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GenCore version 5.1.6
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OM protein - protein search, using sw model

September 15, 2003, 17:16:01 ; Search time 36.7714 Seconds
(without alignments)
112.231 Million cell updates/sec Run on:

US-09-544-664-1

138 1 NIWAAQRYGRELRRMSDEFEGSFKGL (26 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1107863 seqs, 158726573 residues Searched:

1107863 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000 Minimum DB : Maximum DB :

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database:

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/SIDS1/gcgdata/geneseq_geneseqp_embl/AA1982.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Res	sult		Query				
	No.	Score	Match 1	Length	DB	ID	Description
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	4	138	100.0	K	21	AAB37056	Bcl2 polypeptide E
	5	138	100.0	28		AAB37055	Bcl2 polypeptide E
X	Ø	138	100.0	162	22	AAB70370	Shorter murine BAL
7	7	138	100.0	204	17	AAR95168	bcl-x(L)/bcl-2 ass
)	8	138	100.0	204	19	AAW61315	Murine BCL-XL/BCL-
	თ	138	100.0	(204/	19	AAW61316	Mutant BCL-XL/BCL-
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Huang Z, Wang J, Zhang Z, Shan S,

WPI; 2000-679325/66.

120/ 1V - 120 + 45+12M	t BCL-XL/BCL	e BAD pro	r muri	Murine BAD protein	Bad-DITR apoptosis	Human Bad peptide	PTPC-interacting T	Mutant Bc12 compet	O1	g	Human Bad peptide	BBC6 protein for r	L/Bc	Human cell prolife					ovar	bcl-x(L)/bcl-2 ass	Mutant Bcl2 compet	Bad	BC1	t BC.	Bad	ad J	ಌ		Mutant Bc12 compet	ä		್ತಿ	ಭ	t Bcli	Human Bad peptide	
1	-11	19 AAW588	22 AAB7036	/ 24 ABR3908	/ 22 AAU0022	23 AAU78	23 ABP5	23 ABG7	23 ABG7849	23 AAU7861	23 AAU7862	66 18 AAW3247	68 19 AAW5577	68 21 AAB1351	68 22 AAB7036		68 22 AAG6768	68 24 ABR3908	01 23 ABP4163	17	23	23	23 ABG7848	23 ABG7848	23 AAU7861	23	23 AAU7862	23 ABG7848	23 ABG7849:		23 AAU7861	23 AAU7	23 AAU7862	ABG784		
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ALIGNMENTS

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Cytostatic, neuroprotective; anti-HIV; virucide; cerebroprotective; cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad; apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate; colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma; melanoma; lymphocytic leukemia, neurodegenerative disorder; AIDS; stroke; myocardial infarction.
                                                                                            Bcl2 polypeptide BH3 domain peptide #1.
                      AA.
                     36
                                                                                                                                                                                                                                                                                                                             (UYJE-) UNIV JEFFERSON THOMAS
                   AAB37001 standard; peptide;
                                                                                                                                                                                                                                                                                                    99US-0128202.
                                                                                                                                                                                                                                                                            06-APR-2000; 2000WO-US09352
                                                                    28-FEB-2001 (first entry)
                                                                                                                                                                                                                              WO200059526-A1.
                                                                                                                                                                                                                                                                                                    07-APR-1999;
                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                    12-ocT-2000
                                             AAB37001;
RESULT 1
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The invention relates to a peptide conjugate having the formula:

(R-X)n-peptide where n = 1-10; X = C=0, when the R-X group is attached

(C to the N-terminus of the peptide, or a side chain of the peptide where

(C to the N-terminus of the peptide, or a side chain of the peptide where

(C when the R-X group of the side chain is NH2 or NH or X = O or NH,

(C side chain of the peptide, where the side chain functional group is COOH

(C or CONH2; and R = 2-18C alkyl or alkoxy, 2-14C alkylenyl containing one

(C or CONH2; and R = 2-18C alkyl or alkoxy, 2-14C alkylenyl containing one

(C or CONH2; and R = 2-18C alkyl or alkoxy, 2-14C alkylenyl containing one

(C or CONH2; and R = 2-18C alkyl or alkoxy, 2-14C alkylenyl containing one

(C or CONH2; and R = 1-5C straight or branched chain

(C or CONH2; and R = 1-5C straight or branched chain

(C or Expression of the conjugate. The peptides represent examples

(C of a Bcl-2 superfamily polypeptide conresponding to amino acids 72-97 of

(C of a Bcl-2 superfamily polypeptide conresponding to amino acids 72-97 of

(C of a Bcl-2 superfamily polypeptide conresponding to amino acids 72-97 of

(C of a Bcl-2 superfamily polypeptide conresponding to amino acids 72-97 of

(C of a Bcl-2 superfamily polypeptide conjugate is useful for treating a

(C subject afflicted with a cancer cells. It is also useful for inhibiting Bcl-2

(C consenses Bcl-2. The cancer includes prosterized by cancer cells that

(C express Bcl-2. The cancer includes prosterized by cancer cells that

(C consenses Bcl-2. The cancer includes prosterized by cancer cells in a cancer consense includes prosterized by cancer cells in a conjugate is also useful for treating disorders characterized by

(C conjugate is also useful for treating disorders characterized by

(C conjugate is also useful for treating disorders characterized by
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                    New peptide conjugates for modulating apoptosis or for inhibiting cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for treating neurodegenerative disorders, stroke, or cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            increased apoptosis, e.g. neurodegenerative disorders, acquired immunodeficiency syndrome (AIDS), stroke or myocardial infarction.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 138; DB 21;
100.0%; Pred. No. 2e-14;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bcl2 polypeptide BH3 domain peptide #2.
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                                                                                                                  Claim 18; Page 17; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB37002 standard; peptide; 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     stroke; myocardial infarction
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Best Local Similarity 100.(
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26 AA;
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The invention relates to a peptide conjugate having the formula:

(R-X)n-peptide where n = 1-10; X = C=0, when the R-X group is attached

to the N-terminus of the peptide, or a side chain of the peptide where

the functional group of the side chain is NHZ or OH; or X = O or NH,

when the R-X group is attached to the C-terminus of the peptide, or a

side chain of the peptide, where the side chain functional group is COOH

cor CONHZ; and R = 2-18C alkyl or alkoxy, 2-14C alkylenyl containing one

or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally

cor two double peptide or also the peptides represent examples

cor the peptide portion of the conjugate is represent analogues

cof a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of

the BH3 domain of the cell death agonist Bad. The peptide conjugate is

conserved bonds apoptosis in the cells of a subject, or for

reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of

reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of

creversing b cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of

corresponds in cancer cells. It is also useful for inhibiting acids

corresponds acids and correct characterized by cancer cells that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             express Bcl-2. The cancer includes prostate, colorectal, gastric, non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide conjugate is also useful for treating disorders characterized by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                 New peptide conjugates for modulating apoptosis or for inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                increased apoptosis, e.g. neurodegenerative disorders, acquired immunodeficiency syndrome (AIDS), stroke or myocardial infarction.
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                                                                                                                      cell'lymphoma/leukemia 2 (Bcl-2) function, especially useful for
treating neurodegenerative disorders, stroke, or cancer
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Shan S,
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Wang J, Shang Z,
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Huang Z,
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06-APR-2000; 2000WO-US09352.
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(R-X)n-peptide where n = 1-10; X = C=0, when the R-X group is attached to the N-terminus of the peptide, or a side chain of the peptide where the functional group of the side chain is MH2 or OH; or X = O or NH, when the R-X group is attached to the C-terminus of the peptide, or a side chain functional group is considered to the C-terminus of the peptide, where the side chain functional group is COH or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally one crowdistituted with a 1-5c straight or branched chain alkyl group, or benzyl. The peptides AAB37001-B37058 represent examples of the peptide portion of the conjugate. The peptides represent analogues of the peptide portion of the conjugate. The peptide conjugate is alkyl group, or benzyl. The peptide corresponding to amino acids 72-97 of the BH3 domain of the cell death agonist Bad. The peptide conjugate is useful for modulating apoptosis in the cells of a subject, or for reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of subject afflicted with a cancer characterized by cancer cells that cancer characterized by cancer cells that cancer includes prostate, colorectal, gastric, non-small lung, remain or thyroid cancers, neuroblastoma, melanoma, or acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide conjugate is also useful for treating disorders acquired increased apoptosis, e.g. neurodegenerative disorders, acquired immunodeficiency syndrome (AIDS), stroke or myocardial infarction.
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                                                                                                                                      New peptide conjugates for modulating apoptosis or for inhibiting cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for treating neurodegenerative disorders, stroke, or cancer
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                                                          Lu Z;
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                                                        Wang J, Zhang Z, Shan S,
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                  (UYJE-) UNIV JEFFERSON THOMAS.
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Matches 26; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                          Huang Z,
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The invention relates to a peptide conjugate having the formula:

(R-X)n-peptide where n = 1-10; X = C-0, when the R-X group is attached to the N-terminus of the peptide, or a side chain of the peptide where the functional group of the side chain is MH2 or OH; or X = O or NH, when the R-X group is attached to the C-terminus of the peptide, or a side chain of the peptide, where the side chain functional group is considered to the C-terminus of the peptide, or a side chain of the peptide, where the side chain functional group is COCH or two double bonds, cyclobutyl, cyclopentyl, cyclopentyl cyclopentyl cyclopentyl cyclopentyl cyclopentyl cyclopentyl cyclopentyl cyclopentyl cyclopentyl cyclopentyl, cyclopentyl optionally monosubstituted with a 1-5C straight or branched chain alkyl group, or benzyl. The peptides AAB37001-B37058 represent examples of the peptide pertion of the conjugate. The peptides represent analogues of the BH3 domain of the coll death agonist Bad. The peptide conjugate is useful for modulating apoptosis in the cells of a subject, or for reversing B cell lymphoma/leukemia 2 (BCl-2)-mediated blockage of apoptosis in cancer cells. It is also useful for inhibiting Bol-2 conversing B cell lymphoma/leukemia 2 (BCl-2)-mediated blockage of apoptosis in cancer cells. It is also useful for inhibiting Bol-2 conversing a subject afflicted with a cancer characterized by cancer cells that cancer includes prostate, colorectal, gastric, acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide conjugate is also useful for treating disorders characterized by cancer cells conjugate is conjugate is also useful for treating conjugate conjugate is characterized by cancer colorectal, gastric, colorectal, gastric, acute conjugate is conjugate is characterized by cancer colorectal, gastric, acute conjugate is also useful for treating conjugate conju
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                      New peptide conjugates for modulating apoptosis or for inhibiting B cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for treating neurodegenerative disorders, stroke, or cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective; cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad; apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate; colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma; melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS; stroke; myocardial infarction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    increased apoptosis, e.g. neurodegenerative disorders, acquired immunodeficiency syndrome (AIDS), stroke or myocardial infarction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ó
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                                                                                                                                                               Lu Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bcl2 polypeptide BH3 domain peptide #55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 NLWAAQRYGRELRRMSDEFEGSFKGL 26
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                                                                                                                                                               Wang J, Zhang Z, Shan S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 18; Page 19; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB37055 standard; peptide; 28
                                                                                 (UYJE-) UNIV JEFFERSON THOMAS
99US-0128202,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-FEB-2001 (first entry)
                                                                                                                                                                                                                                         WPI; 2000-679325/66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27 AA;
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07-APR-1999;
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                                                                                                                                                               Huang Z,
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Best Local 9
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Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a peptide conjugate having the formula:

(R-X)n-peptide where n = 1-10; X = C=0, when the R-X group is attached

to the N-terminus of the peptide, or a side chain of the peptide where

to the N-terminus of the spetide, or a side chain of the peptide where

the functional group of the side chain is NH3 or OH; or X = O or NH,

when the R-X group is attached to the C-terminus of the peptide, or a

side chain of the peptide, where the side chain functional group is COH

cor CONH2; and R = 2-18C alkyl or alkoxy, 2-14C alkylenyl containing one

or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally

cor CONH2; and R = 2-18C alkyl or alkoxy, 2-14C alkylenyl containing one

cor two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally

cor consistinted with a 1-5C straight or branched chain alkyl group,

phenyl optionally monosubstituted with a 1-5C straight or branched chain

alkyl group, or benzyl. The peptides ABB37001-B37058 represent examples

cof a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of

the BH3 domain of the cell death agonist Bad. The peptide conjugate is

cof a Bcl-2 superfamily polypeptide conjugate is useful for freating a

corresponding to modulating apoptosis in the cells of a subject, or for

corpusing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of

subject afflicted with a cancer characterized by cancer cells that

corpuses Bcl-2. The cancer includes prostate, colorectal, gastric,

conjugate is also useful for treating disorders characterized by

increased apoptosis, e.g. neurodegenerative disorders, acquired

immunodeficiency syndrome (AlDS), stroke or myocardial infarction.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                             New peptide conjugates for modulating apoptosis or for inhibiting cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for treating neurodegenerative disorders, stroke, or cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shorter murine BAD mutant amino acid sequence SEQ ID NO:3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 138; DB 21;
100.0%; Pred. No. 2.1e-14;
Live 0; Mismatches 0;
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                                                                                                                                                                                                    Huang 2, Wang J, Zhang 2, Shan S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB70370 standard; protein; 162 AA
                                                                                                                                                                                                                                                                                                                                                                                        Claim 18; Page 19; 74pp; English.
                                                                                                                                                         (UYJE-) UNIV JEFFERSON THOMAS
                                                              06-APR-2000; 2000WO-US09352.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-MAY-2001 (first entry)
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                                                                                                                                                                                                                                                  WPI; 2000-679325/66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28 AA;
                 12-OCT-2000.
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The present invention describes an isolated or synthetic polypeptide

(1) comprising a less than full length amino acid sequence of a mutant

Bel-XL/Ed-2 associated cell death regulator polypeptide (BAD) or its

fragment, which contains amino acid substitutions at Seril8 of a human

BAD, SeriS5 of a murine BAD. (1) has immunostimulant, neuroprotective,

BAD (shorter murine BAD). (1) has immunostimulant, neuroprotective,

nootropic, antiischeamic, vulnerary, cytostatic, antiviral,

antiarthritic, antiinflammatory and immunosuppressive activities, and

can be used as an apoptosis inducer or inhibitor. BAD polypeptides and

polynuclectides can be used for screening candidate compounds and drugs

for activity that promote cell survival or apoptosis. Other uses include

inducing or inhibiting apoptosis in a cell. Candidate compounds

identified and (mutant) BAD polypeptides are useful in treating

immunodeficiency diseases, neurodegenerative diseases, ischemmic cell

death, reperfusion cell death, wound healing, cancer, viral infections,

lymphoproliferative conditions, arthritis, infertility inflammation and

caltoimmune diseases. The present sequence represents a specifically

calaimed shorter murine BAD mutant amino acid sequence from the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Epitope; murine; bcl-x(L)/bcl-2 associated death promoter; Bad; stroke; polypeptide; bcl-x; cell death; regulate; BH1; BH2; apoptotic cell death; cytokine deprivation; IL-3 dependent cell line; immunodeficiency; AIDS; neurodegenerative disease; senescence; ischaemia; neoplasia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New mutant Bol-XL/Bol-2 Associated Cell Death Regulator polypeptide, useful for screening for candidate compounds which induce or inhibit apoptosis, comprises amino acid substitutions at Serl18, Serl55 or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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100.0%; Pred. No. 1.5e-13;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                             (APOP-) APOPTOSIS TECHNOLOGY INC
                                                                                                                                                                                                                                                                                                                99US-0136783.
                                                                                                                                                                                                                                30-MAY-2000; 2000WO-US11864
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                                                                     WO200110888-A1.
                                                                                                                                                                                                                                                                                                                28-MAY-1999;
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Synthetic.
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Best Local S
Matches 26
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The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell death regulator) proteins, having an amino acid other than Ser at position 112 and/or 136, relative to the murine BAD 204 as sequence. The present sequence is the murine BAD protein. Also described are: (1) fragments of mutant BAD protein able to decrease cell viability; (2) fusion proteins of mutant BAD with a heterologous polypeptide that increases intracellular delivery. Mutant BAD proteins are used to treat or prevent diseases associated with reduced apoptosis, e.g. cancer, viral infection, lymphoproliferation, arthritis, infertility, ancest inflammation and autoimmune disease. Polynucleotide sequences encoding mutant BAD proteins can be used similarly by gene therapy or to produce transgenic animals for use as disease models or in drug screening. BAD proteins phosphorylated at specified Ser are used to screen for enhancers and inhibitors of serine-phosphatase. Inhibitors are potentially useful in treatment of excessive apoptosis such as ALDS, neurodegeneration, aging or ischaemic cell death. The apoptotic status of cells is determined by measuring relative amounts of phosphorylated and non-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Murine, mouse, BCL-XL/BCL-2 associated cell death regulator; BAD protein, serine substituted mutant; apoptosis; cancer; viral infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        phosphorylated BAD, by usual immunoassays. Wutant BAD proteins have greater death-promoting activity than wild-type BAD which can become phosphorylated on the specified Ser, forming a product that does not heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family proteins in the cytosol, thus promoting cell survival. The mutants with Ser substituted cannot bind 14-3-3.
                                                                                                                                                                                                                                                                                                                                         New mutant BAD polypeptide with phosphorylatable serine replaced useful for, e.g. treating reduced apoptosis such as in cancer or viral infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mutant BCL-XL/BCL-2 associated cell death regulator #1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Fig 10; 95pp; English.
                                                                                          97WO-US19175
                                                                                                                                      96US-0733505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-OCT-1998 (first entry)
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                                                                                                                                                                                   UNIW ) UNIV WASHINGTON
                                                                                                                                                                                                                                                                          WPI; 1998-261422/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          204 AA;
                                                                                                                                                                                                                                                                                                  N-PSDB; AAV27833
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                                                                                                                                                                                                                                 (orsmeyer SJ;
                                                                                                                                      18-OCT-1996;
                                                                                          17-0CT-1997;
WO9817682-A1
                                             30-APR-1998,
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Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW61316;
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AAW61316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents the murine bcl-x(L)/bcl-2 associated death promoter (Bad) gene. Bad is a 22.1 kD protein which interacts with bcl-2 and bcl-x proteins and regulates cell death. It has homology to the bcl-2-related family clustered in the BH1 and BH2 domain. Bad has been found to hybridise to bcl-x(L) and bcl-2 in yeast two-hybrid assays and in vivo in mammalian cells. Overexpressed Bad counters the death inhibitory activity of bcl-x(L), but is much less effective at countering the death inhibitory activity of bcl-2. Bad expression can accelerate apoptotic cell death induced by cytokine deprivation in an IL-3 dependent cell line expressing bcl-x(L), and its also counters the death repressor activity of bcl-x(L). Bad competes with Bax for binding to bcl-x(L). Bad may be used to identify agents which inhibit its binding to bcl-x(L) or bcl-x(L) to form heterodimers. Such agents may be used to treat neurodegenerative diseases, immunodeficiency diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Polynucleotide encoding bcl-x(L)/bcl-2 associated death promoter useful to treat neoplasia and apoptosis and to identify agents inhibiting its binding to bcl-2 or bcl-x(L) to form heteromultimers
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1,9e-13;
hes 0;
                                                                         /note= "BH2 conserved amino acids"
38..61
                                             'note= "BH1 conserved amino acids"
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                                                                                                                                      "PEST sequence"
                                                                                                                                                                                   /note= "PEST sequence"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 3; Fig 1; 130pp; English.
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                                                                                                                                                                                                                                                                                                                                                                   94US-0333565.
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                                                                                                                                        /note= "P
111..130
                                                                .192
                       147..149
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N-PSDB; AAT29479.
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Best Local Similarity
Matches 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     204 AA;
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Region
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Gaps

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100.0%; Score 138; DB 19; Length 204; 100.0%; Pred. No. 1.9e-13; ive 0; Mismatches 0; Indels 0;

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30-APR-1998.
30-APR-1998
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                                                                                                                                                                                                                                                                                                                                                            The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell death regulator) proteins, having an amino acid other than Ser at position 112 and/or 136, relative to the murine BAD 204 as sequence. The present sequence represents a mutant BAD protein. Also described are: (1) fragments of mutant BAD with a heterologous polypeptide that increases intracellular delivery. Mutant BAD proteins are used to treat or prevent diseases associated with reduced apoptosis, e.g. cancer, viral infection, lymphoproliferation, arthritis, infertility, cancer, viral infection, lymphoproliferation, arthritis, infertility, infammation and autoimmune disease. Polynucleotide sequences encoding mutant BAD proteins can be used similarly by gene therapy or to produce transgenic animals for use as disease models or in drug screening. BAD proteins phosphorylated at specified Ser are used to screen for enhancers and inhibitors of serine-phosphatase. Inhibitors are potentially useful in treatment of excessive apoptosis such as AIDS, neurodegeneration, eletermined by measuring relative amounts of phosphorylated and nongetermined by measuring relative amounts of phosphorylated and nongetermined by measuring relative amounts of phosphorylated each-promoting activity than wild-type BAD which can become phosphorylated on the specified Ser, forning a product that does not proteins in the cytosol, thus promoting cell survival. The mutants with the ser substituted cannot bind 14-3-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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                                                                                                                                                                                                                                                        New mutant BAD polypeptide with phosphorylatable serine replaced useful for, e.g. treating reduced apoptosis such as in cancer or
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100.0%; Pred. No. 1.9e-13;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                Claim 7; Page 59; 95pp; English.
                                                     97WO-US19175.
                                                                                         96US-0733505.
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Best Local Similarity 100.0
Matches 26; Conservative
                                                                                                                             (UNIW ) UNIV WASHINGTON
                                                                                                                                                                                                   WPI; 1998-261422/23.
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                                                                                                                                                                                                                        N-PSDB; AAV27834
                                                                                                                                                                                                                                                                                            viral infection
                                                                                                                                                                 Korsmeyer SJ;
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                                                      17-0CT-1997;
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Synthetic.
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The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell death regulator) proteins, having an amino acid other than Ser at position 112 and/or 136, relative to the murine BAD 204 as sequence. The position 112 and/or 136, relative to the murine BAD 204 as sequence. The present sequence represents a mutant BAD protein. Also described are: (1) fragments of mutant BAD protein able to decrease cell viability; (2) fusion proteins of mutant BAD with a heterologous polypeptide that increases intracellular delivery. Mutant BAD proteins are used to treat or prevent diseases associated with reduced apoptosis. e.g. cancer, viral infection, lymphoproliferation, arthritis, infertility, infertility, infertility, arthritis, infertility, infertility, infertility, and autoimmune disease. Polynucleotide sequences encoding mutant BAD proteins can be used similarly by gene therapy or to produce transgenic animals for use as disease models or in drug screening. BAD proteins phosphorylated at specified Ser are used to screen for enhancers or intraatment of excessive apoptosis such as AIDS, neurodegeneration, attended and intraatment of excessive apoptosis such as AIDS, neurodegeneration, appropriated BAD, by usual immunoassays. Mutant BAD proteins have greater death-promoting activity than wild-type BAD which can become phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have greater death-promoting activity than wild-type BAD which can become phosphorylated cannot bind 14-3-3 family by substituted cannot bind 14-3-3.
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    97WO-US19175
                                                                                    96US-0733505
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N-PSDB; AAV27835.
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17-0CT-1997;
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Seguence
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                                                                                                                                                                                                                                                          death regulator) proteins, having an amino acid other than Ser at death regulator) proteins, having an amino acid other than Ser at death regulator) proteins, having an amino acid other than Ser at position 112 and/or 136, relative to the murine BAD 204 as sequence. The present sequence represents a mutant BAD protein. Also described are: (1) fragments of mutant BAD protein able to decrease cell viability; (2) fusion proteins of mutant BAD proteins are used to treat or prevent diseases associated with reduced apoptosis, e.g. cancer, viral infection, lymphoproliferation, arthritis, infertility, inflammation and autoimmune disease. Polynucleotide sequences encoding untant BAD proteins can be used similarly by gene therapy or to produce transgenic animals for use as disease models or in drug screening. BAD proteins phosphorylated at specified Ser are used to screen for enhancers and inhibitors of serine-phosphatase. Inhibitors are potentially useful in treatment of excessive apoptosis such as AIDS, neurodegeneration, a ding or ischaemic cell death. The apoptotic status of cells is determined by measuring relative amounts of phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have greater death-promoting activity than wild-type BAD which can become phosphorylated on the specified Ser, forming a product that does not heterodimerise with BCL-2 or BCL-XL bit instead binds to 14-3-3 family proteins in the cytosol, thus promoting cell survival. The mutants with conservative cannot bind 14-3-3.
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                                                                                                                                                                                                                                       The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell death regulator) proteins, having an aming and all constants.
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                                                                                                                                                                     New mutant BAD polypeptide with phosphorylatable serine replaced useful for, e.g. treating reduced apoptosis such as in cancer or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 204;
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100.0%; Pred. No. 1.9e-13;
trive 0; Mismatches 0;
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                                                                                                                                                                                                                         Claim 7; Page 60-61; 95pp; English.
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             97WO-US19175.
                                       96US-0733505
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                                                                     (UNIW ) UNIV WASHINGTON
                                                                                                                           WPI; 1998-261422/23.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
nes 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                204 AA;
                                                                                                                                           N-PSDB; AAV27836.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9809643-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-JUL-1998
                                                                                               Korsmeyer SJ;
             17-0CT-1997;
                                         18-0CT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW58832;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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This sequence represents a novel serine-phosphorylated protein, BAD

(Bc1-X1/Bc1-2 associated cell death regulator). The serine residue is
phosporylated in a post-translational modification and allows binding

to the 14-3-3 protein which is a signal transduction regulator.

Modulators of phosphorylated BAD, which act through inhibition/activation

of a phosphoserine phosphatase, are useful for preventing/tracting

Increased/decreased apoptosis. In a cell. The increased apoptosis may

result from immunodeficiency diseases, senescence, neurodegenerative

disease, ischaemic cell death, reperfusion cell death, infertility and

wound-healing. Decreased apoptosis may result from cancer, viral

infection, lymphoproliferative conditions, arthritis, infertility,

inflammation and autoimmune diseases. Measuring the amount of

phosphorylated compared to unphosphorylated BAD polypeptide and/or total

C. BAD in a cell is useful for determining the apoptotic state of a cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immunostimulant; neuroprotective; nootropic; antischaemic; vulnerary; cytostatic; antiviral; antiarthritic; antinflammatory; wound healing; immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer; immunodeficiency disease; neurodegenerative disease; viral infection; ischaemic cell death; reperfusion cell death; arthritis; infection; lymphoproliferative condition; inflammation; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                         Serine-phosphorylated Bcl-X-1/Bcl-2 Associated cell Death regulator polypeptide - useful for modulation of apoptosis associated with, e.g. cancer and immunodeficiency diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 138; DB 19; Length 204; 100.0%; Pred. No. 1.9e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Longer murine BAD mutant amino acid sequence SEQ ID NO:2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        140 NLWAAQRYGRELRRMSDEFEGSFKGL 165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 3; Fig 8; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0136783.
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97WO-US15871
                                                                             96US-0707868
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26; Conservative
                                                                                                                                                       (UNIW ) UNIV WASHINGTON.
                                                                                                                                                                                                                                                                                                               WPI; 1998-207049/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   204 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200110888-A1.
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                                                                                                                                                                                                                                        Korsmeyer SJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-MAY-1999;
09-SEP-1997;
                                                                             09-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-MAY-2001
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.6-AUG-1999;
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                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                     AAU00220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Region
                                                                                                                                                                                                                                                                                                                                                                                     AAU00220
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                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes an isolated or synthetic polypeptide

(I) comprising a less than full length amino acid sequence of a mutant

Bel-XL/Bcl-2 associated cell death regulator polypeptide (BAD) or its

fragment, which contains amino acid substitutions at Serl18 of a human

EAD, Ser155 of a murine BAD). (I) has immunostimulant, neuroprotective,

BAD (shorter murine BAD). (I) has immunostimulant, neuroprotective,

nootropic, antisofhemmic, vulnerary, cytostatic, antiviral,

antiarthritic, antiniflammatory and immunosuppressive activities, and

can be used as an apoptosis inducer or inhibitor. BAD polypeptides and

polynucleotides can be used for screening candidate compounds and drugs

for activity that promote cell survival or apoptosis. Other uses include

inducing or inhibiting apoptosis in a cell. Candidate compounds

ideath, ineperfusion cell death, wound healing, cancer, viral infections,

lymphoproliferative conditions, arthritis, infertility, inflammation and

cutoimmune diseases. The present sequence represents a specifically

claimed longer murine BAD mutant amino acid sequence from the present
                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Murine; BAD; herpes simplex virus; HSV; US3; herpes virus; apoptosis; virucide; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                          New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide, useful for screening for candidate compounds which induce or inhibit apoptosis, comprises amino acid substitutions at Ser118, Ser155 or
                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                        Length 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 138; DB 22;
100.0%; Pred. No. 1.9e-13;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 NLWAAQRYGRELRRMSDEFEGSFKGL 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABR39082 standard; Protein; 204 AA.
                                                                                                                                 Claim 4; Page 148; 157pp; English.
          (APOP-) APOPIOSIS TECHNOLOGY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Murine BAD protein SEQ ID NO:4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-JUL-2002; 2002WO-US24177.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-JUL-2001; 2001US-308929P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.
Best Local Similarity 100.
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Munger J, Roizman B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYCH-) UNIV CHICAGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-248168/24.
                                                     WPI; 2001-138734/14
                                                                                                                                                                                                                                                                                                                                                                                    204 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2003012049-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-FEB-2003.
                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABR39082;
                                Zhou X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
ABR39082
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse; Bad-DTTR; apoptosis; cancer; spinal muscular atrophy; diphtheria toxin receptor binding domain; DTR; neoplasm; tumour; hyper-proliferation; Alzheimer's disease; neurodegenerative disorder; transient ischaemic neuronal injury; stroke; spinal cord injury;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                Inducing apoptosis in a cell infected with herpes simplex virus, HSV, by administering to the cell, a composition comprising an agent that inhibits phosphorylation of pro-apoptotic polypeptide BAD by HSV US3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 204;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 138; DB 24; 100.0%; Pred. No. 1.9e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bad-DTTR apoptosis-modifying fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "10x histidine tag"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HARD ) HARVARD COLLEGE.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  140 NLWAAQRYGRELRRMSDEFEGSFKGL 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 NLWAAQRYGRELRRMSDEFEGSFKGL 26
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Chimeric - Corynebacterium diptheriae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU00220 standard; Protein; 567 AA.
                                                                                                                                                                                                                   Claim 15; Page 168; 192pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Youle RJ, Liu X, Collier RJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chimeric - Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-218343/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         204 AA;
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N-PSDB; ABZ81201
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Novel fusion protein for modifying apoptosis in target cell and reducing apoptosis after transient ischaemic neuronal injury, has two domains which targets protein to a cell and modifies apoptotic response of cell
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Claim 4; Page 59-61; 65pp; English.

The sequence represents the amino acid sequence of Bad-DTTR apoptosismodifying fusion protein comprising Bad gene sequence fueed via a short
linker to diphtheria toxin translocation domain (DTTR). The
functional apoptosis-modifying fusion protein is capable of binding a
crarget cell and integrating into or crossing a cellular membrane of the
target cell. The apoptosis-modifying fusion protein comprises at least
two domains: the DTR domain, which modifies an apoptotic response
target cell and the BC1-XI domain, which modifies an apoptotic response
target cell and the BC1-XI domain, which modifies an apoptotic response
the target cell. The fusion protein is useful for modifying
thibiting or enhancing) apoptosis in a target cell, such as neuron,
lymphocyte, cancer, neoplasm, macrophage, epithelial, stem, tumour or
hyper-proliferative cell or an adipocyte. It is also useful for reducing
typoptosis in a subject after transient ischaemic neuronal injury,
apoptosis in a subject after transient ischaemic neuronal injury,
aspecially spinal cord injury. The fusion protein may be used to treat
various diseases and injury conditions through inhibition or enhancement
of apoptotic cellular response, including neurodegenerative disorders
such as Alzheimen's disease, Huntington's disease, spinal muscular
atrophy, stroke episodes and unrequiated cell growth as in tumours and
various cancers. The apoptosis-modifying fusion protein can be delivered
ceffectively throughout the body and targeted to selective tissue and

567 AA; Sequence

0; Gaps 0; Length 567; Indels Query Match 100.0%; Score 138; DB 22; Best Local Similarity 100.0%; Pred. No. 6.1e-13; Matches 26; Conservative 0; Mismatches 0;

161 NLWAAQRYGRELRRMSDEFEGSFKGL 186 1 NLWAAQRYGRELRRMSDEFEGSFKGL 26 g Š

Search completed: September 15, 2003, 17:22:13 Job time : 37.7714 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

September 15, 2003, 17:22:21; Search time 13.5571 Seconds (without alignments) 81.144 Million cell updates/sec Run on:

138 1 NIWAAQRYGREIRRMSDEFEGSFKGI 26 Perfect score: Sequence:

US-09-544-664-1

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

328717 segs, 42310858 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 00% Maximum Match 100% Listing first 45 summaries

Database :

/cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/fe_COMB.pep:*
/cgn2_6/ptodata/1/iaa/fe_COMB.pep:* Issued_Patents_AA:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		6/6			COLUMNIC	
Result		Query	:			
No.	Score	Match	Length	B :	OI.	Description
₽	m	100.0	CA	٦	-333-565-	2,
7	$^{\circ}$	00	CA	7	8-661-47	Sequence 2, Appli
m	3	00.	(1	7	33-505A-	() ()
4	3	00	(4	7	-08-733-505A-1	e 12,
Ŋ	138	100.0	(1	N	-08-733-505	ce 13,
φ	$^{\circ}$	00	(4	C)	S-08-733-505A-	e 14,
7	3	97.8	(4	7	-717-123	'n
σ	$^{\circ}$	97.8	.,	ヤ	-09-375-257	m
ത	114	82.6	166	Н	4	
10	Н	82.6	П	7	-717-123	2
11	4	82.6	L-3	n	-08-985-335	H
12	114	82.6		'n	-985-335	7,
13	$\overline{}$	82.6	~	'n	-09-410-372	'n
14		82.6	П	m	9-410-372	7,
15		82.6	П	Ţ	-09-375-257-2	equence 2,
79	-1	81.9		Н	-333-565	e 10,
17		81.9		~	-08-661-479	equence 10,
18	\sim	73.9		7	-08-733-505A-5	equence 55,
19	102	73.9		N	-08-733-505A-	equence 56
20	$^{\circ}$	73.9		N	-08-733-505A-5	57
21	\sim	73.9		7	8-733-505A-5	53
22	86	62.3		-	-08-333-565-2	26
23	86	62,3		N	-08-661-479-2	56
24	19	44.2		N	8-733-505A-3	34
25	61	44.2		N	-08-706-741B-	69
26	61	44.2		N	08-924-695A-6	69
27	51	37.0		N	-08-867-087B-4	40

Sequence 4656, Ap	Sequence 3, Appli				Sequence 23807, A	Sequence 5164, Ap	Sequence 2, Appli	Sequence 4, Appli	Seguence 17508, A			Seguence 27, Appl				
US-09-328-352-4656	US-09-074-579-3	US-09-388-774-3	US-09-546-153-1	US-09-252-991A-31458	US-09-252-991A-23807	US-09-328-352-5164	US-09-235-103-2	US-09-235-103-4	US-09-252-991A-17508	US-09-252-991A-28775	US-09-328-352-7449	US-09-651-656-27	US-09-650-855-27	US-09-206-551-20	US-09-252-991A-18729	US-09-252-991A-18296
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904	946	946	946	906	229	303	356	356	1064	903	125	263	263	877	1125	467
35.1	 	33.3	33.3	33.0	32.6	32.6	32.6	32.6	32.6	32.2	31.9	31.9	31.9	31.9	31.9	31.5
48.5	46	46	46	45.5	45	45	45	45	45	44.5	44	44	44	44	44	43.5
28	30	31	32	33	34	35	36	37	38	9	40	4.1	42	43	44	45

ALIGNMENTS

US-0B-33-565-2
Sequence 2, Application US/0833565
Fatent No. 5622852
GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
TITLE OF INVENTION: REGULATOR
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COMPUTER READABLE FORM:
MEDIUW TYPE: California
COMPUTER READABLE FORM:
MEDIUW TYPE: Ploppy disk
COMPUTER READABLE FORM:
MEDIUW TYPE: Ploppy disk
COMPUTER READABLE FORM:
MEDIUW TYPE: Ploppy disk
COMPUTER READABLE FORM:
MEDIUW TYPE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/33,565
FILING DATE: 31-COT-1994
CLASSIFICATION NUMBER: 15726A-000700
TELECOMMUNICATION INFORMATION:
TELEPRONE: (415) 326-2440
TELEPRONE: (415) 326-240
TELEPRONE: MINDRER: LEGEN DING: 2: SEQUENCE CHARACTERISTICS:
LEMCTH: SALID amino acids
LEMCTH: SALID MOLECULE TYPE: protein FEATURE: NAME/KEY: Protein TYPE: amino acid STRANDEDNESS: sin linear RESULT 1 US-08-333-565-2

Query Match

100.0%; Score 138; DB 1; Length 204;
Best Local Similarity 100.0%; Pred. No. 5.8e-14;
Matches 26; Conservative 0; Mismatches 0; Indels 0 LOCATION: 1..204
CTHER INFORMATION: /note= "Deduced amino acid sequence CTHER INFORMATION: of mouse BAD."
US-08-333-565-2

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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
FTILING DATE:
CLASSIPICATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REGISTRATION NUMBER: 965458
TELECOMMUNICATION INPORMATION:
TELEPHONE: (314) 727-5188
TELEPHONE: (314) 727-6092
INPORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
  F: HOWELL & HAFERKAMP, L.C. 7733 FORSYTH BLVD., SUITE 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               140 NLWAAQRYGRELRRMSDEFEGSFKGL 165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 965458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-733-505A-12; Sequence 12, Application US/08733505A; Patent No. 5856445; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 530
                                              ST. LOUIS
: MISSOURI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RY: USA
63105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                   63105
    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-733-505A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 4
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APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: BERINE SUBSTITUTED MUTANTS OF
TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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                                                                                                                                                                                                     GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
TITLE OF INVENTION: REGULATOR
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Deduced amino acid sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/661,479
FILING DATE: 11-JUN 1995
CLASSIFICATION 1435
PRICR APPLICATION DATA:
APPLICATION NUMBER: US 08/333,565
FILING DATE: 31-0CT-1994
ATTORNEY/AGENT INFORMATION:
NAME: SMith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726A-000700
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 138; DB 2; Best Local Similarity 100.0%; Pred. No. 5.8e-14; Matches 26; Conservative 0; Mismatches 0;
                        140 NLWAAQRYGRELRRMSDEFEGSFKGL 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              140 NIWAAQRYGRELRRWSDEFEGSFKGL 165
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1 NLWAAQRYGRELRRMSDEFEGSFKGL 26
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                                                                                                                 RESULT 2
US-08-661-479-2
; Sequence 2, Application US/08661479
; Patent No. 5834209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
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LOCATION: 1.204
COHER INFORMATION:
US-08-661-479-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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US-08-733-505A-1
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APPLICATT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
                                                                    0
Query Match 100.0%; Score 138; DB 2; Length 204; Best Local Similarity 100.0%; Pred. No. 5.8e-14; Matches 26; Conservative 0; Mismatches 0; Indels (
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us-09-544-664-1.rai

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TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                      Gaps
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APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: BERINE SUBSTITUTED MUTANTS OF
TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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                                                                                                                                                 Length 204;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPER FIPOPPY disk
COMPUTER: FID PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE:
FILING DATE:
                                                                                                                                              100.0%; Score 138; DB 2; ilarity 100.0%; Pred. No. 5.8e-14; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 138; DB 2;
100.0%; Pred. No. 5.8e-14;
ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         140 NLWAAQRYGRELRRMSDEFEGSFKGL 165
                                                                                                                                                                                                                                            1 NLWAAQRYGRELRRMSDEFEGSFKGL 26
                                                                                                                                                                                                                     1 NLWAAQRYGRELRRMSDEFEGSFKGL 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 965458
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTER/STICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-733-505A-14; Sequence 14, Application US/08733505A; Patent No. 5856445
                                                                                                                                                                                                                                                                                                                                                  Sequence 13, Application US/08733505A Patent No. 5856445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: KORSMEYER, STANLEY J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 204 amino acids amino acids
                 LENGTH: 204 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.
Best Local Similarity 100.
Matches 26, Conservative
 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                        ; MOLECULE TYPE: peptide US-08-733-505A-12
                                                                          linear
                                                                                                                                              Query Match
Best Local Similarity
Matches 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                RESULT 5
US-08-733-505A-13
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                                                                        TOPOLOGY:
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Gaps
SERINE SUBSTITUTED MUTANTS OF
BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
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Patent No. 5965703
GENERAL INFORMATION:
APPLICANT: Horne, William A.
APPLICANT: Oltersdorf, Tilman
TITLE OF INVENTION: Human BAD Polypeptides, Encoding Nucleic
TITLE OF INVENTION: Acids and Methods of Use
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 138; DB 2; Length 204; Best Local Similarity 100.0%; Pred. No. 5.8e-14; Matches 26; Conservative 0; Mismatches 0; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PSTEM: PC-DOS/MS-DOS
SOFFWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/717,123
                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DCS/MS-DOS
SOFTWARE: PATCHILD Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
                                              NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: USA
ZIP: 63105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 140 NLWAAQRYGRELRRMSDEFEGSFKGL 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 NLWAAQRYGRELRRMSDEFEGSFKGL 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPAX: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 20-SEP-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: San Dicy-
STATE: California
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ATTORNEY/AGENT INFORMATION: NAME: Saliwanchik, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 4370 La Jo
CITY: San Diego
STATE: California
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                                                                                                                                                                                                                  amino acid
                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                       STRANDEDNESS:
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APPLICANT: Xudong, Yin
TITLE OF INVENTION: Gene and Protein for Regulation of Cell Death
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Horne, William A.
APPLICANT: Oltersdorf, Tilman
TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC
TITLE OF INVENTION: ACIDS AND METHODS OF USE
FILE REFERENCE: 480140.428D1
CURRENT APPLICATION NUMBER: US/09/375,257
CURRENT FILING DATE: 1999-08-16
NUMBER OF SEQ IN NOS: 15
SOFTWARE: FASTERQ for Windows Version 4.0
; SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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                                                                                                                                                                                                                                       97.8%; Score 135; DB 2; Length 204; 96.2%; Pred. No. 1.7e-13; tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDESSES: Saliwanchik & Saliwanchik STREET: 2421 N.W. 41st Street, Suite A-1 CITY: Gainesville STATE: 12010 N.W. 41st Street, Suite A-1 STATE: Florida COUNTR: USA COUNTR: USA COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERAIING SYSTEM: PC-DOS/M-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURENT APPLICATION DATA: APPLICATION NUMBER: US/08/665,617 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                140 NLWAAQRYGRELRRMIDEFEGSFKGL 165
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; Sequence 2, Application US/08665617
; Patent No. 5663316
                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-375-257-3
; Sequence 3, Application US/09375257
; Patent No. 6504022
REFERENCE/DOCKET NUMBER: P-II
TELECOMMUNICATION INPORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS;
                                                                                           .... 3:
....weTH: 204 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-717-123-3
                                                                                                                                                                                                                                           Query Match
Best Local Similarity 96.23
Matches 25; Conservative
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CORGANISM: Mus musculus
US-09-375-257-3
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                                                                                                                                                                                                                                                                                                                             82.6%; score 114; DB 1; Length 166; 91.7%; Pred. No. 2.5e-10; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 114; DB 2; Length 168; Pred. No. 2.6e-10; 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER CALIFORMIS

COMPUTER READABLE FORM:

MEDIOM TYPE: Floppy disk

COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/717,123
FILING DATE: 20-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: 31,815
FELECOMMUNICATION INFORMATION:
TELEBHONE: (619) 5535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       103 NLWAAQRYGRELRRMSDEFVDSFK 126
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                                                                                                                                                                                                                                                                                                                                                                                                                    1 NLWAAQRYGRELRRMSDEFEGSFK 24
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: CL-8
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 375-800
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACIERISTICS:
LENGTH: 166 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
US-08-717-123-2
; Sequence 2, Application US/08717123
; Patent No. 5965703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Horne, William A.
APPLICANT: Oltersdorf, Tilman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82.6%;
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TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 91.70,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       i: 168 amino acids amino acids
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Best Local Similarity 91.7
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: protein US-08-717-123-2
                                                                                                                                                                                                                         single
                                                                                                                                                                                                                                                                , MOLECULE TYPE: protein US-08-665-617-2
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Query Match 82.6%; Score 114; DB 3; Length 168; Best Local Similarity 91.7%; Pred. No. 2.6e-10; Matches 22; Conservative 0; Mismatches 2; Indels
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; Sequence 1, Application US/09410372
; Patent No. 6281334
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
; APPLICANT: Stah, Pureti
; APPLICANT: Stah, Pureti
; APPLICANT: Society, Neil C.
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
; TITLE OF INVENTION: PROLIFERATION
NUMBER OF SEQUENCES:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                       OPERATING SYSTEM: DOS SOFTWARE: FRASESQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,335
FILING DATE: Filed Herewith PRIOR APPLICATION DATA:
APPLICATION NUMBER: FILESTA:
ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTATION NUMBER: 36,749
REGENENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 18-08-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/410,372 FILING DATE:
               CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         103 NLWAAQRYGRELRRMSDEFVDSFK 126
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                                                                                                                                    ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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COMFUTER: IBM Compatible
OPERATING SYSTEM: DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid STRANDEDNESS: sir
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LIBRARY: Genba...
                                                                               Palo Alto
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IMMEDIATE SOURCE:
                                                                                                                        USA
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US-08-985-335-7
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US-09-410-372-1
                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
                                                                             CITY:
STATE:
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us-08-985-335-1
; Sequence 1, Application US/08985335
; Patent No. 6080847
; GENERAL INFORMATION:
    APPLICANT: Hillman, Jennifer L.
    APPLICANT: Yea, Henry
    APPLICANT: Al, Preeti
    APPLICANT: Shah, Purvi
    APPLICANT: Orley, Neil C.
    TITLE OF INVENTION: PROTEINS
    TITLE OF INVENTION: PROTEINS
    NUMBER OF SEQUENCES: 9
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: ADDRESS:
    ADDRESSEE: ADDRESS:
    CITY: Palo Alto
    STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROTEINS ASSOCIATED WITH CELL PROLIFERATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPPERATIOS SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,335 |
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0421 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEPHONE: 650-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           103 NLWAAQRYGRELRRMSDEFVDSFK 126
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APPLICANT: Yue, Henry
APPLICANT: Shah, Purvi
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: PROLIFERATION
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/08985335 Patent No. 6080847 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 168 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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IMMEDIATE SOURCE:
LIBRARY: SYNORA
CLONE: 358673
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TYPE: PRT
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US-09-410-372-7
Sequence 7. Application US/09410372
Petent No. 6281334
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: PROLIFERATION
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPOTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/09/410,372
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/985,335
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0421 US
TELEPOMUNICATION INFORMATION:
TELEPRONE, 650-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
TYPE: amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PF-0421 US
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APPLICATION NUMBER: 08/985,335
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Bilings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0421
TELEPHONE: 650-855-0555
TELEPHONE: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: SYNORAB01
CLONE: 358673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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COUNTRY: US
ZIP: 94304
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APPLICANT: Horne, William A.
APPLICANT: Oltersdorf, Tilman
TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC
TITLE OF INVENTION: ACIDS AND METHODS OF USE
FILE REPERENCE: 480140.12811
CURRENT APPLICATION NUMBER: US/09/375,257
CURRENT APPLICATION NUMBER: US/09/375,257
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 168
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                                                                                                                                        Query Match 82.6%; Score 114; DB 3; Length 168; Best Local Similarity 91.7%; Pred, No. 2.6e-10; Matches 22; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: September 15, 2003, 17:45:05 Job time: 14.5571 secs
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                                                                                                                                                                                                                                                                                                                                                             RESULT 15
US-09-375-257-2
; Sequence 2, Application US/09375257
; Patent No. 6504022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Homo sapiens
US-09-375-257-2
                ; INMEDIATE SOURCE;
; LIBRARY: GenBank
; CLONE: 1683637
US-09-410-372-7
TOPOLOGY: linear
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Sequence 2, Appli

Sequence 18, Appl Sequence 236, Appl Sequence 162, App Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 62, Appli Sequence 62, Appli Sequence 198, Appli Sequence 198, Appli Sequence 13485, Appli Sequence 13485, Appli Sequence 13485, Appli Sequence 13485, Appli Sequence 11813, Appli Sequence 11813, Appli

4 US-10-008-355-8 US-09-815-242-12463 US-10-369-294-20 US-09-843-846-18 US-09-841-752A-238 US-09-149-045-2 US-09-149-045-2 US-09-149-045-2 US-09-149-045-2 US-09-149-045-2 US-09-149-045-2 US-09-149-045-2 US-09-149-045-2 US-09-149-045-2 US-09-181-2 US-09-331-631A-22 US-09-331-631A-22 US-09-331-631A-22 US-09-331-631A-22 US-09-389-723-501 US-09-989-723-501 US-09-989-723-501 US-09-989-723-501

610

Sequence 501, App Sequence 501, App

US-09-989-731-501 US-09-989-732-501 US-09-991-073-501 US-09-909-320-292 US-09-990-442-501 US-09-993-604-501

ALIGNMENTS

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APPLICAMT: Horne, William A. APPLICAMT: Oltersdorf, Tilman TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC TITLE OF INVENTION: ACIDS AND METHODS OF USE TITLE OF INVENTION: ACIDS AND METHODS OF USE TILE REFERENCE: 480140.428D3
CURRENT APPLICATION NUMBER: US/09/922,378
CURRENT FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/10066179
; Publication No. US20020115631A1
; GENERAL INFORMATION:
APPLICANT: HOTHE, William A.
APPLICANT: Oltersdorf, Tilman
; TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC
; TITLE OF INVENTION: ACIDS AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 140 NLWAAQRYGRELRRMTDEFEGSFKGL 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 NLWAAQRYGRELRRMSDEFEGSFKGL 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-922-378-3; Sequence 3, Application US/09922378; Patent No. US20020037869A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 97.8
Best Local Similarity 96.2
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Mus musculus
204
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  LENGIH:
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Sequence 258, Appl
Sequence 2, Appli
Sequence 1, Appli
Sequence 7, Appli
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Sequence 9145, App
Sequence 1, Appli
Sequence 241, App
Sequence 1077, App
Sequence 3, Appli
Sequence 11541, A
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                                                                                                  (without alignments)
184.034 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                     September 15, 2003, 17:25:56; Search time 20.6143 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2,
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                                                                                                                                                                                                                                                                                                                                                                  Published_Applications_AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_LEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US06_LEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US06_LEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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12: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
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18: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
         GenCore version 15.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-10-059-261-258

US-09-222-378-2

US-09-894-657-1

US-09-894-657-1

US-09-894-657-7

4 US-10-066-179-2

5 US-10-176-761-9145

5 US-10-156-761-11541

US-10-128-075-241

US-10-288-075-1077

US-10-288-075-1077

US-10-186-761-11541

US-09-815-242-5704
                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                              541936 segs, 145912426 residues
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                                                                                                                                                     138
1 NLWAAQRYGRELRRMSDEFEGSFKGL
                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                             using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                 Minimum DB seq length: 0 Maximum DB seq length: 2000000000
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Match Length DB
                                                                                                                                         US-09-544-664-1
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946
272
426
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Gaps

0

Length 204

97.8%; Score 135; DB 9; Length 20 96.2%; Pred. No. 3.3e-12; Live 1; Mismatches 0; Indels

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COUNTRY: USA
ZIP: 94304
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                   ; ORGANISM: Homo sapiens
US-09-922-378-2
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US-09-894-657-7
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US-09-894-657-1
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US-10-059-261-258
US-10-059-261-258
SQUENCE 258, Application US/10059261
SPUDIcation No. US20030077826A1
GENERAL INFORMATION:
APPLICANT: EDELANN, LENA
TITLE OF INVENTION: SPECIFIC CELLS AND A MODULE REGULATING THE APPLICANT:
TITLE OF INVENTION: PUTCHING OF THE PERMEABILITY TRANSITION PORE COMPLEX
TITLE OF INVENTION: PUTCHING OF THE PERMEABILITY TRANSITION PORE COMPLEX
TITLE OF INVENTION: (PTPC)
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
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                                                                                                                                                                                                                                                                                                                                                                                            97.8%; Score 135; DB 14; Length 204; llarity 96.2%; Pred. No. 3.3e-12; Conservative 1; Mismatches 0; Indels
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ilarity 91.7%; Pred. No. 4.8e-10;
Conservative 0; Mismatches 2;
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Sequence 2, Application US/09922378
Sequence 2, Application US/09922378
Sequence 10. US20020037869A1
GENERAL INFORMATION:
APPLICANT: Horne, William A.
APPLICANT: Oltersdorf, Tilman A.
TITLE OF INVENTION: HOMAN BAD POLYPEPTIDES, EN.
TITLE OF INVENTION: ACIDS AND METHODS OF USE
FILE REFERENCE: 480140.428D3
CURRENT APPLICATION NUMBER: US/09/922,378
CURRENT APPLICATION NUMBER: US/09/922,378
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 168
FILE REFERENCE: 480140,428C1
CURRENT APPLICATION NUMBER: US/10/066,179
CURRENT FILING DATE: 2002-02-01
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 204
TYPE: PRT
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                                                                                                                                                                                                                                                                                                ORGANISM: Mus musculus
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nes 22; Conserva
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Matches 25; Conserv
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US-09-922-378-2
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Matches
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 Length 168,
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Pred. No. 3.4e-09;
0; Mismatches 2; Indels
                                        2; Indels
                                                                                                                                                                                                                                                                                   PPLICANT: HILLING...,
Yue, Henry
Lal, Preeti
Shah, Purvi
Corley, Neil C.
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
PROLIFERATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: SYSTEM: DOS
COMPUTER: FRASESO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION UNMER: US/09/894,657
FILING DATE: 28-Jun-2001
PRIOR APPLICATION DATA:
Score 114; DB 9;
Pred. No. 3.4e-09;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 09/410,372
FILING DATE: CURROWN>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0421 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-894-657-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             103 NLWAAQRYGRELRRMSDEFVDSFK 126
                                                                                                      103 NIWAAQRYGRELRRMSDEFVDSFK 126
                                                                                1 NLWAAQRYGRELRRMSDEFEGSFK 24
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TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                         Sequence 1, Application US/09894657; Patent No. US20020098569A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 1:
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Best Local Similarity 91.7%;
Matches 22; Conservative (
Query Match
Best Local Similarity 91.7%;
Matches 22; Conservative (
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Gaps

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TITLE OF INVENTION: CONTEXT-INDEPENDENT ANTIBODIES COUPLED WITH DATABASE SEARCHIN TITLE OF INVENTION: CONTEXT-INDEPENDENT ANTIBODIES COUPLED WITH DATABASE SEARCHIN FILE REFERENCE: CST-138 CIP3
CURRENT APPLICATION NUMBER: US/10/174,105A
CURRENT FILING DATE: 1998-09-04
PRIOR FILING DATE: 1998-09-04
PRIOR FILING DATE: 1998-09-04
PRIOR FILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 193
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 147
LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COCATION: (8)...(8)
CTHER INFORMATION: PHOSPHORYLATION; serine at position 8 is phosphorylated US-10-174-105A-147
                                                                                                             Length 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 15,
                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                      82.6%; Score 114; DB 14;
91.7%; Pred. No. 3.4e-09;
tive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 51.4%; Score 71; DB 15; 1
Best Local Similarity 100.0%; Pred. No. 0.00061;
Matches 14; Conservative 0; Mismatches 0;
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APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLECTIDES
FILE REPERBANCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR PRILING DATE: 2001-05-30
PRIOR PLILING DATE: 2001-05-30
PRIOR PRILICATION NUMBER: JP 2001-272697
                                                                                                                                                                                                                                                                                                                                                                     Sequence 147, Application US/10174105A Publication No. US20030068652A1 GENERAL INFORMATION:
APPLICANT: Cell Signaling Technology, Inc. APPLICANT: COMB, Michael J. APPLICANT: TAN, Yi
                                                                                                                                                                                                                                 103 NLWAAQRYGRELRRMSDEFVDSFK 126
                                                                                                                                                                                                    1 NLWAAQRYGRELRRMSDEFEGSFK 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Synthetic Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 9145, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GRELRRMSDEFEGS 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 GRELRRMSDEFEGS 22
                                                                                                    Query Match
Best Local Similarity 91.73
Matches 22; Conservative
        ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-066-179-2
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US-10-156-761-9145
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US-10-174-105A-147
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    APPLICANT: Horne, William A.
    APPLICANT: Horne, William A.
    TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC; TILE OF INVENTION: ACIDS AND METHODS OF USE; FILE REFERENCE: 480140.428C1; CURRENT APPLICATION NUMBER: US/10/066,179; CURRENT FILING DATE: 2002-02-01; NUMBER OF SEQ ID NOS: 15; SOFTWARE: FastSEQ for Windows Version 4.0; SEQ ID NO 2; LENGTH: 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 168;
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91.7%; Pred. No. 3.4e-09;
tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDINA TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastESD for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/894,657
FILING DATE: 28-Jun-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/410,372
FILING DATE: CURNOWN>
APPLICATION NUMBER: 09/410,372
FILING DATE: CURNOWN>
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 36,749
                                                                                                                                        Shah, Purvi
Corley, Neil C.
TITLE OF INVENTION: PROLIFERATION
                                                                                                                                                                                                                                                                                             ADDRESSEE: Incyte Pharmaceuticals, Inc
STREET: 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: PF-0421 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-845-0555
TELEPHONE: 650-845-4166
INFORMATION POR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE DESCRIPTION: SEQ ID NO: 7: US-09-894-657-7
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Sequence 7, Application US/09894657
Patent No. US20020098569A1
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer
Yue, Henry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 168 amino acids
TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
                                                                                                                               Lal, Preeti
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CLONE: 1683637
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Best Local Similarity 91.79
Matches 22; Conservative
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STATE: CA
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RESULT 13
US-09-828-423-3
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Pred. No. 20;
3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/10092750
FUDLICATION NO. US20030032157A1
GENERAL INFORMATION:
APPLICANT: Hammond, Philip W.
APPLICANT: Alpin, Julia
APPLICANT: Application Wigher: US/10/092,750
CURRENT FILING DATE: 2002-03-07
PRIOR PILING DATE: 2001-03-08
NUMBER: OF SEQ ID NOS: 253
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    > Sequence 241, Application US/10092750
; Publication No. US20030032157A1
; GENERAL INFORMATION:
; APPLICANT: Hammond, Philip W.
; APPLICANT: Hammond, Philip W.
; APPLICANT: Alpin, Julia
; APPLICANT: Mright, Martin C.
; TITLE OF INVENTION: Polypeptides Interactive with BCL-XI
FILE REFERENCE: 50036/050002
; CURRENT APPLICATION NUMBER: US/10/092,750
; CURRENT FILING DATE: 2001-03-07
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 241
; LENGTH: 138
; TYPE: RTT
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                                                                                                                                                                            TYPE: PRT; ORGANISM: Streptomyces avermitilis US-10-156-761-9145
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45.5%;
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PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 9145
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; ORGANISM: Homo sapiens
US-10-092-750-1
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US-10-092-750-241
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Best Local Similarity
Matches 10; Conserv
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US-10-092-750-241
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US-10-092-750-1
                                                                                                                                   LENGTH:
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RESULT 12
US-10-238-075-1077
Sequence 1077, Application US/10238075
Publication No. US20030148324A1
Sequence 1077, Application US/10238075
Publication No. US20030148324A1
INDERINATION:
TITLE OF INVENTION:
TITLE OF INVENTION: E.col., and biological uses of these polynucleotides and of 1
FILE REFERENCE: BLANDINE
CURRENT APPLICATION NUMBER: US/10/238,075
CURRENT PILING DATE: 2002-09-10
PRIOR APPLICATION NUMBER: 0003145
PRIOR REPLING DATE: 2000-09-10
PRIOR FILING DATE: 2000-09-10
NUMBER OF SEQ ID NOS: 1576
SOFTWARE: Patentin version 3.1
SEQ ID NO 1077
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TITLE OF INVENTION: GROWTH-ASSOCIATED TRYPSIN-TYPE
INHIBITOR HEAVY CHAIN PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Cerrone, Michael C
RECISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: 9P-0505 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 46; DB 12;
Pred. No. 1.5e+02;
5; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: WORD Perfect 6.1/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/828,423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 05-Apr-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/388,774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :||||| | :: |: | |||
610 IWAAQRNGAKVPRYRNGFTSMDIGL 634
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ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
                      APPLICANT: Hillman, Jennifer L.
2 LWAAQRYGRELRRMSDEFEGSF 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/09828423
; Patent No. US20020099178A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33.3%;
40.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 40.0°
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Escherichia coli
US-10-238-075-1077
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                                                                                                                                                                                                                                                        Query Match 33.3%; Score 46; DB 9; Length 946; Best Local Similarity 30.8%; Pred. No. 2.1e+02; Matches 8; Conservative 5; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 11541, Application US/10156761
Fublication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: ISHTKAWA, JUN
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIVUKI
APPLICANT: SAKAKI, YOSHIVUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT FILING DATE: 2002-05-29
PRIOR PHILNG DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 11541
LENGTH: 272
                                                                                                                                                            CLONE: 9133985
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-828-423-3
                                                                                                                                                                                                                                                                                                                                                                            212 DVWVIEPOGLRFLHVPDTFEGHFDGV 237
                                                                                                                                                                                                                                                                                                                                       1 NLWAAQRYGRELRRMSDEFEGSFKGL 26
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Patent No. US20020061569A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Streptomyces avermitilis
                                                          LENGTH: 946 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | | :| ||| :|
29 WIAAAHGAELRRAAD 43
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APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W
                                                                                                                                                        LIBRARY: GENEBANK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Conservative
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Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
US-10-156-761-11541
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US-09-815-242-5704
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APPLICANT:
APPLICANT:
APPLICANT:
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| FILE REFERENCE: ELITRA.011A
| CURRENT APPLICATION NUMBER: US/09/815,242
| CURRENT INLING DATE: 2001-03-21
| PRIOR APPLICATION NUMBER: 60/2191,078
| PRIOR APPLICATION NUMBER: 60/206,848
| PRIOR FILING DATE: 2000-05-23
| PRIOR FILING DATE: 2000-05-23
| PRIOR FILING DATE: 2000-05-23
| PRIOR FILING DATE: 2000-05-26
| PRIOR FILING DATE: 2000-10-23
| PRIOR FILING DATE: 2000-11-27
| PRIOR FILING DATE: 2000-11-27
| PRIOR PLICATION NUMBER: 60/257,931
| PRIOR FILING DATE: 2001-12-22
| PRIOR FILING DATE: 2001-02-16
| PRIOR FILING DATE: 2003, 17:47:52
| PRIOR FILING DATE: 2003, 17:47:52
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
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protein search, using sw model t OM protein September 15, 2003, 17:18:16 Run on:

6; Search time 11.7 Seconds (without alignments) 213.708 Million cell updates/sec

138 1 NLWAAQRYGRELRRMSDEFEGSFKGL US-09-544-664-1 Perfect score: Sequence: Title:

26

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 segs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_76:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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		Description	protein - mo	r-alpha	$\overline{}$	inter-alpha-inhibi	2-dehydro-3-deoxy-	floral homeotic pr	ine/putre	probable threonine	ed hypothe	Ig kappa chain - h	annexin P35 - maiz	transforming prote	O)		(D	Ĺ	7		Antho-RFamide prec	ical p	-	7	-1	ted	41	· pare	Antho-RFamide neur	hypothetical prote	σ
		A																				T09486		IYHU2	$\overline{}$	8139	6951	∞	3917	147	8331
		80	~	C4	C1	7	7	N	(7	C1	N	N	7	~	(7)	~	N	7	N	7	7	7	N	Н	7	~	7	7	a	N	7
		Length	20															96			4	1140				3					
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		Score	13	54	53	53	52	51	20	50	49	48.5	œ	48	48	48	47	47	47	Ġ	46.5	46.5	46	46	46	46	ď.	45.5	'n.	'n	•
	Result	No.		7	m	4	N	9	7	∞	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

30	chlorocruorin chai	conserved hypothet	conserved hypothet	xo dwnd uoi wipos	oxaloacetate decar	oxaloacetate decar	oxaloacetate decar	probable membrane	env polyprotein -	hypothetical prote	NADH dehydrogenase					
45 32.6 165 455 32.6 465 32.6 465 32.6 465 32.6 591 45 32.6 591 45 32.6 591 45 32.6 596 44.5 32.2 532 546 555 510 510 510 510 510 510 510 510 510	S59899	F83201	H95406	B44465	AB0509	AE0909	A28088	S52675	VCLJG4	T19472	128811	T15566	T01993	D83264	AG1482	G91024
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তে এ এ বি	165	295	346	591	591	591	596	715	864	1263	1557	2325	75	455	536	910
	32.6	32.6	32.6	32.6	32.6	32.6	32.6	32.6	32.6	32.6	32.6	32.6	32.2	32.2	32.2	32.2
0 H G E 4 E 6 F 8 9 0 H G E 4 E	45	45	45	45	45	45	45		45	45	45	45	44.5	44.5	44.5	44.5
(1) (1) (1) (1) (1) (1) (1) (1) (1) (1)	30	3	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1

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Dad protein - mouse C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Species: Musrul95 #sequence_revision 03-Mar-1995 #text_change 05-Nov-1999
C.Accession: A55671
R.Yang, E.; Zha, J.; Jockel, J.; Boise, L.H.; Thompson, C.B.; Korsmeyer, S.J.
C.A.I. 180, 285-291, 1995
A,Title: Bad, a heterodimeric partner for Bcl-x-L and Bcl-2, displaces Bax and paraference number: A55671; MulD:95136361; PMID:7834748
A.Accession: A55671
A.Status: preliminary; not compared with conceptual translation
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                                                                                                                                                                                                                                                                                                                                                                                     A)Cross-references: GB:L37296; NID:q639778; PIDN:AAA64465.1; PID:g639779
C; Keywords: heterodimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ·
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 100.0%; Score 138; DB 2; Local Similarity 100.0%; Pred. No. 7e-13; les 26; Conservative 0; Mismatches (
                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-204 <YAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
A55671
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Best Loca Matches

140 NLWAAORYGRELRRMSDEFEGSFKGL 165 1 NLWAAQRYGRELRRMSDEFEGSFKGL 26 qq QΫ

RESULT :

inter-alpha-trypsin inhibitor heavy chain 2 - golden hamster C, Species: Mesocricetus auratus (golden hamster)
C, Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 20-Jun-2000
C, Date: 25-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 20-Jun-2000
C, Accession: JC5575; PC4485
C, Accession: JC5575; PC4485
A, Title: Molecular clouhing and sequencing of cDNAs encoding three heavy-chain precurs in inhibitor heavy chain family.
A, Reference number: JC5574; MJD:97420688; PMID:9276673
A, Accession: JC5575
A, Moleculer type: mRNA
A, Residues: 1-946 <NAK>
A, Residues: 1-946 <NAK>
A, Residues: 1-946 <NAK>
A, Cross-references: DDBJ:D89286; NID:g1694689; PIDN:BAA13939.1; PID:g1694690
A, Experimental source: liver

A; Accession: PC4485

A.Molecule type: protein A.Residues: 55-64;140-146;151-156;424-447;500-528;577-605 <NA2> C.Comment: In the plasma three inter-alpha-trypsin inhibitor heavy chains 1, 2 and 3 that the complexes play important role for panceatic cancer. C.Superfamily: inter-alpha-trypsin inhibitor complex component II F:261-264,717-916/Disulfide bonds: #status predicted

Score 54; DB 2; Length 946; Pred. No. 8.8; 39.18; 34.68; Query Match Best Local Similarity

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A;Cross_references: EMBL:Z36118; NID:9536664; PIDN:CAA85212.1; PID:9536665; MIPS:YBR; R;Ruenzler, M.; Paravicini, G.; Egli, C.M.; Irniger, S.; Braus, G.H. A;714, 1992
A; Pitle: Cloning, primary structure and regulation of the ARO4 gene, encoding the tyr A;Reference number: JN0322; MUID:92225349; PMID:1348717
A;Accession: JN0322
                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-370 <ALJ>
A; Residues: 1-370 <ALJ>
A; Cross-references: EMBL: Z36118; NID: 9536664; PIDN: CAA85212.1; PID: 9536665; MIPS: YBR;
R; Aigle, M.; Baclet, M.C.; Barthe, C.; Biteau, N.; Crouzet, M.; Doignon, F.
submitted to the Protein Sequence Database, August 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      \ddot{\circ}
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A;Title: The complete sequence of a 6794 bp segment located on the right arm of chrom A;Reference number: S38185; MUID:94078675; PMID:8256522 A;Accession: S38185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-204,208-370 < KUE>
A; Cross-references: EMBL:X61107
B; Kuenzler, M.; Balmelli, T.; Egli, C.M.; Paravicini, G.; Braus, G.H.
B; Kuenzler, 175, 5548-5558, 1993
A; Title: Cloning, primary structure, and regulation of the HIS7 gene encoding a bifur A; Reference number: A48651; MUID:93374850; PMID:8366040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C: Comment: This enzyme catalyzes the condensation of phosphoenolpyruvate and D-erythm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            floral homeotic protein APETALA3 (AP3) - Arabidopsis thaliana
Nyalternate names: homeotic protein APETALA3; MAD5-box regulatory protein AP3
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C;Accession: A42095; S52633; T47593
E;Jack, T.; Brockman, L.L.; Meyerowitz, E.M.
Cell 68, 683-697, 1992
A;Title: The homeotic gene APETALA3 of Arabidopsis thaliana encodes a MADS box and A;Reference number: A42095; MUID:92154682; PMID:1346756
A;Accession: A42095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A.Description: aldehyde-lyase; carbon-carbon lyase
A.Pathway: aromatic amino acid blosynthesis; shikimate pathway
A.Note: first step in shikimate pathway
C.Superfamily: phospho-2-dehydro-3-deoxyheptonate aldolase
C.Keywords: aldehyde-lyase; aromatic amino acid blosynthesis; carbon-carbon lyase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ó
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                                                                                                                                                                              A) Cross-references: GB:L20296; NID:g311101; PIDN:AAA65607.1; PID:g311102 R;Aljinovic, G.; Pohl, F.M.; Pohl, T.M. submitted to the Protein Sequence Database, August 1994 A;Reference number: S45906 A;Accession: S46126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: SGD:ARO4
A;Cross-references: SGD:S0000453; MIPS:YBR249c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37.7%; Score 52; 47.6%; Pred. No. (
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                                                                                                  A; Status: translation not shown
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A, Residues: 352-370 <KU2>
A, Cross-references: GB:X61107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: S45940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 10; Conserv
                                                                                                                           A; Molecule type: DNA
A; Residues: 1-370 <DOI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-370 <AIG>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: S46130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Accession: B48651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Map position: 2R
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                                                                                                                                                                                                                                                                                           Expecies: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: D70760
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whiteheac, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S
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Cipate: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 20-Aug-1999
Cipate: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 20-Aug-1999
Cipate: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 20-Aug-1999
Cipate: 54354 #. Reguence, G.; Salier, J.P.
Biochem, J. 306, 505-512, 1995
A;Title: The three heavy-chain precursors for the inter-alpha-inhibitor family in mouse: A;Recession: S54353 #MID:95194326; PMID:7534067
A;Recession: S54354
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:Z74025; GB:AL123456; NID:g3261586; PIDN:CAA98415.1; PID:e1299911; A;Experimental source: strain H37Rv
C;Genetics:
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A; Cross-references: EMBL: X70392; NID: 9695633; PIDN: CAA49842.1; C; Superfamily: inter-alpha-trypsin inhibitor complex component
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 223;
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     12;
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2.8;
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Pred. No. 12;
5; Mismatches
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     Mismatches
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                                                                                                  212 NVWIVELOGMRFLHVPDTFEGHFOGV 237
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Pred. No.
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                                                             1 NLWAAQRYGRELRRMSDEFEGSFKGL
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58.8%;
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34.6%;
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Best Local Similarity 34.6'
Matches 9; Conservative
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Best Local Similarity 58.8
Matches 10; Conservative
     Conservative
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C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C;Accession: A96753
B;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L.
Anthors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Althel: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Accession: A96753
A;Actatus: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conserved hypothetical protein PA1031 [imported] - Pseudomonas aeruginosa (strain PA0 C; Species: Pseudomonas aeruginosa C; Species: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C; Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C; Accession: B83517 R; Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L.; Lory, S.; Olson, M.V.
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A; Accession: E83517
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  H
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C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: $40376
R;Klein, R:; Jaenichen, R.; Zachau, H.G.
Bur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: $40312; MUID:94080891; PMID:8258341
A;Accession: $40376
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Pred. No. 23;
4; Mismatches
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Pred. No. 18;
7; Mismatches
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65 WASERQGREEELRRLASE
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Best Local Similarity 35.3
Matches 12; Conservative
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Best Local Similarity 55.6
Matches 10, Conservative
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A; Molecule type: DNA
A; Residues: 1-453 <STO>
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A; Residues: 1-516 <STO>
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S40376
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A; Residues: 1-232 </rd>
A; Residues: 1-232 </rd>
A; Residues: 1-232 </rd>
A; Cross-references: GB:886397; NID:g166607; FIDN:AAA32740.1; PID:g166608
A; Experimental source petals, stamens
A; Note: sequence extracted from NCB1 backbone (NCBIN:82520, NCBIP:82521)
B; Okamoto, H.; Yano, A.; Shiralshi, H.; Okada, K.; Shimura, Y.
Plant Mol. Biol. 26, 465-472, 1994
A; Pitle: denetic complementation of a floral homeotic mutation, apetala3, with an Arabid A; Accession: S52633; MUD:95036018; PMID:7948893
A; Status: preliminary
A; Mchecule type: DNA
A; Residues: 1-63 < CORA
A; Cross-references: GB: DD2125
A; Residues: 1-63 < CORA
A; Cross-references: GB: DD2125
B; Bloceker H.; Mewes, H.; Lemcke, K.; Mayer, K.F.X.; Quetier, F.; Salanoubat M.Mewes, Submitted to the Protein Sequence Database, March 2000
A; Residues: 1-232 < CBLO
A; Residues: 1-232 < CBLO
A; Cross-references: RMBL:AL132971
A; Residues: 1-232 < CBLO
A; Cross-references: RMBL:AL132971
A; Residues: 1-232 < CBLO
A; Cross-references: RMBL:AL132971
A; Reperimental source: cultivar Columbia; BAC clone T12E18
C; Genetics:
A; Map position: 3
A; Introns: 63/2; 85/3; 106/2; 139/3; 153/3; 168/3
A; Note: T12E18 30
C; Superfamily: transcription factor squa; serum response factor DNA-binding domain homol C; Keywords: DNA binding; nucleus; transcription regulation
C; Keywords: DNA binding; nucleus; transcription regulation
F; 2-57/Domain: serum response factor DNA-binding domain homology <SRF>
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C'Species: O2-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C'Species: O2-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C'Species: C84338
R'NG, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jable Jung, K.H.; Alam, M.; Freitas, T.
Froc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li A; A; Reference number: A64160; MUID:20504483; PMID:11016950
A;Accession: C84338
A;Accession: C84338
A;Molecule type: DNA
A;Residues: 1-374 <STO>
A;Cross-references: GB:AE004437; NID:910581314; PIDN:AAG20071.1; GSPDB:GN00138
C;Genetics:
A;Gene: potA2
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A96753
probable threonine synthase [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
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Pred. No. 1
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76.9%;
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Matches 12; Conserv
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Best Local Similarity
Matches 10; Conser
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A/Cross references: EMBE.AL050352; GSPDB:GN00062; ATSP:F27B13.80
A/Experimental source: cultivar Columbia; BAC clone F27B13
B/Curien, G.; Dumas, R.; Ravanel, S.; Douce, R.
FEBS Lett. 390, 85-90, 1996
A/Fitle: Characterization of an Arabidopsis thaliana cDNA encoding an S-adenosylmethi A/Reference number: S71362; MUID:96314555; PMID:8706836
                                                                                                                                                                      oxidoreductase, sol/devB family - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: F72289
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hic Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:AE001772; GB:AE000512; NID:94981693; PIDN:AAD35230.1; PID:9498
A;Experimental source: strain MSB8
                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 399, 323-329, 1999
A; Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome A; Reference number: A72200; MUID:99287316; PMID:10360571
A; Accession: F72289
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A;Residues: 'L',3-526 <CUR>
A;Cross-references: EMBL:L41666; NID:g1448916; PIDN:AAB04607.1; PID:g1448917
A;Accession: S74307
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C;Keywords: carbon-oxygen lyase; chloroplast
F;1-39/Domain: transit peptide (chloroplast) #status predicted <TNP>
F;40-526/Product: threonine synthase #status experimental <MAT>
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Pred. No. 15;
8; Mismatches 7; Indels
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Pred. No. 37;
6; Mismatches
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111 ACEKYEREIRSATDQFDLAILGM 133
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REIRRMNKEQEGRSKG 184
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35.3%;
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Matches 8; Conservative
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A;Accession: T08545
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A, Residues: 40-54 <CUI>
C, Genetics:
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A; Residues: 1-526 <BEV>
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A; Residues: 1-220 <ARN>
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169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       annexin P35 - maize
C; Species: Zea mays (maize)
C; Species: Zea mays (maize)
C; Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jul-2000
C; Satety, N.H.: James, N.C.; Greenland, A.J.
Plant Physiol. 112, 1391-1396, 1996
A; Title: CDNA isolation and gene expression of maize annexins P33 and P35.
A; Recession: T02975
A; Rocession: T02975
A; Rocession: T02975
A; Ranslates: Parallainary; translated from GB/EMBL/DDBJ
A; Rocession: T1314 -RBAT
A; Roserides: 1314 -RBAT: X98245; NID:g1370602; PIDN:CAA66901.1; PID:g1370603
A; Experimental source: cultivar clipper; root tip
C; Superfamily: annexin repeat homology
F; 14-85/Domain: annexin repeat homology
                                                                                                                                                                                                                                                                                                                     <u>:</u>
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                   A. Residues: 1-134 <KLE>
A. Cross-references: EMBL:X72486; NID:g441440; PIDN:CAA51154.1; PID:g441441
C. Superfamily: immunoglobulin V region; immunoglobulin homology
C. Keywords: heterotetramer; immunoglobulin
F:34-113/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          58 WFRORPGRSPRRLIYNVSKRDSGVSDRFSGSGSG 91
                                                                                                                                                                                                                                         Score 48.5; DB Pred. No. 7.8; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 19;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 48.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 AQRYGRE-LRRMSDEFEGSFK 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54 AEAYGKELLRALGDEIHGKFE 74
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47.6%;
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                                                                                                                                                                                                                                            35.1%;
38.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 47.69
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                  13; Conservative
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Best Local Similarity
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Best Local Similarity
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Matches
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T02975
                                                                                                                                                                                                                                                                                                               Matches
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QΥ g Q.

0;

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RESULT 15
682308
oxalcacetate decarboxylase, alpha chain VC0550 [similarity] - Vibrio cholerae (strain NI C, Species: Vibrio cholerae
C, Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C; Accession: G82308
R; Heidelberg, J.F.; Bisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F.
I, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A; Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A; Reference number: A82035; MUD:20406833; PMID:10952301
A; Accession: G82308
A; Molecule type: DNA
A; Resperimenty
A; Molecule type: DNA
A; Resperimental source: serogroup 01; strain N16961; biotype El Tor
C; Genetics:
A; Genet
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34.1%; Score 47; DB 2; Length 597;

Best Local Similarity 47.4%; Pred. No. 60;

Matches 9; Conservative 4; Mismatches 6; Indels
| ||:|: :||| ||:
272 YFREVRKKYAKFEGOLKGV 290
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Search completed: September 15, 2003, 17:27:00 Job time : 12.7 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model,

September 15, 2003, 17:16:55; Search time 6.12857 Seconds
(without alignments)
199.507 Million cell updates/sec Run on:

US-09-544-664-1 138 1 NLWAAQRYGREIRRMSDEFEGSFKGL 26 Title: Perfect score: Seguence:

BLOSUM62 . Gapext 0.5 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 seqs, 47026705 residues Searched:

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Q61337 mus musculu O35147 rattus norv		Q61703 mus musculu P32449 saccharomyc	arab	Q8k2h3 mus musculu O62092 ledum palus	rhodoc					09mt28 solanum tub	Q9s7b5 arabidopsis	043521 homo sapien	Q16994 anthopleura		P19823 homo sapien	Q46124 campylobact	P21259 polyorchis	Q01133 calliactis				klebsi	Q13049 homo sapien	simian	g		P33900 salmonella	STO IIITS
QI	BAD_MOUSE BAD_RAT	SAD_HUMAN ITH2_MESAU	ITH2_MOUSE	AP3.ARATH	CE05_MOUSE	MATK_RHOFR	MATK_RHOTS	RMUC_PSEAE	RAS3_RHIRA	6PGL_THEMA	THRC_SOLTU	THRC_ARATH	BIM_HUMAN	FMR2_ANTEL	FMR1_ANTEL	ITH2_HUMAN	RPOB_CAMJE	PRFA_POLPE	FMRA_CALPA	MATK_LOIPR	SNF4_KLULA	DCOA_SALTY	DCOA_KLEPN	HT2A_HUMAN	ENV_SIVAT	LML1_CAEEL	NUOG_ECOLI	NUOG_SALTY	- 1
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Score	13.00	~ სე	л 33	27	ഗ	49.5	9	49	48	₹ †	48	48	47	ŝ	•	46	4	45.5	'n	•	45	45	45	45	45	45	4	44.5	
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088498 rattus norv	vaxyco escherichia P50465 escherichia	Q8z8d2 salmonella	Q8zqu6 salmonella	P27757 simian immu	P27977 simian immu	Q9nyf5 homo sapien	Q9nu22 homo sapien	Q8nf91 homo sapien	P73327 synechocyst	Q9z507 streptomyce
BIM_RAT	END8_ECOS/ END8_ECOLI	END8_SALTI	END8_SALTY	ENV_SIVA1	ENV_SIVAG	CE05_HUMAN	MDN1_HUMAN	SNE1_HUMAN	UREF_SYNY3	UVRA_STRCO
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196	262	262	262	768	877	915	5596	8797	217	1014
31.9	31.9	31.9	31.9	31.9	31.9	31.9	31.9	31.9	31.5	31.5
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ε. 4.1	3 2 3 0 3 0	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
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"Interference of BAD (Bcl-xL/Bcl-2-associated death promoter)-induced
apoptosis in mammalian cells by 14-3-3 isoforms and P11.";
Mol. Endocrinol. 11:1858-1867(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D'Agata V., Magro G., Travali S., Musco S., Cavallaro S.; "Cloning and expression of the programmed cell death regulator BAD in
Ser-136 is the major site of AKT/PKB phosphorylation, Ser-155 the major site of protein kinase A (CAPK) phosphorylation. SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain. SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                        S->A: NO PHOSPHORYLATION.
S->A: NO PHOSPHORYLATION.
S->A: NO PHOSPHORYLATION; INTERACTS WITH BCL-X(L).
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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                                                                                                                                                                                                                                                                                                                                         PHOSPHORYLATION (BY PKA AND PKB).
PHOSPHORYLATION (BY PKA AND PKB).
PHOSPHORYLATION (BY PKA AND PKB).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Bcl2-antagonist of cell death (BAD) (Bcl-2 binding component
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 138; DB 1; Length 204; 100.0%; Pred. No. 1.5e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND MUTAGENESIS OF SER-113 AND SER-137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        6C2BA910205053F7 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6) (Bcl-xL/Bcl-2 associated death promoter).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORMS ALPHA AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 NLWAAQRYGRELRRMSDEFEGSFKGL 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IISSUE=Brain;
MEDLINE=21109372; PubMed=11161472;
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                                                                                                                                                                                                                                        MGD; MGG109634; IG57.
MGD; MGI1096330; Bad.
InterPro; IPR000712; Bc12_BH.
PROSITE; PS01259; BH3; FALSE_NEG.
Apoptosis; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=98034386; PubMed=9369453;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat).
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1136
1136
1136
1136
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nes 26; Conserv
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MUTAGEN
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Matches
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Hamner S., Arumae U., Yu L.-Y., Sun Y.-F., Saarma M., Lindholm D.;
Thuctional characterization of two splice variants of rat BAD and
their interaction with Bcl-w in sympathetic neurons.";
Mol. Cell. Neurosci. 17:97-106(2001).

Mol. Cell. Neurosci. 17:97-106(2001).

Dinding to Bcl-x(L), Bcl-2 and Bcl-w, thereby affecting the level
of heterodimerization of these proteins with BAX. Can reverse the
death repressor activity of Bcl-x(L), but not that of Bcl-2 (By
similarity). Appears to act as a link between growth factor
creceptor signaling and the apoptotic pathways.

receptor signaling and the apoptotic pathways.

receptor signaling and the apoptotic pathways.

113/Ser-137 phosphorylated form binds ld-3-3 proteins, Bcl-
subcombinity noter mitochondrial membrane. Upon
phosphorylation, locates to the cytoplasm (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                        IsoId=05147-2; Sequence=VSP_000534;

-!- TISSUE SPECIFICITY: Expressed in all tissues tested, including brain, liver, spleen and heart. In the brain, restricted to epithelial cells of the choroid plexus. Isoform alpha is the more abundant form.

-!- DOMAIN: Intact BH3 domain is required by BIK, BID, BAK, BAD AND BAX for their pro-apoptotic activity and for their interaction with anti-apoptotic members of the Bcl-2 family.

-!- PTM: Phosphorylated on Ser-137 promotes heterodimerization with 14-3-3 profeins. This interaction then facilitates the phosphorylation at Ser-137 promotes heterodimerization to the release of Bcl-x(L) and the promotion of cell survival. Ser-137 is the major site of AKT/PKB phosphorylation, Ser-156 the major site of protein kinase A (CAPK) phosphorylation (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LPRPKSAGTATQMRQSASWTRIIQSWWDRNLGKGGSTPSQ
-> EELTYSVEFLPVRAIAMEGWPLLWSFQSFPHTLPPTPP
EVAMFPLRYWTALRRLC (in isoform Beta).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROTEINS. NO EFFECT ON HETERODIMERIZATION WITH BCL2 NOR WITH PROTEIN P11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S->A: NO EFFECT ON HETERODIMERIZATION WITH 14-3-3 PROFEINS.
S->A: NO HETERODIMERIZATION WITH 14-3-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BY SIMILARITY).
PHOSPHORYLATION (BY PKA AND PKB)
PHOSPHORYLARITY).
PHOSPHORYLATION (BY PKA AND PKB)
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PHOSPHORYLATION (BY PKA AND PKB)
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7AFA71DAE9CF4A81 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    similarity).
-!- SIMILARITY: Contains | Bcl-2 homology 3 (BH3) domain.
-!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                                                                                                                                                                                                       Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Phosphorylation; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /FTId=VSP_000534
                                                                                                                                                                                                                                                                                                                                                         IsoId=035147-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000712; Bcl2_BH.
PROSITE; PS01259; BH3; FALSE_NEG.
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22228 MW;
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205 AA;
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                                                                                                                                                                                                                                                                                                                                         Name=Alpha;
                                                                                                                                                                                                                                                                                                                                                                               Name=Beta;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VARSPLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP;
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A Manusherz R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Klausherz R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Aptichul S.F., Jordan H., Moore T., Wans J., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Botachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Raha S.S., Loguellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gay L.J., Hilyk S.W., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hilyk S.W., Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Shench J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Rotriguez A.C., Grimwood J., Schmutz J., Marra M.A.; Schein J.E., Schmutz J., Marra M.A.; Schein J.E., Jones S.J.M., Marra M.A.; Reneration and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                Yin D.X., Li 2., Huang B., Chen S., Zhou H., "A human protein that interacts with Bcl-2 and have homology to mouse
                                                                                                                                                           092934: 014803; Created)
10-NOV-1997 (Rel. 35, Created)
115-SEP-2003 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
BCl2-antagonist of cell death (BAD) (Bcl-2 binding component 6) (Bcl-BAD) OR BECG OR BCL2L8.
                                       Gaps
                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Bone marrow;
MEDLINE=98049554; PubMed=9388232;
MCtilie S., Diaz J.-L., Horne W., Chang J., Wang Y., Wilson G.,
Chang S., Weeks S., Fritz L.C., Oltersdorf T.;
"Dimerization properties of human BAD.";
J. Biol. Chem. 272:30866-30872(1997).
                                   ó
          Length 205;
                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=97083574; PubMed=8929532; Wang H.-G., Rapp U.R., Reed J.C.; "Bcl-2 targets the protein kinase Raf-1 to mitochondria.";
                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Takayama S., Reed J.C.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                      Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases
          Score 138; DB 1;
Pred. No. 1.6e-13;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                   [2]
SEQUENCE FROM N.A., AND PHOSPHORYLATION BY RAF-1.
                                                                                                                                                     168 AA.
                                                                            1 NLWAAQRYGRELRRMSDEFEGSFKGL 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND DIMERIZATION.
                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Lung;
MEDLINE=22388257; PubMed=12477932;
          100.0%;
100.0%;
                                     26; Conservative
                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Cell 87:629-638(1996).
                                                                                                                                                                                                                                                         Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                             [3]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                     BAD_HUMAN
                                                                                                                                                                                                                                                                                                                                                         BAD.
                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity).

1. SUBCELLUIAR LOCATION: Outer mitochondrial membrane. Upon phosphorylation, locates to the cytoplasm.

1. TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARETY OF TISSUES.

1. DOMAIN: Intact BH3 domain is required by BIK, BID, BAK, BAD AND BAX for their pro-apoptotic activity and for their interaction with anti-apoptotic members of the Bcl-2 family.

2. PTM: Phosphorylation on Ser-79 promotes heterodimerization with 14-3-3 proteins. This interaction then facilitates the phosphorylation at Ser-118, a site within the BH3 domain, leading to the release of Bcl-x(L) and the promotion of cell survival.

2. Ser-99 is the major site of AKT/PKB phosphorylation, Ser-118 the major site of protein kinase A (CAPK) phosphorylation (by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         similarity).
-! SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
-! SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
-!- CAUTION: Ref.1 sequence differs from that shown due to frameshifts in position 64 and 91.
                                                                                                                                                                                                             mitagenesis, and biophysical studies.";
Protein Sci. 9:2528-2534(2000).
-!-FUNCTION: Promotes cell death. Successfully competes for the binding to Bcl-x(L), Bcl-2 and Bcl-w, thereby affecting the level of heterodimerization of these proteins with BAX. Can reverse the death repressor activity of Bcl-x(L), but not that of Bcl-2 (By similarity). Appears to act as a link between growth factor receptor signaling and the apoptotic pathways.
-!- SUBUNIT: Forms heterodimers with the anti-apoptotic proteins, Bcl-x(L), Bcl-2 and Bcl-w. Also binds protein Si00Al0 (By similarity). The Ser-75/Ser-99 phosphorylated form binds 14-3-3 proteins (By
STRUCTURE BY NMR OF 103-127.
MEDLINE=21073561; Pubmed=11206074;
Petros A.M., Nettesheim D.G., Wang Y., Olejniczak E.T., Meadows R.P., Mack J., Swift K., Matayoshi E.D., Zhang H., Thompson C.B.,
                                                                                                                                                                               peptide complex formation from structure,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PKB) (BY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY).
A -> S (in dbSNP:3729933).
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18392 MW; 69FD8D27DDEE3241 CRC64;
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EMBL, AF021792; AAB72092.1; -
EMBL; AF031523; AAB88124.1; -
EMBL; BC001901; AAH01901.1; -.
PDB; 1G5J; 07-FEB-01.
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                                                                                                                                              Fesik S.W.;
"Rationale for Bcl-xL/Bad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    106
168 AA;
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Score 114; DB 1; Length 168;

82.6%;

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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nakatani T., Suzuki Y., Yamamoto T., Sinohara H.; Molecular cloning and sequencing of cDNAs encoding three heavy-chain precursors of the inter-alpha-trypsin inhibitor in Syrian hamster: implications for the evolution of the inter-alpha-trypsin inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBDINIT: 1-ALPHA-I PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN, BIKUNIN. INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2 BIKUNIN, INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-I) OF H2 AND BIKUNIN, AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN. PRH H3 NT PRELINKED WITH BIKUNIN VIA A CHONDROITIN 4-SULFATE BRIDGE TO THE THEIR C-TERMINAL ASPARTATE (BY
                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN, INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Biochem. 120:145-152(1996).
                                                                                                                                                                                                                             15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Inter-alpha-trypsin inhibitor heavy chain H2 precursor (III heavy chain H2) (Inter-alpha-inhibitor heavy chain 2) (HC2).
ITHE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 55-64; 140-146; 151-156; 424-447; 500-528 AND 577-605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yamamoto T., Yamamoto K., Sinohara H.;
"Inter-alpha-trypsin inhibitor and its related proteins in Syrian
                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                         6
                         Indels
                     5
     5e-10;
                                                                                                                                                                                              946 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: BELONGS TO THE ITIH FAMILY.
   Pred. No. 5e-1
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                             Mesocricetus auratus (Golden hamster).
                                                                                 1 NLWAAQRYGRELRRMSDEFEGSFK 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=97018241; PubMed=8864857;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97420688; PubMed=9276673;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biochem. 122:71-82(1997).
 91.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; D89286; BAA13939.1; -
PIR; JC5575; JC5575.
InterPro; IPR006587; VIT.
InterPro; IPR002035; VWF_A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hamster urine and plasma.";
                       22; Conservative
                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00092; vwa; 1.
SMART; SM00609; VIT; 1.
Best Local Similarity Matches 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chain family
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                     Mesocricetus.
NCBI_TaxID=10036;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   - i - SUBUNII:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Liver
                                                                                                                                                                                          ITH2_MESAU P97279;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           heavy
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RC STRAIN-C57BL/6N. TISSUE-Liver;

RX MEDLINE-9519426; PubMed=7554067;

RA Chan P., Risler J.-L., Raquenez G., Salier J.-P.;

RA Chan P., Risler J.-L., Raquenez G., Salier J.-P.;

RT Three theavy-chain precursors for the inter-alpha-inhibitor family in mouse: new members of the multicopper oxidase protein group with differential transcription in liver and brain.";

RI Jochem J. 306:50-512(1959).

R L. FUNCION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A BIONING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN,

C. INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE LOCALIZATION, SYMTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY SUBLYNIY: I-Alpha I PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM ONE OR TWO HEAVY CHAINS (H., H. OR H3) AND ONE LIGHT CHAIN,

BIKUNIN, INTER-ALPHA-INFE INHIBITOR (I-ALPHA-II) OF H3 AND BIKUNIN.

C. TISSUE SPECIFICITY: EXPRESSED IN BOTH LIVER AND BIKUNIN.

C. TISSUE SPECIFICITY: EXPRESSED IN BOTH LIVER AND BRUNIN.

C. TISSUE BRIDGE TO THE THEIR C-TERMINAL ASPARFATE (BY CTERMINAL ASPARFATE (BY CTERMINAL ASPARFATE (EXPRESSED IN BOTH LIVER (BY CHAINS (BY CTERMINAL ASPARFATE (EXPRESSED IN BOTH LIVER (BY CTERMINAL ASPARFATE (EXPRESSED IN BOTH LIVER (BY CTERMINAL ASPARFATE (EXPRESSED CTERMINAL ASPAR
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                                                                                                          BY SIMILARITY.
INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                               (POTENTIAL).
CROSS-LINK SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus...iusculus (Mouse).
Eukaryota; Metagoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciuroguathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-301-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Inter-alpha-trypsin inhibitor heavy chain H2 precursor (III heavy chain H2) (Inter-alpha-inhibitor heavy chain 2).
                                                                                                                                                                                                                                                              (POTENTIAL).
                                                                                                                                                                                                                                       (POTENTIAL).
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                                                                                                                                                                                                                    (POTENTIAL)
                                           Serine protease inhibitor; Repeat; Signal; Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 54; DB 1; Length 946;
                                                                                                                                                                                                                                                                               N-LINKED (GLCNAC. . .) (POTE:
CHONDROITIN 4-SDLFAIE, CROSS
(BY SIMILARITY).
V -> Y (IN REF. 2).
E -> I (IN REF. 2).
E -> I (IN REF. 2).
MW; CA8BF565458E7B2E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12; Indels
                                                                                                                                                                                                                                                            (GLCNAC. . .)
                                                                                                                                                                                                                                       (GLCNAC. . .)
                                                                                                                                                                                         WWFA.

N-LINKED (GLCNAC...

N-LINKED (GLCNAC...

N-LINKED (GLCNAC...

N-LINKED (GLCNAC...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          946 AA.
                                                                                                                                                                          SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 3.4
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           212 NVWIVELOGMRFLHVPDIFEGHFOGV 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 NLWAAQRYGRELRRMSDEFEGSFKGL 26
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                                                                                                                                                                                                                                                                                                                                                                                         106580 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                   39.1%;
34.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 34.6 tes 9; Conservative
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SM00327; VWA; 1.
                                                                                                                                                                                                                                                                                                                                               510
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                                                                                                                                                                                                                                                                                                                                                                  595
946 AA;
                      PROSITE; PS50234;
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15-JUL-1998 (
28-PEB-2003 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ITH2_MOUSE
Q61703;
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                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                         CARBOHYD
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                                                                                                                                                                                                                                                                                                                                               CONFLICT
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CHAIN
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us-09-544-664-1.rsp

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Matches
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     SOW WENT WAR WANTED TO THE CONTROL OF THE CONTROL O
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY.
INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

MEDLINE=92225349; PubMed=1348717;

Kuenzler M., Paravicini G., Egli C., Irniger S., Braus G.H.;

Kuenzler M., primary structure and regulation of the ARO4 gene, encoding the tyrosine-inhibited 3-deoxy-D-arabino-heptulosonate-7-phosphate synthase from Saccharomyces cerevisiae.";

Gene 113:67-74(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Doignon F., Biteau N., Aigle M., Crouzet M., "The complete sequence of a 6794 bp segment located on the right arm of chromosome II of Saccharomyces cerevisiae. Finding of a putative dUTPase in a yeast.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHONDROITIN 4-SULFATE, CROSS-LINK SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-ocr-1993 (Rel. 27, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Phospho-2-dehydro-3-deoxyheptonate aldolase, tyrosine-inhibited
(EC 4.1.2.15) (Phospho-2-Reto-3-deoxyheptonate aldolase) (DAHP
synthetase) (3-deoxy-D-arabino-heptulosonate 7-phosphate synthase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomyces cerevisiae (Baker's yeast).

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                      Serine protease inhibitor; Repeat; Signal; Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38.4%; Score 53; DB 1; Length 946; 34.6%; Pred, No. 4.8; ive ~.5; Mismatches 12; Indels
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Submitted (NOV-1993) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY).
40DB6716433ED9DC CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  212 NVWIIEPQGMRFLHVPDIFEGHFQGV 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 NLWAAQRYGRELRRMSDEFEGSFKGL 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BY
                                                                                                                                                                                           MGD; MGI:96619; Itih2.
InterPro; IPR006587; VIT.
InterPro; IPR002035; VWE_A.
Pfam; PF00092; VWA_1.
SMART; SM00609; VIT; 1.
SMART; SM00327; VWA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 34.00,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ARO4 OR YBR249C OR YBR1701.
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                                                                                                                                          EMBL; X70392; CAA49842.1;
                                                                                                                                                                                                                                                                                                                                                                             VWFA; 1.
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54
702
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REVISIONS TO 205-207.
                                                                                                                                                                        PIR; S54354; S54354
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                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS50234;
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308
1118
263
702
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P32449;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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PROPEP
CHAIN
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DOMAIN
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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GO; GO:0003849; F:2-dehydro-3-deoxyphosphoheptonate aldolase . . .; IDA.
InterPro; IPR006219; AroFGH.
InterPro; IPR006218; DAHP1/KDSA.
                                                                                                                                     Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: STEREOSPECIFIC CONDENSATION OF PHOSPHOENOLDFRUVATE (PEP)
AND D-ERYTHROSE-4-PHOSPHATE (E4P) GIVING RISE TO 3-DEOXY-D-ARABINO-HEPTULOSONATE-7-PHOSPHATE (DAHP).
-!- CAPALYTIC ACTIVITY: 2-dehydro-3-deoxy-D-arabino-heptonate 7-phosphate + phosphate = phosphoenolpyruvate + D-erythrose 4-phosphate + H(2)O.
-!- ENZYME REGULATION: INHIBITED BY TYROSINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 232 AA.
P35632; Q39003; Q8LB79; Q9S7Q3; Q9SQ14; Q9SQ15; Q9SQ16; Q9SQ17;
P35632; Q39003; Q8LB79; Q9S7Q3; Q9SQ14; Q9SQ15; Q9SQ16; Q9SQ17;
Q9SQ18; Q9SQ19; Q9SQ20; Q9SQ21; Q9SX13;
O1-JUN-1994 (Rel. 29, Last sequence update)
O1-JUN-1994 (Rel. 29, Last annotation update)
I5-SEP-2003 (Rel. 42, Last annotation update)
Floral homeotic protein APETALA3.
AP3 OR AT3654340 OR T12E18_30.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
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ProDom; PD005060; AroFGH; 1.
TIGRRAMS; TIGRO0034; aroFGH; 1.
Aromatic amino acid biosynthesis; Lyase; Multigene family.
SEQUENCE 370 AA; 39749 MW; 594ED48F24175979 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           first step.
-!- INDUCTION: By amino acid starvation.
-!- SIMILARITY: BELONGS TO CLASS-I DAHP SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37.7%; Score 52; DB 1; Length 370;
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; Mismatches
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EMBL; L20296; AAA65607.1; -.
EMBL; 236118; CAA85212.1; -.
PIR; S38185; S38185.
HSSP; P00886; LQR7.
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Yeast 9:1131-1137(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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                                                                    FROM N.A.
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NCBI_TaxID=3702;
                                                                                                             STRAIN-S288c;
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                                                                       SEQUENCE
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EMBL;
EMBL;
   RN PEDURKCE FROM N.A.

RY SEQURKCE FROM N.A.

STRAIN-CV. Columbia;

RX MEDINE=21016720; PubMed=11130713;

RA MEDINE=21016720; PubMed=11130713;

Salanoubat M., Lemcke K., Rieger M., Ansorge W., Unseld M.,

RA Fartmann B., Valle G., Bloecker H., Perez-Alonso M., Obermaier B.,

RA Fartmann B., Valle G., Bloecker H., Perez-Alonso M., Obermaier B.,

Belseny M., Boutry M., Grivell L.A., Mache R., Pulydomenech P.,

RA Mincker P., Cattolico L., Waissenbach J., Saurin W., Oberier F.,

RA Wincher P., Cattolico L., Waissenbach J., Saurin W., Oberier F.,

RA Wincher P., Cattolico L., Waissenbach J., Saurin W., Benes V.,

RA Wiedelmann R., Kranz H., Vorsa H., Holland R., Brandt P., Nyakatura G.,

RA Wiedelmann R., Rranz H., Yanger S., Simionati B.,

Conrad A., Hornischer K., Kauer G., Loehnert T.-H., Nordsiek G.,

RA Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,

RA Reichelt J., Scharfe M., Schoof H., Terol J., Climent J.,

RA Mavarro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,

RA Mannangh G., Haase D., Raper-Illauro C., Purnelle B., Masuy D.,

RA Mannangh G., Haase D., Raper-Illauro C., Purnelle B., Masuy D.,

RA Mannangh G., Haase D., Raper-Illauro C., Purnelle B., Masuy D.,

RA Mannangh G., Malti R., Wu D., Perezoral P., Johner J., Shea T.P.,

RA Rooney T., Rizzo M., Walts A., Utterback T., Fujii C.Y., Shea T.P.,

RA Rooney T., Rizzo M., Walts A., Utterback T., Fujii C.Y., Shea T.P.,

RA Rooney T., Rizzo M., Walts A., Utterback T., Fujii C.Y., Shea T.P.,

RA Preser C.M., Kannan W.C., Salzberg S.L., White O., Venter J.C.,

RA Preser C.M., Kannan W.C., Salzberg S.L., White O., Venter J.C.,

RA Fraser C.M., Kanawa R., Matsumoto M., Matsumo A., Muraki A.,

RA Rayama S., Nakazaki M., Shinpo S., Takenchi C., Wada T.,

RA Matanbe A., Yanada M., Yakada M., Tabata S.;

RY Matanbe B., Mannanda M., Tabata S.;

RY Matanbe B., Sanado M., Tabata S.;

RY Mathala M., Matsunoto M., Matsuno C., Matania P.,

RA Matanbe M., Matsunoto M., Matsuno C., Matania M.,

Reidenece and analysis of chromosome
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MEDLINE=99311297; PubMed=10382288;
Brunel D., Froger N., Pelletier G.;
"Development of amplified consensus genetic markers (ACGM) in Brassica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=cv. Columbia;
Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
"RIKEN Arabidopsis full length cDNA clones (RAFLs) sequenced by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Purugganan M.D., Suddith J.I.; "Molecular population genetics of floral homeotic loci: departures from the equilibrium-neutral model at the APETALA3 and PISTILLATA genes of Arabidopsis thallana."; Genetics 151:839-848(1999).
                                                                    STRAIN-cv. Landsberg erecta;
MEDLINE=95036018; PubMed=7948893;
Okamato H., Tano A., Shiraishi H., Okada K., Shimura Y.;
"Genetic complementation of a floral homeotic mutation, apetala3, with an Arabidopsis thaliana gene homologous to DEFICIENS of
                                                                                                                                                                                                                                                                                                                                                                                             SIRALINE. SINCE THE STATE OF TH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Full-length cDNA from Arabidopsis thaliana."; Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               consortium (Salk/Stanford/PGEC)
                                                                                                                                                                                                                                                                                             . 26:465-472(1994).
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND VARIANTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 36-128 FROM N.A.
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[2]
SEQUENCE FROM N.A.
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Feldmann K.,
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=8643482;
Riecimann J.L., Krizek B.A., Meyerowitz E.M.;
Riecimann J.L., Rrizek B.A., Meyerowitz E.M.;
"Dimerization specificity of Arabidopsis MADS domain homeotic proteins APETALA1, APETALA3, PISTILLATA, and AGAMOUS.";
Proc. Natl. Acad. Sci. U.S.A. 93:4793-4798(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 409:525-529 (2001).

Nature 409:525-529 (2001).

-I-FUNCTION: Probable transcription factor involved in the genetic control of flower development. Is required for normal development of petals and stamens in the wild-type flower. Forms an heterodimer with PISTILIATA that is required for autoregulation of both AP3 and PI genes. AP3/PI heterodimer interacts with AP3/PI or SEPALLATA3 to form a ternary complex that could be responsible for the regulation of the genes involved in the flower
                                                                                                                                                                                                                 Krizek B.A., Meyerowitz E.M.;
"The Arabidopsis homeotic genes APETALA3 and PISTILLATA are sufficient to provide the B class organ identity function.";
Development 122:11-22(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- SUBCELLUCAR LOCATION: Nuclear.
-1- TISSUE SPECIFICITY: Expressed in petals and stamens.
-1- TISSUE SPECIFICITY: Expressed in petals and stamens.
-1- INDUCTION: Positively regulated by the meristem identity proteins APETALAI and LEARY with the cooperation of UFO.
-1- MISCELLANEOUS: Mutations in the carpels.
into sepals and stamina into carpels.
-1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Honma T., Goto K., "Complexes of MADS-box proteins are sufficient to convert leaves into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=11283333;
Ng M., Yanofsky M.F.;
"Activation of the Arabidopsis B class homeotic genes by APETALA1.";
Plant Cell 13:739-753(2001).
from Arabidopsis thaliana sequences of known biological
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                                                                                       Genome 42:387-402(1999).
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                                                                                                                                                                                                PubMed=8565821;
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EMBL; AB012751; BAA25872.1; -.
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062992;
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MEDIAIN-1978, Magner L., Shenmen C.M., Schuler G.D., Strausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Alausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., A Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Bosak S.A., McEwan P.J., McKernan K.J., Abramson R.D., Mullahy S.J., Bosak S.A., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00350; MADS_BOX_1; 1.
PROSITE; PS50066; MADS_BOX_2; 1.
Flowering; Transcription regulation; Activator; Developmental protein;
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M -> T (in, strain cv. Bretagny).
N -> D (in strain cv. Corsacalla-1).
L -> S (in strain cv. Li-8).
L -> V (in strain cv. Kas-1).
E -> K (in strains cv. Chi-1 and cv. Gr-3).
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15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Protein C5orf5 homolog.
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                                                                                                                                                                                                                                                                                TRANSFAC; T01776; -.
INTERFYO; IPR002487; TF_Xbox.
InterPro; IPR002100; TF_MADSbox.
Pfam; PF01486; K-box; 1.
Pf00319; SRF-TF; 1.
             EMBL, AF115811, AAD51900.1;
EMBL, AF115812, AAD51900.1;
EMBL, AF115813, AAD51901.1;
EMBL, AF115814, AAD51902.1;
EMBL, AL132971, CAR81799.1;
EMBL, AY087369, AAM64919.1;
EMBL, AY142590, AAM13159.1;
EMBL, AY42095, AA2095.
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SMART; SM00432; MADS; 1.
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TRANSFAC; T01776;
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VARIANT
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CE05_MOUSE
ACC CRE05_MOUSE
DT 15-SEP

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                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; Ericales; Ericaceae; Ericoideae; Rhodoreae; Rhododendron.
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.W., Krzywinski M.L., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDMA sequences.", proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- SIMILARITY: Belongs to the FAMA3 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- FUNCTION: Probably assists in splicing chloroplast group II introns (By similarity).
-!- SIMILARITY: BELONGS TO THE INTRON MATURASE FAMILY 2. MATK
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Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                % Match 36.2%; Score 50; DB 1; Length 851; Local Similarity 45.5%; Pred. No. 12; les 10; Conservative 5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unvestigation of sectional relationships in the genus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          851 AA; 97054 MW; C2B26669FB6DB2CE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rhododenáron (Ericaceae) based on matK seguences.
Shokubutsu Kenkyu Zasshi 73:143-154(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             506 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; BC031465; AAH31465.1; -. InterPro; IPR000198; RhoGAP. Pfam; PF00620; RhoGAP; 1. SMART; SM00324; RhOGAP; 1. PROSIŢĖ; PS50238; RHOGAP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ledum palustre (Wild rosemary).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTPase activation. DOMAIN 23
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RESULT 12
RMUC_PSEAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Investigation of sectional relationships in the genus Rhododendron (Ericaceae) based on matk Sequences."; Shokubutsu Kenkyu Zasshi 73:143*154(1998).
--- FUNCTION: Probably assists in splicing chloroplast group II introma (By similarity).
--- SIMILARITY: BELONGS TO THE INTRON MATURASE FAMILY 2. MATK
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Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
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                                                                                                         1; Length 506;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7; Indels
                                                                                                                                        Indels
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SEQUENCE 506 AA; 60534 MW; ADA44B25E92436E8 CRC64;
          InterPro; IPRO02866, Matk.N.
Pfam; PF01348; Intron_maturas2; 1.
Pfam; PF01824; Matk.N; 1.
mRNA processing; Chloroplast.
SEQUENCE 506 AA; 60412 MW; CFEA926307DAC85E CRC64;
                                                                                                                                                                                                                                                                                                            28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                         ВВ
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                                                                                                       35.9%; Score 49.5; DI
36.7%; Pred. No. 8.2;
iive 5; Mismatches
                                                                                                                                                                                      506 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 LWAA-----QRYGRELRRMSDEFEGSFK 24
                                                                                                                                                                      2 LWAA-----QRYGRELRRMSDEFEGSFK 24
                                                                                                                                                                                                                                                                                                                                                                                          Rhododendron ferrugineum (Alpenrose).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000442; Intron_maturse2.
InterPro; IPR002866; Matk_N.
Pfam; PF01348; Intron_maturas2; 1.
Pfam; PF01824; Matk_N; 1.
InterPro; IPR000442; Intron_maturse2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MATK_RHOTS STANDARD;
062991;
28-FEB-2003 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AB012741; BAA25862.1; -.
                                                                                                                                                                                                                                                                                                                                                            Maturase K (Intron maturase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 36./r,
Thes 11; Conservative
                                                                                                        Query Match
Best Local Similarity 36.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBFAMILY.
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MEDLINE-20437337; PubMed=10984043;

MEDLINE-20437337; PubMed=10984043;

MEDLINE-20437337; PubMed=10984043;

MECKEY M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., A Hickey M.J., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., A Garber R.L., Coulter S.M., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., A Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;

R. Complete genome sequence of Pseudomonas aeruginosa PAO1, an RI opportunistic pathogen.";

R. Nature 406:959-964(2000).
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                                                                                                                                                                                                                                      Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots;
Asteridae, Ericales, Ericaceae, Ericoideae, Rhodoreae, Rhododendron.
                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Investigation of sectional relationships in the genus Rhododendron (Ericaceae) based on matK sequences."; Shokubutsu Kenkyu Zasshi 73:143-154(1998).
-!- FUNCTION: Probably assists in splicing chloroplast group II introns (By similarity).
-!- SIMILARITY: BELONGS TO THE INTRON MATURASE FAMILY 2. MATK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35.9%; Score 49.5; DB 1; Length 506; 36.7%; Pred. No. 8.2;
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi
Yukawa T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7; Indels
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SEQUENCE 506 AA; 60569 MW; AEE12FF8809C223E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            091403;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
DNA recombination protein rmuC homolog.
28-FEB-2003 (Rel. 41, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Maturase K (Intron maturase).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interpro; IPR000442; Intron_maturse2. Interpro; IPR002866; MatK_N.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 30...
Lag 11; Conservative
                                                                                                                           Rhododendron tsusiophyllum. Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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                                                                                                                                                                                                                                                                                                          NCBI_TaxID=49629;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBFAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yukawa
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PRINTS; PR00449; RASTRNSFRMNG.
SMART; SM00173; RAS; 1.
TIGRFAMS; TIGRE0231; small_GTP; 1.
                                           TIGRFAMS; TIGR00231; small GTP-binding; Prenylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6PGL_THEMA
Q9XON8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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NP_BIND
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
6PGL_THEMA
                                                                                                                                                                             LIPID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBCELLULAR LOCATION: Piasma membrane.
-!- DEVELOPMENTAL STAGE: IN SPORULATING MYCELLUM AND MUCH LESS IN GERMLING AND YEAST.
-!- SIMILARITY: BELONGS TO THE SMALL GIPASE SUPERFAMILY. RAS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rhizomucor racemosus (Mucor circinelloides f. lusitanicus).
Eukaryota, Fungi, Zygomycota; Zygomycetes; Mucorales; Mucoraceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     2;
 FUNCTION: Involved in DNA recombination (By similarity). SIMILARITY: BELONGS TO THE RMUC FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                                                                                                     PIR; B3517; B3517.
InterPro; IPR003798; DUF195.
Pfam; PF02646; Rmuc; 1.
DNA recombination; Coiled coil; Complete proteome.
DOMAIN
SEQUENCE 453 AA; 51539 MW; 1E7EA97E8ZECSE4B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                         35.5%; Score 49; DB 1
55.6%; Pred. No. 8.6;
Live 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 205 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro: IPR003577; GTPase_Ras.
InterPro: IPR001806; Ras_trnsfrmng.
InterPro: IPR005225; Small_GTP.
Pfam; PF00071; ras; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 WAAQRYGR--ELRRMSDE 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65 WASEROGREEELRRLASE 82
                                                                                                                                                                                                                                     EMBL; AE004535; AAG04420.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M55177; AAA83379.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 55.6 les 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; C36365; C36365.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ras-like protein 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-AICC 1216B;
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NCBI_TaxID=4841;
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                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation-the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

STRAIN-MSB8 / DSM 3109;

MEDLINE-99287316; Pubmed=10360571;

MEDLINE-99287316, Pubmed=10360571;

Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,

Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Recchum K.A.,

McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,

Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,

Heidelberg J., Sutton G.G., Fleischmann R.D., Elsen J.A., White O.,

Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;

"Evidence for lateral gene transfer between Archaea and Bacteria from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   phospho-D-gluconate.
-!- PATHWAY: Pentose phosphate pathway; second step.
-!- SIMILARITY: BELONGS TO THE GLUCOSAMINE/GALACTOSAMINE-6-PHOSPHATE ISOMERASE FAMILY. 6-PHOSPHOGLUCONOLACTONASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- CATALYTIC ACTIVITY: 6-phospho-D-glucono-1,5-lactone + H(2)0 = 6-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga. NCBL_TaxID=2336;
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                                                                                                                                                                                                                                  DB 1; Length 205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -:- FUNCTION: HYDROLYSIS OF 6-PHOSPHOGLUCONOLACTONE TO 6-
                                                                                                                                                                                                                                                                                             4; Indels
                                                                                                             EFFECTOR REGION (PROBABLE).
FARNESYL (BY SIMILARITY).
DBF086466F090F50 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9BOFD07EE01E60C3 CRC64;
                      GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
6-phosphogluconolactonase (EC 3.1.1.31) (6PGL).
PGL OR DEVB OR TM1154.
                                                                                                                                                                                                                                     Score 48; DB 1
Pred. No. 5.1;
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genome sequence of Thermotoga maritima." Nature 399:323-329(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR005148; Gluc_gal_isom.
InterPro; IPR005900; Phosphogluconlac.
Pfam; PF01182; Glucosamine_iso; 1.
TIGRFAMS; TIGR01198; pgl; 1.
Lipoprotein.
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SEQUENCE 220 AA; 25325 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE001772; AAD36230.1; -.
                                                                                                                                                                          23408 MW;
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168 REIRRMNKEQEGRSKG 183
                                                                                                                                                                                                                                  Query Match 34.8%;
Best Local Similarity 62.5%;
Matches 10; Conservative 2
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67
125
46
202
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122
132
38
202
205 AA;
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HSSP; Q9STB5; LE3X.
InterPro; IPR001926; B6_enzyme_beta.
InterPro; IPR004450; Thr_synthase.
Fram; PF00291; PALP; 1.

TIGRFAMS; TIGR00260; thrc; 1.

PROSITE; P800165; DEHYDRATASE_SER_THR; 1.

Threonine biosynthesis; Lyase; Pyridoxal phosphate; Allosteric enzyme; Chloroplast; Transit peptide.
TRANSIT 1.
                                                                                                                                                                                                                                                                                                                                      TISSUE-Leaf;
PubMed=10940468;
Casazza A.P., Basner A., Hoefgen R., Hesse H.;
Expression of threonine synthase from Solanum tuberosum L. is not metabolically regulated by photosynthesis-related signals or by nitrogenous compounds.",
Plant Sci. 157:43-50(2000).
-! CATALYTIC ACTIVITY: O-phospho-L-homoserine + H(2)0 = L-threonine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Solanum tubercosum (Potato).
Solanum tubercosum (Potato).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; lamiids; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHLOROPLAST (BY SIMILARITY).
THREONINE SYNTHASE.
PYRIDOXAL PHOSPHATE (BY SIMILARITY).
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                                                                                                                                                                                  28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Threonine synthase, chloroplast precursor (EC 4.2.3.1) (TS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34.8%; Score 48; DB 1; Length 519; 35.3%; Pred. No. 14; tive 6; Mismatches 8; Indels
7; Indels
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                                                                                                                                       519 AA.
Mismatches
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                                               4 AAQRYGRELRRMSDEFEGSFKGL 26
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Matches 12; Conservative
8; Conservative
                                                                                                                                       STANDARD;
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Matches
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0919n2 brachydanio
08vjs3 mycobacteri
010843 mycobacteri
080016 mycobacteri
082v71 pyrobaculum
09seg0 arabidopsis
09sq20 arabidopsis
09sq17 arabidopsis
09sq19 arabidopsis
09sq19 arabidopsis
09sq19 arabidopsis
09sq16 arabidopsis
                                                             (without alignments)
237.680 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                     ; Search time 28.2286 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                138
1 NLWAAQRYGRELRRMSDEFEGSFKGL 26
                                                                                                                                                        830525 seqs, 258052604 residues
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                                                     September 15, 2003, 17:17:31
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                                   using sw model
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Gapop 10.0 , Gapext 0.5
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sp_unclassified:*
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sp_human:*
sp_invertebrate:*
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Maximum Match 100%
Listing first 45 su
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sp_mhc:*
sp_organelle:*
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1: sp_archea:*
2: sp_bacteria:*
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Maximum DB seq length: 2000000000
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sp_rodent:*
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047149 rhododendro
047171 rhododendro
062982 rhododendro
062972 rhododendro
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047155 rhododendro
047152 rhododendro
047173 rhododendro
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                     chimpanzee
halobacteri
                                  09ssp5 arabidopsis
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Q9ub33 anopheles g
                                                  anopheles g
       shewanella
                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-20373792; PubMed=10917738;
Inohara N., Nunez G.;
"Genes with homology to mammalian apoptosis regulators identified in zebrafish.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                       Brachydanio rerio (2ebrafish) (Danio rerio).
Eukaryota: Metazoa; Chordata: Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
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                    037056
09hnz9
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65.2%; Pred. No. 5.3e-05;
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EMBL, AF231017; AAF66962.2; -.

HSSP; Q92934; 1G5J.

ZFIN; ZDB-GENE-000616-1; bad.

SEQUENCE 146 AA; 16546 MW; 28A5650BB5107ECB CRC64;
                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
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      Q8E134
Q8K316
Q9K316
Q9HNZ9
Q9K2H3
Q9UB33
Q9UB33
Q9UB3
Q4714
Q47141
Q63960
Q62975
Q62975
Q62975
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047155
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047173
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047170
047174
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062980
062981
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01-0CT-2000 (TrEMBLrel. 15, 01-DEC-2001 (TrEMBLrel. 19, 01-OCT-2002 (TrEMBLrel. 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 65.2 les 15; Conservative
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68
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Q919N2;
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Matches
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0919N2
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ID Q8
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Thermoproteaceae, Pyrobaculum
NCBI_TaxID=13773;
                                                   17
                                                   1 NLWAAQRYGRELRRMSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00609; VIT; 1.
SMART; SM00327; VWA; 1.
PROSITE; PS50234; VWFA; 1.
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Matches 9; Conservative
  10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Miller J.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  aerophilum."
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Q8K016;
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  Matches
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                                                     QΫ
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C. -:-SIMILARITY: TO M.PARATUBERCULOSIS IS900.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
Bishai W.;
"Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium tuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773;
                                                                                                                                                       Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Mycobacteriaceae, Mycobacterium.
NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AE007058; AAK46348.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003346; Transposase_20.
Pfam: PF02371; Transposase_20; 1.
Hypothetical protein; Complete protecme.
SEQUENCE 223 AA; 24132 MW; 70456750017FEF37 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro: INTO/)
InterPro: IPRO03346; Transposase_20.
Pfam: PF02371; Transposase_20; 1.
SEQUENCE 196 AA: 21349 MW; C145ABD836FD9C2D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein Rv2014.
Rv2014 OR MTCX39.03C.
Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 53; DB 16;
Pred. No. 8.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38.4%; Score 53; DB 16; 58.8%; Pred. No. 7.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       223 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                 Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 58.8
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tuberculist; Rv2014;
                                                                                IS1607, transposase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TIGR; MT2070;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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Q10843
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                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria: Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12; Indels
  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC034341; AAH34341.1; -.
MGD; MGI:96619; Itih2.
InterPro; IPR002035; VWF_A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         946 AA; 105945 MW; 8B17DBA71B85BC5C CRC64;
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EMBL; AE009793; AAL63125.1; -.
Interpro; IPR006638; Elp3.
Interpro; IPR00182; CCN5acetyltransf.
SMART; SM00729; Elp3; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 471 AA; 52952 WW; 3B1E36E8AEE2EFOA CRC64;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-NAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein PAE0922.
                                                                                                                                                                                                                                                                                  01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Inter-alpha trypsin inhibitor, heavy chain 2.
ITIH2.
9
                                                                                                                                                                                                                                  946 AA.
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5; Mismatches
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38.4%; Score 53; 34.6%; Pred. No. 4
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SEQUENCE FROM N.A.
STRAIN-IMZ / ATCC 51768 / DSM 7523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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PROSITE; PS00350; MADS_BOX_1; 1.
PROSITE; PS50066; MADS_BOX_2; 1.
DNA-binding; Nuclear protein; Transcription; Transcription regulation.
SEQUENCE 232 AA; 27342 MW; BDFDCB59B73F4601 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE: PS00350; MADS_BOX_1; 1.
PROSITE; PS50066; MADS_BOX_2; 1.
DNA-binding; Nuclear protein; Transcription; Transcription regulation.
SEQUENCE 232 AA; 27267 MW; 42A852D697E22A65 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta; eudicotyledons, core eudicots; Rosidae, eurosids II; Brassicales; Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-CV. Li-8;
MEDLINE-99126449; PubMed=9927474;
Purugganan M.D., Suddith J.I.;
"Molecular population genetics of floral homeotic loci. Departures from the equilibrium-neutral model at the APETALA3 and PISTILLATA genes of Arabidopsis thaliana.";
Genetics 151:839-848(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
"Molecular population genetics of floral homeotic loci. Departures from the equilibrium-neutral model at the APETALA3 and PISTILLATA genes of Arabidopsis thaliana."; Genetics 151:839-848(1999).
                                                             -1- SUBCELLUIAR LOCATION: NUCLEAR (BY SIMILARITY).
-1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 232;
                                                                                                                                                                                                                                                                                                                    DB 10; Length 232;
18;
                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Floral homeotic protein AP3.
                                                                                                                                                                                                                                                                                                                                                    4,
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Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           232 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Mismatches
                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                 107 QRLGECLDELDIQELRRLEDEMENTFK 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 QRYG-----RELRRMSDEFEGSFK 24
                                                                                                                                                                                                                                                                                                                    37.0%; Score 51; 44.4%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                 6 ORYG-----RELRRMSDEFEGSFK 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Interpro: IPR002487; TF_Kbox.
InterPro: IPR002100; TF_MADSbox.
Pfam: PF01486; K-box; 1.
Pfam: PF00319; SR-TF; 1.
PRINTS: PR00404; MADSDOMAIN.
SMART; SM00432; MADS; 1.
                                                                                                                                           InterPro; IPR002487; TF_Kbox.
InterPro; IPR002100; TF_MADSbox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF115801; AAD51890.1; -.
HSSP; P11746; 1MNM.
                                                                                                             EMBL; AF115806; AAD51895.1; -.
HSSP; P11746; 1MNM.
                                                                                                                                                                       Pfam; PF01486; K.box; 1.
Pfam; PF00319; SRF-TF; 1.
PRINTS; PR00404; MADSDOMAIN.
SMART; SW00432; MADS; 1.
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Best Local Similarity 44.4
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity '
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NON_TER 231 231
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta; eudicotyledons, core eudicots, Rosidae,
eurosids II; Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                  Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnollophyta, eudicotyledons, core eudicots, Rosidae, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                        MOL. Biol. Evol. 16:1037-1045(1999).
-! SUBCELLUIAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=99404148; PubMed=10474900;
Lawton-Rauh A.L., Buckler E.S. IV, Purugganan M.D.;
"Patterns of molecular evolution among paralogous floral homeotic
                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 51; DB 10; Length 231;
Pred. No. 18;
    DB 17; Length 471;
                                 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27176 MW; A67CAE1EEBD8F7AA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                     01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     232 AA.
                                                                                                                                                                           231 AA.
                                 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           107 QRLGECLDELDIQELRRLEDEMENTFK 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 QRYG-----RELRRMSDEFEGSFK 24
    Score 52;
                  Pred. No
                                                                                     404 WQHSGMGREIMRLAEEIAGEFGAL 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY 2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequel-OCT-2002 (TrEMBLrel. 22, Last anno Floral homeotic protein AP3.
                                                                 3 WAAQRYGRELRRMSDEFEGSFKGL 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                             PRT;
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SEQUENCE FROM N.A.
STRAIN-CV. COISCALIA;
MEDLINE-99126449; PubMed-9927474;
Purugganan M.D., Suddith J.I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002487; TF Kbox.
InterPro; IPR002100; TF_MADSbox.
Pfam; PF01486; K-box; 1.
Pfam; PF00319; SRF-TF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PRO0404; MADSDOMAIN.
SMART; SM00432; MADS; 1.
PROSITE; PS50066; MADS_BOX_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF143380; AAF25590.1; -. HSSP; P11746; 1MNM.
 37.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 44.4 nes 12; Conservative
                                 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                231 AA;
 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                       Apetala3 (Fragment)
                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=59689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                    Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                 genes."
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Q9SEG0
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232 AA
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Interpro; IPR002100; TF_MADSbox.
Pfam; PF01486; K-box; 1.
PRam; PF00319; SRF-TF; 1.
PRAMS; PR00404; MADSDMAIN.
SMART; SM00432; MADS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=cv. Kent;
MEDLINE=99126449; Pubmed=9927474;
   Arabidopsis thaliana.";
                                                                                                                InterPro; IPR002487; TF_Kbox.
InterPro; IPR002100; TF_MADSbox.
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                                                                                 EMBL; AF115807; AAD51896.1; -. HSSP; P11746; 1MNM.
                                                                                                                                                                                                                                                                                        37.0%;
                                                                                                                                                                                                                                                                                                         44.48;
                                                                                                                                                                                                                                                                                                    Local Similarity 44.4 tes 12; Conservative
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                                                                                                                                                   Pfam; PF01486; K-box; 1
Pfam; PF00319; SRF-TF;
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les 12; Conserv
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                                                                   FACTORS
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Best Local S
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PROSITE; PS50066; MADS_BOX_2; 1.
DNA-binding; Nuclear protein; Transcription; Transcription regulation.
SEQUENCE 232 AA; 27284 MW; 04FCFC55B73C7729 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana (Mouse-ear cress).

Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                 Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae, eurosids II; Brassicales, Brassicaceae, Arabidopsis.
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MEDLINE=99126449; PubMed=9927474;
Purugganan M.D., Suddith J.I.;
"Molecular population genetics of floral homeotic loci. Departures from the equilibrium-neutral model at the APETALA3 and PISTILLATA
                                                                                                                                                                                                                                                                                                                                 STRAIN=CV. Lisse,
MEDLINE-99126449; PubMed=9927474;
Puruganan M.D., Suddith J.I.;
Puruganan M.D., Suddith J.I.;
"Molecular population genetics of floral homeotic loci. Departures from the equilibrium-neutral model at the APETALA3 and PISTILLATA genes of Arabidopsis thaliana.";
Genetics 15:1839-848(1999).
- : SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
- : SUBCILLULAR LOCATION: PACTORS.
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Pred. No. 18;
3; Mismatches 4; Indels
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Last annotation update)
                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
Floral homeotic protein AP3.
                                                                                                  232 AA.
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6 QRYG------RELRRMSDEFEGSFK 24
                                                                                                                                                                                                                 Arabidopsis thaliana (Mouse-ear cress).
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InterPro; IPR002100; TF_MADSbox.
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Pfam; PF00319; SRF-TF; 1.
PRINTS; PR00404; MADSDOMAIN.
SMART; SM00432; MADS; 1.
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nes 12; Conservative
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01-MAY-2000 (TrEMBLrel. 13,
01-MAR-2003 (TrEMBLrel. 23,
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SEQUENCE FROM N.A.
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Query Match

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PRINTS; PRO0404; MADSOMAIN.
SWART; SW00432; MADS; I.
PROSITE; PS50066; WADS_BOX_2; I.
DNA-binding; Nuclear protein; Transcription; Transcription regulation.
SEQUENCE 232 AA; .27311 MW; 71AE593FB8A67EC3 CRC64;
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PROSITE; PS50066; MADS_BOX_2; 1.
DNA-binding; Nuclear protein; Transcription; Transcription regulation.
SEQUENCE 232 AA; 27286 NW; 66976305B8BB63E3 CRC64;
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Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
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Pred. No. 18;
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01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CCT-2002 (TrEMBLrel. 22, Last annotation update)
Floral homeotic protein AP3.
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Query Match
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Q9SQ15
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                                                                            U1-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
Floral homeotic protein APETALA3 (AP3).
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBL_TAXID=3702;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Full-Length cDNA from Arabidopsis thaliana.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLUIAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.
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MEDLINE-99126449; PubMed-9927474;
Purugganan M.D., Suddith J.I.;
"Molecular population genetics of floral homeotic loci. Departures from the equilibrium-neutral model at the APETALA3 and PISTILLATA genes of Arabidopsis thaliana.";
                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
Haas B.J., Volforsky N., Town C.D., Troukhan M., Alexandrov N., Fadmann K.A., Flavell R.B., White O., Salzberg S.L.;
"Full-length messenger RNA sequences greatly improve genome annotation.";
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&
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Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.
Feldmann K.;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Floral homeotic protein AP3.
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Pred. No. 18;
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                                                                232 AA.
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InterPro; IPR002100; TF_MADSbox.
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44.4%;
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SMART; SMO0432; MADS; 1.
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Pfam; PF00319; SRF-TF; 1.
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                                                                PRELIMINARY;
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Q9SQ16
                 RESULT 12
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SEQUENCE 232 AA; 27314 MW; DB8CAIFC835557D6 CRC64;
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Enkaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBL_TaxID=3702;
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SEQUENCE 232 AA; 27300 MW; 5CA05FD44F824DF0 CRC64;
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"Molecular population genetics of floral homeotic loci. Departures from the equilibrium neutral model at the APETALA3 and PISTILLATA genes of Arabidopsis thaliana.";
Genetics 151:839-848(1999).
-!- SUBCELLULAR LOCATION: UNCLEAR (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
Genetics 151:839-848(1999).
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
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Pred. No. 18;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   107 QRLGECLDELDIQELRRLEDEMENTFK 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, AF115812; AAD51901.1; -. HSSP; P11746; 1MNM.
InterPro; IPR002100; TF_MADSbox.
Pfan; PF01486; K-box; 1.
Pfan; PF00319; SRF-TF; 1.
PRINTS; PR00404; MADSDOMAIN.
                                                                                                    EMBL, AF115810; AAD51899.1; -. HSSP; P11746; 1MNM.
InterPro; IPR002487; TF_Kbox.
Interpro; IPR002100; TF_MADSbox.
Pfan; PF01486; K-box; 1.
Pfan; PF00319; SRF-TF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=cv. Kas-1;
MEDLINE=99126449; PubMed=9927474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00432; MADS; 1.
PROSITE; PS00350; MADS_BOX_1; 1.
PROSITE; PS50066; MADS_BOX_2; 1.
                                                                                                                                                                                                                                                                                         SWART; SM00432; MADS: 1.
PROSITE; PS00350; WADS_BOX_1; 1.
PROSITE; PS50066; MADS_BOX_2; 1.
                                                                                                                                                                                                                                                                     PRINTS; PR00404; MADSDOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             37.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 44.4 tes 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2002 (TrEMBLrel. Floral homeotic protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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us-09-544-664-1.rspt

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PROSITE; PS50066; MADS_BOX_2; 1.
DNA-binding; Nuclear protein; Transcription; Transcription regulation.
SEQUENCE 232 AA; 27340 MW; 6690703F9F9CFD63 CRC64;
                                                                                                   APETALA3.

Arabidopsis thaliana (Mouse-ear cress).

Branidopsis thaliantae, Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                              .;
&
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 37.0%; Score 51; DB 10; Length 232; Best Local Similarity 44.4%; Pred. No. 18; Matches 12; Conservative 3; Mismatches 4; Indels
                                               01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Floral homeotic protein AP3.
                        232 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: September 15, 2003, 17:25:45 Job time: 30.2286 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 QRYG-----RELRRMSDEFEGSFK 24
                         PRT;
                                                                                                                                                                                                                                                                                                                                     EMBL; AF115803; AAD51892.1; --
EMBL; AF115798; AAD51887.1; --
HSSP; P11746; 1MNM.
InterPro; IPR002487; TF_Kbox.
InterPro; IPR002100; IF_MADSbox.
Pfam; PF01486; K-box; 1.
Pfam; PF00119; SRF-TF; 1.
PRINTS; PR00404; MADSDOMAIN.
SMART; SM00432; MADS; 1.
                        PRELIMINARY;
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RESULT 15
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89.4
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                                                                                                                                                                                                                                      September 23, 2003, 09:43:16; Search time 86 Seconds (without alignments) 49.833 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /SIDSI/gogdata/genesed/genesedp-embl/AA1988.DAT:*
/SIDSI/gogdata/genesed/genesedp-embl/AA1989.DAT:*
/SIDSI/gogdata/genesed/genesedp-embl/AA1989.DAT:*
/SIDSI/gogdata/geneseq/geneseqp-embl/AA1990.DAT:*
/SIDSI/gogdata/geneseq/geneseqp-embl/AA1992.DAT:*
/SIDSI/gogdata/geneseq/geneseqp-embl/AA1992.DAT:*
/SIDSI/gogdata/geneseq/geneseqp-embl/AA1992.DAT:*
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/SIDS1/gcgdata/geneseq/genesegp-embl/AA2001.DAT:
/SIDS1/gcgdata/geneseq/genesegp-embl/AA2002.DAT:
/SIDS1/gcgdata/geneseq/genesegp-embl/AA2003.DAT:
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                                 GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
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                                                                                                                                                                                                                                                                                                                                                                                              US-09-544-664B-2
142
1 NLWAAGÉYGRELRRMSDEFVDSFKKGL/27
1 NJY-56QÍÝ410 ÚJŠEKUÞBBENDSFKKGL/27
A 5 3 4 5 6QÍÝ410 ÚJŠEKUÞBBENDSFKKGL/27
BLOSUM62
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                   using sw model
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                     Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Searched:
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                                                                                                                                                                                                                                                          Run on:
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SUMMARIES

Human BAD mutant a Human Bad protein. Amino acid sequenc Human BAD protein BBC6 protein for r Human Bcl-xL/Bcl-2 Human cell prolife Human ovarian anti PTPC-interacting T Description AAW55779 AAB13512 AAB70368 AAB48287 AAG67688 ABR39081 ABP41630 ABP56161 AAW32476 A DB Length Query Match Score 137 137 137 137 137 137 Result 80.

Mutant Bc12 compet Human Bad peptide Mutant Bc12 compet Human Bad peptide Mutant Bc12 compet Mutant Bc12 compet Human Bad peptide Mutant Bc12 compet Human Bad peptide Human Bad peptide Mutant Bc12 compet Human Bad peptide Bc12 polypeptide B Bc12 polypeptide B Bc12 polypeptide B	an.
ABG78484 AAU78610 ABG78498 AAG78617 AAG78615 AAG78616 AAU78616 AAU78620 AAU78620 AAU78620 AAU78620 AAU78621 AAU78621 AAU78621 AAU78621 AAU78622 AAU78622 AAU78622 AAU78622 AAU78622 AAU78623	ALIGNMENTS 166 AA. 19cle; Bcl2; hum 1 protein that
889.9.4.4.8.8.8.9.9.6.6.6.6.6.6.6.6.6.6.6.6.6.6.6	standard; Protein;] 998 (first entry) tein for regulating o e; cell death; cell o 6-A. 996; 96US-0665617. 996; 96US-0665617. 7-447980/41. AAT91561. ABECG gene - encodes
110 127 127 13 14 15 16 17 17 17 17 17 17 17 17 18 17 17 17 17 17 17 17 17 17 17	1 6 W32476 W32476 -JAN-1 C6 pro C6 gen C6 gen C6 Gen C7 1566331 -SEP-1 -JUN-1 -JUN-1 -JUN-1 -JUN-1
Zig.	RESULT AAW3247 LD AAW3247 XX AAW3

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detection and diagnosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                     02-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US6080847-A.
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                                                                                                                                                                                                                                                                                                                AAB13512;
                                           Sequence
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                                                                             Query Match
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Matches
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                                                     sequence is disclosed as being a protein called BBCS which requires cell death through interaction with Bcl-2. The DNA may be used for the production of the recombinant protein, which can be used in unspecified therapeutic or diagnostic procedures, as a molecular weight marker, and to raise antibodies that can be used in unspecified diagnostic or therapeutic applications and to reduce or eliminate the biological activity of the BBC6 protein in vivo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is the human Bcl-xL/Bcl-2 associated death promoting polypeptide, Bad, the binding of which to Bcl-Xl results in the induction of programmed cell death, i.e. apoptosis. Bad can be used in screening assays for compounds to treat or prevent diseases characterised by apoptotic cell death, such as neurodegenerative disorders, e.g. Alzheimer's and Parkinson's disease, amyotrophic lateral sclerosis, retinitis pigmentosa and cerebellar degeneration, and myelodysplastic syndromes, e.g. aplastic anaemia and ischemic injury including myocardial infarction, stroke and reperfusion injury. Assays can also be used to obtain apoptosis enhancing compounds to treat or prevent diseases characterised by the loss of apoptotic cell death, such as an energy and hormone dependent tumours, autoimmune
                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bad gene mediating apoptosis - used to develop products for treating e.g. neurodegenerative disease, cancers or autoimmune disease
                                          The present sequence represents a protein of 166 amino acids. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; Bcl-xL/Bcl-2 associated death promoting polypeptide; Bad; programmed cell death; apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diseases, e.g. systemic lupus erythematosus and immune-mediated glomerulonephritis and viral infections, e.g. herpesvirus, poxvirus or adenovirus infection. Bad can also be used for
                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                        Length 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human Bcl-xL/Bcl-2 associated death promoting polypeptide.
                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                          1.1e-12;
                                                                                                                                                                                                                                        Score 137.; -- BB-18.
                                                                                                                                                                                                                                                            Pred No. 1.16
0; (Mismatches
                                                                                                                                                                                                                                                                                                                                                101 NLWAAGRIGRELRRMSDEFVDSFKKGL 127
                                                                                                                                                                                                                                                                                             1 NEWAAGEFGRELRRMSDEFVDSFKKGL 27
Claim 1; Column 11-12; 7pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW55779 standard; Protein; 168 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 8; Fig 1; 41pp; English.
                                                                                                                                                                                                                                      96.5%;
ilarity 96.3%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (IDUN-) IDUN PHARM INC.
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                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 26; Conserv
                                                                                                                                                                                                    166 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAV25877
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-JUL-1998
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                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 2
AAW55779
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charter structural and chemical homology with Bel-2, is involved in cell proliferation. Its coding sequence was isolated by screening a synovial tissue cDRA library using a computer search for amino acid sequence alignments. The gene and protein can be used in the treatment of various cancers, disorders with associated inflammation such as Addison's disease, adult respiratory distress syndrome, allergies, anaemia, asthma, atherosclerosis, Crohn's disease, ulcerative colitis, diabetes mellitus, emphysema, glomerulonephritis, gout, Graves' disease, irritable bowel syndrome, lugus erythemation, osteoporosis, rheumatoid arthritis, Sjogren's syndrome and autoimmune thyroiditis, complications of cancer, haemodialysis and extracorporeal circulaing AIDS and other infectious and genetic immunodeficiencies, neurodegenerative diseases such as Alzheimer's disease and Parkinson's disease, ischaemic injuries
                                                                                                               6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      with cell proliferation for diagnosis, prevention and treatment of e.g. cancer, acquired immunodeficiency syndrome, and Parkinson's disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                such as myocardial infarction, and wasting diseases including cachexia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel polynucleotide and polypeptide sequences of proteins associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is the human APOP-1 protein. This protein, which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; cell proliferation; APOP-1; cancer; inflammation; infection; trauma; neurodegenerative disease; ischaemic injury; wasting disease.
                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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                                                      Length 168;
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                                                                                                               Indels
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Pred. No. 1.1e-12;
0; Mismatches 1;
                                                 Score 137; DB 19;
Pred No. 1.1e-12;
); Mismatches 1,
                                                                                                                                                                                                   103 NLWAAQRYGRELRRMSDEFVDSFKKGL 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ů,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human cell proliferation protein APOP-1
                                                                                                                                                                 1 NLWAAQEYGRELRRMSDEFVDSFKKGL 27
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                                                                                                                                                                                                                                                                                                                                                                 AAB13512 standard; protein; 168 AA
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                                                      96.5%;
96.3%;
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Best Local Similarity 96.39
Watches 26; Conservative
                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hillman JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-451230/39
                                                                                Local Similarity
les 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA;
168 AA;
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AAB70368

δ g

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Homo sapiens.
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                                                                                                                                                                                                                      02-APR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zhang H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                  AAB48287
                                                                                                                                                                             AAB48287;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 6
                                                                                            RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes an isolated or synthetic polypeptide

(I) comprising a less than full length amino acid sequence of a mutant

Bel-XL/Bel-2 associated cell death regulator polypeptide (BAD) or its

fragment, which contains amino acid substitutions at Seril8 of a human

fragment, which contains amino acid substitutions at Seril8 of a human

EAD, SeriS5 of a murine BAD. (I) has immunostimulant, neuroprotective,

BAD (shorter murine BAD). (I) has immunostimulant, neuroprotective,

noctropic, antiischaemic, vulnerary, cytostatic, antiviral,

antiarthritic, antiinflammatory and immunosuppressive activities, and

can be used as an apoptosis inducer or inhibitor. BAD polypeptides and

polynucleotides can be used for screening candidate compounds and drugs

for activity that promote cell survival or apoptosis. Other uses include

inducing or inhibiting apoptosis in a cell. Candidate compounds

identified and (mutant) BAD polypeptides are useful in treating

death, reperfusion cell death, wound healing, cancer, viral infections,

intriarment and mutant and mutant, anthritis, infertility, inflammation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      autoimmune diseases. The present sequence represents a specifically claimed human BAD mutant amino acid sequence from the present invention.
                                                                                                                                                                                                                                                                                                                     Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis; immunostimulant; neuroprotective; nootropic; antilschaemic; vulnerary; cytostatic; antiviral; autiarthritic; antinflammatory; wound healing; immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer; immunodeficiency disease; neurodegenerative disease; viral infection; ischaemic cell death; reperfusion cell death; arthritis; infertility; lymphoproliferative condition; inflammation; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide, useful for screening for candidate compounds which induce or inhibit apoptosis, comprises amino acid substitutions at Serl18, Serl55 or Serl13 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Andels
                                                                                                                                                                                                                                                                               Human BAD mutant amino acid sequence SEQ ID NO:1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 137; DB 22;
Pred. No. 1 1e-12;
0; Mismatches 1;
                             27
NIWAAQEYGRELRRMSDEFVDSFKKGL
                                                                                                                                                     AAB70368 standard; protein; 168 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 147; 157pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (APOP-) APOPTOSIS TECHNOLOGY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96.5%;
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                                                                                                                                                                                                                                        (first entry)
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Best Local Similarity 96.39
Matches 26; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           168 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                               AAB70368;
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The invention relates to methods of altering the polypeptide levels in a cell, using proteins selected from S-phase kinase associated proteins 1 and 2 (SKP1, SKP2), SKP2-like proteins (ZF) and CUL-1 (a member of the cullin/ CDC53 family of proteins). The method is useful for altering the level of p27, cyclin E, Max, Mad, c-Myc, MDM2, p53, Bax, Bad or Bcl-2 polypeptide in a cell. SKP2 and SKP2-like protein levels are useful for detecting tumours, and in monitoring tumor treatment in a mammal. Agents that modulate interactions between SKP and target proteins are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modulating polypeptide levels in a cell, diagnosing and treating tumor, involves altering levels of proteins such as S-phase kinase associated proteins 1, 2 and cullin/CDC53 proteins -
                                                                                                                                                                                                                                                                                                                                                                             S-phase kinase associated protein; SKP1; SKP2; SKP2-like protein; ZF; CUL-1; cullin; CDC53; p27; cyclin E; Max; Mad; c-Myc; MDM2; p53; Bax; Bad; Bc1-2; tumour; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; cell proliferation; APOP-1; APOP-2; APOP-3; apoptosis; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Amino acid sequence of protein associated with cell proliferation-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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Pred. No. 1.1e-12;
Mismatches 1
NIMAAQREGERRASDEFVDSFKKGL 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NEWAAQRYGRELRRMSDEFVDSFKKGL 129
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96.3%; Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 5; Page 102-103; 162pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA.
                                                                                                                                                                  standard; protein; 168 AA.
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N-PSDB; AAC84599.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      168 AA;
                                                                                                                                                                                                                                                                                                                             Human Bad protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      treating tumours.
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Human BAD protein SEQ ID NO: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                           168 AA;
                                                                                                                                                                                                                     N-PSDB; ABZ81200.
                                                                          WO2003012049-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mac.
Local Sim.
26;
                                                       Homo sapiens
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                                                                                               13-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 8
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0
                                                              10..13 /note= "potential casein kinase II phosphorylation site"
                                                                                              /note= "potential casein kinase II phosphorylation site"
                                                                                                                                                                                                                 /note= "potential casein kinase II phosphorylation site"
                                                                                                                                        /note= "potential casein kinase II phosphorylation site"
                                                                                                                                                                                             /note= "potential protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents a human protein which is associated with cell proliferation, designated APOP-1. The specification also describes APOP-2 and APOP-3. The APOP polypeptides are useful for diagnosing, preventing or treating disorders associated with abnormal cell proliferation and apoptosis. The polypeptides and composition are particularly useful for treating or preventing cancer (e.g. brain or breat cancer), a disorder associated with an increase in apoptosis (e.g. Alzheimer's disease or Parkinson's disease) or inflammation (e.g. allergies, gout, osteoarthritis or bronchitis).
                                                                                                                                                                                                                                                                                                                                                                                                 New polypeptides associated with cell proliferation, useful for preventing or treating cancer (e.g. brain cancer), a disorder associated with an increase in apoptosis (e.g. Alzheimer's disease) or
brain cancer; breast cancer; Alzheimer's disease; Parkinson's disease;
inflammation; allergy; gout; osteoarthritis; bronchitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                   /note= "potential protein kinase C phosphorylation
                                                                                                                                                            /note= "potential cAMP- and cGMP-dependent protein kinase phosphorylation site"
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96.5%; Score 137; DB 22; Length 168; 96.3%; Pred. No. 1.1e-12; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                Corley NC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   103 NLWAAQRYGRELRRMSDEFVDSFKKGL 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 NLWAAQEKGRELRRMSDEFVDSFKKGL 27
                                                                                                                                                                                                                                                                                                                                                Shah P,
                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example; Fig 1A-C; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABR39081 standard; Protein; 168
                                                                                                                                                                                                                                                                                 99US-0410372.
                                                                                                                                                                                                                                                                                                                           (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                               Lal P,
                                                                                                                                                                                                                                                                                                      97US-0985335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                  115..118
                                                                                                                                                                                  124..126
                                                                                                                                                                                                      153..156
                                                                                                                                                                                                                                                                                                                                                                                                                                    inflammation (e.g. gout)
                                                                                                                                                                                                                                                                                                                                               Hillman JL, Yue H,
                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-569961/64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 26; Conser
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                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAH78430.
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                                                              Modified-site
                                                                                                        Modified-site
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                                                                                                                                                  Modified-site
                                                                                                                                                                                                      Modified-site
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                                                                                                                                                                                                                                                                                                      04-DEC-1997;
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                                 Homo sapiens
                                                                                                                                                                                                                                       US6281334-B1
                                                                                                                                                                                                                                                            28-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour; ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; infection; cardiovascular disorder; respiratory disorder; neurological disorder; cardiovascular disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antiinflammatory; gynaecological; reproductive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes a method (MI) for inducing apoptosis in a cell infected with herpes simplex virus (HSV), which comprises administering to the cell, a composition having an agent that inhibits phosphorylation of pro-apoptotic polypeptide BAD by HSV US3. Also described is a method (M2) for treating a patient infected with HSV, by administering to the patient, a composition comprising a peptide comprising a sequence of 4-100 continuous amino acids of a 168 residue amino acid sequence (see ABB39081), where the peptide comprises seril2, seril5, or their combinations. BAD has virucide activity. MI is useful for inducing apoptosis in a cell infected with HSV, where the cell is in a human. M2 is useful for treating a patient infected with HSV. The present sequence represents human BAD, which is used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Inducing apoptosis in a cell infected with herpes simplex virus, HSV, by administering to the cell, a composition comprising an agent that inhibits phosphorylation of pro-apoptotic polypeptide BAD by HSV US3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
Human; BAD; herpes simplex virus; HSV; US3; herpes virus; apoptosis;
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Pred. No. 1.1e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human ovarian antigen HCE4K28, SEQ ID NO:2762.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 NLWAAØEYGRELRRMSDEFVDSFKKGL 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 15; Page 166-167; 192pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABP41630 standard; Protein; 201 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96.5%;
                                                                                                                                                                                                                                                                                                                                                                         31-JUL-2002; 2002WO-US24177.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-JUL-2001; 2001US-308929P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Munger J, Roizman B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYCH-) UNIV CHICAGO
                                           virucide; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-248168/24
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Human; Bc12; Bc1X1; programmed cell death; apoptosis; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-619260/66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25 AA;
                                                                                                                                                                                                                                  WO200261105-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-NOV-2002
                                                                                                                                                                                                                                                                             08-AUG-2002.
                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABG78484;
                                                                                                                                                                                                                                                                                                                                                                                                   (INSP )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
ABG78484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP4228) and to cDNAs encoding them (ABD54131-ABO56305), and also encompasses polypeptides 90% identical and polynuclectides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen to polynuclectides and polypeptides in diagnosing, and the use of ovarian antigen polynuclectides and polypeptides in diagnosing, treating, prognosing or preventing various ovary and/or breast-related disorders. Such conditions include ovarian cancer and breast cancer, and metastatic tumours of ovarian or breast origin, reproductive system disorders (e.g., infertility, disorders of pregnancy, anovulation, polycystic ovary syndrome, ovarian cysts, and dysmeorrhoea), endorine disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and immunodeficiencies, autoimmune opphoritis, systemic lupus erythematosus), blood-related disorders (e.g., anaemia), cardiovascular disorders and urinary system disorders, neurological disorders, gastrointestinal disorders and urinary system and also he used in forman antigen polypeptides and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polynucleotides may also be used in screening for compounds which modulate ovarian antigen expression or activity. The polynucleotides may further be used for gene therapy, chromosome mapping, in the identification of individuals and in forensic analysis, and the polypeptides may be used as food additives or to prepare antibodies useful in disease diagnosis, drug targeting and phenotyping. The present sequence represents a human ovarian antigen of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                              Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96.5%; Score 137; DB 23; 96.3%; Pred. No. 1.3e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 11; SEQ ID No 2762; 2922pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          111 NLWAAQRYGRELRRWSDEFVDSFKKGL 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 NLWAAÓEÝGRELRRMSDEFVDSFKKGL 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABP56161 standard; peptide; 25 AA.
                                                                                                                                                                                         07-JUN-2000; 2000US-209467P.
                                                                                                                                             07-JUN-2001; 2001WO-US18569.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-MAR-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best_Local Similarity 96.3
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 neurological diseases
                                                                                                                                                                                                                                (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                                         Birse CE, Rosen CA;
                                                                                                                                                                                                                                                                                                                   WPI; 2002-147878/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          201 AA;
                                                                                                                                                                                                                                                                                                                                        N-PSDB; ABO54707
                                                           WO200200677-A1.
                   Homo sapiens.
                                                                                                      03-JAN-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABP56161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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The present invention describes a chimeric bifunctional molecule (I) comprising at least a first functional molecule covalently linked to a second functional molecule, which is able to modulate the activity of the permeability transition pore complex (PPFC) of the mitochondria.

(I) has the function of specifically targeting and entering a tissue call population. The second functional molecule has the function of specifically targeting and entering a tissue call by apoptosis by requlating the opening or the closing of the PPFC of the mitochondria or its fragment. (I) has virucide, neuroprotective, vasotropic and cytostatic activities, and can be used as a mitochondrial permeability transition pore complex (PPPC) modulator. (I) is useful for treating or preventing a pathological infection or disease. (I) is also useful for regulating cell death regulatory molecules, specifically the apoptogenic function of the PPPC, for treating e.g. cancer, isobaemia, neurodegenerative diseases, fulminant hepatitis or viral infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents a PTPC-interacting TOX peptide which is given in the exemplification of the present invention.
                                                                                                                                                                                                                                               apoptogenic; ischaemia; neurodegenerative disease; fulminant hepatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                       permeability transition pore complex; virucide; neuroprotective; vasotropic; cytostatic; infection; cell death regulation; apoptosis; mitochondrial permeability transition pore complex modulator; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New chimeric bifunctional molecules that target specific cells and regulate the apoptosis function of the permeability transition pore complex of the mitochondria, useful for treating or preventing e.g. cancer or ischemia -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                 Mitochondrial membrane permeabilisation; mitochondrion; PTPC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred, No. 4.2e-12
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89.4%; Score 127;
96.0%; Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 NLWAAQEYGRELRRMSDEFVDSFKK 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIMAAQRYGRELRRMSDEFVDSFKK 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABG78484 standard; Peptide; 25 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Briand J;
PTPC-interacting TOX peptide #27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 9; Page 11; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-2002; 2002WO-EP01633.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-FEB-2001; 2001US-265594P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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Best Local Similarity 96.0
Matches 24; Conservative
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DXX E

Qy 음 Η;

Shang

Matayoshi E,

Swift KM,

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Nettesheim DG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-NOV-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABG78490;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fesik SW,
                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                    bind
                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABG78490
 g
                                                                                                                                                                                                                                                                                                                                                                                                       QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                            This invention relates to a novel mutant protein which is derived from a wild type human Bc1-2 protein. The mutant is created by replacing a sequence of amino acid residues comprising a flexible loop from the wild type Bc1-2 protein with an amino acid sequence comprising at least two acidic amino acids. The mutant Bc1-2 protein comprises a 166 residue shown in the specification. The invention also comprises an assay for identifying substances that bind to the Bc1-2 protein. The protein sequences of the invention are useful in biological assays to identify substances that block the ability of Bc1-2 to inhibit programmed cell death or apoptosis. The present sequence represents a human Bc12 peptide of the invention.
                                                                                                                                                                                                                                             New mutant Bcl-2 proteins derived from a wild type human Bcl-2 protein, useful in biological assays to identify substances that block the ability of Bcl-2 to inhibit programmed cell death or apoptosis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; Bad; Bcl-2; apoptosis; cancer; inducer; degenerative disease;
ischemic injury; suppressor; BH3 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human Bad peptide #10 which binds to a member of the Bcl-2 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Joseph MK, Olejniczak ET, Petros AM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89.4%; Score 127; DB 23; 96.0%; Pred. No. 4.2e-12;
                                                                                                                                                                                           Nettesheim DG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 NLWAAQEYGRELRRMSDEFVDSFKK 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A.A
                                                                                                                                                                                                                                                                                                     Example 2; Page 17; 36pp; English
                                                                                                                                                                                           Yoon H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU78610 standard; Peptide; 25
                                                                                                        15-NOV-2001; 2001WO-US45693.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-SEP-2001; 2001WO-US27410.
                                                                                                                                   20-NOV-2000; 2000US-0716395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 96.0
nes 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Meadows RP,
                                                                                                                                                                                           Petros AM,
                                                                                                                                                                                                                  WPI; 2002-490141/52.
                                                                                                                                                               (ABBO ) ABBOTT LAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ABBO ) ABBOTT LAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25 AA;
                                                   WO200240530-A2.
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           Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                              23-MAY-2002
                                                                                                                                                                                        Fesik SW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fesik SW,
                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU78610;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 11
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The present invention relates to new peptides that are derived from a wild-type human Bad peptide and are able to bind to a member of the Bol-2 protein family. The peptides are useful, when labelled, in competitive/displacement assays for identifying substances that bind to members of the Bol-2 family and may induce or suppress apoptosis so are potentially useful for treating cancer (inducers) or degenerative diseases or ischemic injury (suppressors). The peptides of the invention have high helix propensity, maintain the contacts of the wild-type Bad peptide and, compared with the Bad peptide, may have better physical properties, particularly solubility. The present sequence represents one of a collection of Bad peptides (AAU78601-AAU78631) that were derived from the BH3 domain of the human wild-type Bad peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention relates to a novel mutant protein which is derived from a wild type human Bcl-2 protein. The mutant is created by replacing a sequence of amino acid residues comprising a flexible loop from the wild type Bcl-2 protein with an amino acid sequence comprising at least two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New mutant Bcl-2 proteins derived from a wild type human Bcl-2 protein, useful in biological assays to identify substances that block the ability of Bcl-2 to inhibit programmed cell death or apoptosis
                                                                   derivatives of Bad peptide, useful for identifying compounds that 1 to Bcl-2 proteins, potential agents for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; Bcl2; BclX1; programmed cell death; apoptosis; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mutant Bcl2 competitive binding assay peptide #7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.2e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nettesheim DG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 127;
Pred. No. 4
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                                                                                                                                                                                                        Claim 18; Page 18; 31pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89.48;
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                                                                                                                                           degenerative disease
WPI; 2002-292254/33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to new peptides that are derived from a wild-type human Bad peptide and are able to bind to a member of the Bol-2 protein family. The peptides are useful, when labelled, in competitive/displacement assays for identifying substances that bind to members of the Bol-2 family and may induce or suppress apoptosis so are potentially useful for treating cancer (inducers) or degenerative diseases or ischemic injury (suppressors). The peptides of the invention have high helix propensity, maintain the contacts of the wild-type Bad peptide and, compared with the Bad peptide, may have better physical properties, particularly solubility. The present sequence represents one of a collection of Bad peptides (AAU78601-AAU78631) that were derived from the BH3 domain of the human wild-type Bad peptide.
acidic amino acids. The mutant Bcl-2 protein comprises a 166 residue shown in the specification. The invention also comprises an assay for identifying substances that bind to the Bcl-2 protein. The protein sequences of the invention are useful in biological assays to identify substances that block the ability of Bcl-2 to inhibit programmed cell death or apoptosis. The present sequence represents a human Bcl2 peptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          wew uerlvatives of Bad peptide, useful for identifying compounds that bind to Bcl-2 proteins, potential agents for treating cancer and degenerative disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                     Human; Bad; Bcl-2; apoptosis; cancer; inducer; degenerative disease; ischemic injury; suppressor; BH3 domain.
                                                                                                                                                                                                                                                                                                                                                            Human Bad peptide #17 which binds to a member of the Bcl-2 family.
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                                                                                                                                   Score 124; DB 23; Length 25;
Pred. No. 1.2e-11;
L; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ows RP, Joseph MK, Olejniczak ET,
Swift KM, Matayoshi E, Zhang H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 124; DB 23; 1
Pred. No. 1.2e-11;
1; Mismatches 1;
                                                                                                                                                                                         1 NLWAAQEYGRELRRMSDEFVDSFKK 25
                                                                                                                                                                                                       1 NIWAAQRYGRELRRMSDEFVDAFKK 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 14; 31pp; English.
                                                                                                                                                                                                                                                                               AAU78617 standard; Peptide; 25 AA
                                                                                                                                   87.3%;
92.0%;
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92.0%;
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                                                                                                                              Query Match 87.33
Best Local Similarity 92.09
Matches 23; Conservative
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Best Local Similarity 92.09
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Meadows RP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-292254/33.
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                                                                                                           25 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200220568-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fesik SW,
                                                                                                            Sequence
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This invention relates to a novel mutant protein which is derived from a wild type human Bcl-2 protein. The mutant is created by replacing a sequence of amino acid residues comprising a flexible loop from the wild type Bcl-2 protein with an amino acid sequence comprising at least two acidic amino acids. The mutant Bcl-2 protein comprises a 166 residue shown in the specification. The invention also comprises an assay for identifying substances that bind to the Bcl-2 protein. The protein sequences of the invention are useful in biological assays to identify substances that block the ability of Bcl-2 to inhibit programmed cell death, or apoptosis. The present sequence represents a human Bcl2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New mutant Bcl-2 proteins derived from a wild type human Bcl-2 protein, useful in biological assays to identify substances that block the ability of Bcl-2 to inhibit programmed cell death or apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                          Human; Bcl2; BclXl; programmed cell death; apoptosis; mutant; mutein.
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                                                                                                                                                                                                                                                                                                                                                   Mutant Bcl2 competitive binding assay peptide #5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 123; DB 23;
Pred. No. 1.7e-11;
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0; Mismatches
NLWAAQEYGRELRRMSDEFVDSFKK 25
                             1 NIWAAQRYGREIRRMSDEFVDAFKK 25
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                                                                                                                                                                                      ABG78488 standard; Peptide;
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Best Local Similarity 92.0
Matches 23; Conservative
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Synthetic.
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                                                                                                                                      RESULT 14
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                                                                                                                                                                                                                                                                                                                                    New mutant Bcl-2 proteins derived from a wild type human Bcl-2 protein, useful in biological assays to identify substances that block the ability of Bcl-2 to inhibit programmed cell death or apoptosis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                 Human; Bcl2; BclXl; programmed cell death; apoptosis; mutant; mutein
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Best Local Similarity 92.0%; Pred. No. 1.7e-11;
Matches 23; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                       Yoon H, Nettesheim DG;
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                                                                                                                                                                                                                                                                       Fesik SW, Petros AM,
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                                                  Homo sapiens.
Synthetic.
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Search completed: September 23, 2003, 09:47:13 Job time: 87 secs

Sequence 26276, A Sequence 17508, A Sequence 18296, A Sequence 2, Appli

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LENGTH: 166 amino acids
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Best Local Similarity
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COUNTRY: US,
ZIP: 32606
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Qγ
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Sequence 69, Appl
Sequence 69, Appl
Sequence 18729, A
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1, Appli
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Sequence 2, Appli
                                                                                         September 23, 2003, 09:43:16 ; Search time 30 Seconds
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38.080 Million cell updates/sec
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Sequence 2,
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Sequence 7,
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1:    /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2:    /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3:    /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4:    /cgn2_6/ptodata/1/iaa/BB_COMB.pep:*
5:    /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6:    /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6:    /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
            GenCore version 5.1.6
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US-08-375-257-3
US-08-33-555-110
US-08-733-505A-55
US-08-733-505A-55
US-08-733-505A-56
US-08-733-505A-58
US-08-733-505A-58
US-08-733-505A-58
US-08-733-505A-58
US-08-733-505A-58
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US-08-985-335-7
US-09-410-372-1
US-09-375-257-2
US-08-333-565-2
US-08-733-565-2
US-08-733-505A-1
US-08-733-505A-12
US-08-733-505A-13
US-08-733-505A-13
                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
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142
1 NLWAAQEYGRELRRMSDEFVDSFKKGL/27
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Maximum Match 100%
Listing first 45 summaries
                                                                    protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Lengta
                                                                                                                                                                                                          Scoring table:
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                                                                                                                                                   Title:
Perfect score:
                                                                  OM protein
                                                                                                                                                                                                                                                  Searched:
                                                                                                                                                                               Sequence:
                                                                                             Run on:
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Sequence 56, Appl
Sequence 20, Appl
Sequence 20, Appli
Sequence 7710, Ap
Sequence 7710, Ap
Sequence 1058, Ap
Sequence 1058, Ap
Sequence 6559, Ap
Sequence 8, Appli
Sequence 10, Appli
Sequence 10, Appli
Sequence 23461, Appli
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Sequence 2, Application US/08665617
Patent No. 566316
GENERAL INFORMATION:
APPLICANT: Xudong, Yin
TITLE OF INVENTION: Gene and Protein for Regulation of Cell Death
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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US-09-252-9118-18296
US-09-252-9918-18296
US-08-379-5568-2
US-08-867-087B-40
US-08-867-087B-40
US-09-11-451-56
US-09-252-9918-20008
US-09-328-352-7710
US-09-328-352-7710
US-09-328-352-7449
US-09-328-352-7449
US-09-328-352-7449
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,617
                                                                                                                                                                                                                                                                            US-09-091-501B-8
US-09-091-501B-10
US-09-252-991A-23461
US-08-261-660A-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421-N.W. 41st Street, Suite A-1
CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96.3%; Score 137; DE
96.3%; Pred. No. 5.38
cive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFCATION: 530
ATTORNET/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: CL-8
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEPHONE: (352) 375-800
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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COMPUTER REALABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
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CITY: Palo Alto
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                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: sing
TOPOLOGY: linear
IMMEDIATE SOURCE:
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LIBRARY: SYNCLE
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COUNTRY: U
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                                                         GENERAL INFORMATION:
APPLICANT: Horne, William A.
APPLICANT: Oltersdorf, Tilman
TITLE OF INVENTION: Human BAD Polypeptides, Encoding Nucleic
TITLE OF INVENTION: Acids and Methods of Use
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96.5%; Score 137; DB 2; Length 168; 96.3%; Pred. No.-5.4e-14;
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; Sequence 1, Application US/08985335
; Patent No. 6080847
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
; APPLICANT: Shah, Pureli
; APPLICANT: Shah, Pureli
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
; TITLE OF INVENTION: PROLIFERATION
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Forter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP.
                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: ELOPPY disk
COMPUTER: ELOPPY disk
COMPUTER: ELOPPY disk
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/717,123
FILING DATE: 20-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: P-ID 1929
TELECOMMONICATION INFORMATION:
TELECOMMONICATION INFORMATION:
TELEFRAX: (619) 535-9901
TELEFRAX: (619) 535-9901
TELEFRAX: (619) 535-9901
TELEFRAX: (619) 535-9949
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
TYPE: protein
US-08-717-123-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       103 NLWAAQRYGRELRRMSDEFVDSFKKGL 129
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                   Sequence 2, Application US/08717123 Patent No. 5965703
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                                                                                                                                                                                                                                                      CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
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Best Local Similarity 96.3
Matches 26; Conservative
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MEDIUM TYPE: Diskette
US-08-717-123-2
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CURRENT APPLICATION NAME: U.S. OF WILSOAM VERSION 2.0

APPLICATION WINGER: U.S. OF 98, 335

FILING DATE:

RILLING DATE:

RELIGION DATE:

RESISTATION WINGER: 10, 74

APPLICATION WINGER: 10, 7, 9

RESISTATION WINGER: 10, 7, 10

RESISTATION: 10, 10

RESISTATION WINGER: 10, 10

RESISTATION WINGER: 10, 10

RESISTATION WINGER: 10, 10

RESISTATION: 10, 10

RESISTATION
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LIBRARY: GenBa
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                                                                                                                                                                                                                                                                                                                                                                                            94304
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COUNTRY:
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                                                                                      US-09-410-372-7
                       103
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                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Fenry
APPLICANT: Lal, Preeti
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: PROLIFERATION
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96.5%; Score 137; DB 3; I 96.3%; Pred, No. 5.4e-14.

Live 0; Mismatches 1;
                                                                                                                                                                       96.5%; Score 137; DB 3; 96.3%; Pred No. 5.48-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER REDABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: STESTED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/410,372
                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Dr.
                                                                                                                                                                                                                                                                103 NLWAAQRYGRELRRMSDEFVDSFKKGL 129
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FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Bilings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-04
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEPAX: 650-845-4166
: INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/985,335
                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/09410372
Patent No. 6281334
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
HOMEDIATE SOURCE:
LIBRARY: Genbank
CLONE: 1683637
US-08-985-335-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 168 amino acids TYPE: amino acid STRANDEDNESS: single
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Best Local Similarity 96.3
Matches 26; Conservative
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Best Local Similarity 96.3
Matches 26; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
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APPLICANT: Hillman
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IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; CLONE: 358673
US-09-410-372-1
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Gaps
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; Patent No. 6504022
; GENERAL INFORMATION:
; APPLICANT: Horne, William A.
; APPLICANT: Oltersdorf, Tilman
; TITLE OF INVENTION: HUMN BAD POLYPEPTIDES, ENCODING NUCLEIC
; TITLE OF INVENTION: ACIDS AND METHODS OF USE
; FILE REFERENCE: 480140.428D1
; CURRENT APPLICATION NUMBER: US/09/375,257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 168
                                           GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
APPLICANT: Lal, Preeti
APPLICANT: Call, Preeti
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
TITLE OF ENVENTION: PROLIFERATION
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/410,372
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                                                                                                                                                                                                                                                                                     ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  103 NIWAAQRYGRELRRMSDEFVDSFKKGL 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/985,335
FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: PF-0421
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
Sequence 7, Application US/09410372 Patent No. 6281334
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96.3%;
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MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 168 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 96.3
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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US-08-733-505A-1
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                                                                                                                                                                                     96.5%; Score 137; DB 4; Length 168; 96.3%; Pred. No. 5.4e-14; Live 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08333565
; Patent No. 5622852
; GENERAL INFORMATION:
    APPLICANT: KORSMEYER, Stanley J.
    TITLE OF INVENTION: Bel-x/Bel-2 ASSOCIATED CELL DEATH
    TITLE OF INVENTION: REGULATOR
    NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
    ADDRESSE: Townsend and Townsend Khourie and Crew
    STREET: 379 Lytton Avenue
    CITY: Palo Alto
    STARE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Deduced amino acid sequence of mouse BAD."
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                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE PATENTIN RELEASE #1.0, Version #1.25 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/333,565 FILING DATE: 31-0CT-1994 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: Smith, William M REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 109; DB 1;
Pred. No. 1.7e-09;
0; Mismatches 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 15726A-000700
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
CURRENT FILING DATE: 1999-08-16
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 168
                                                                                                                                                                                                                                                                                            103 NLWAAQRKGRELRRMSDEFVDSFKKGL 129
                                                                                                                                                                                                                                                                    1 NIWAA@BYGRELRRMSDEFVDSFKKGL 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     140 NIWAAQRYGRELRRMSDEFEGSFK 163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 76.8%;
Best Local Similarity 87.5%;
Matches 21; Conservative (
                                                                                                                                                                                                                                26; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
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                                                                                                     TYPE: PRT
CRGANISM: Homo sapiens
US-09-375-257-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: Protein
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                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                           US-08-333-565-2
                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                              Matches
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Patent No. 5856445
GENERAL INFORMATION:
APPLICANT: KORSMENER, STANLEY J.
ATILE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
TITLE OF INVENTION: BCI-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                          GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
IITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
TITLE OF INVENTION: REGULATOR
                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend Khourie and Crew STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patentin Release #1.0, Version #1.25
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APPLICATION NUBBER: US/08/661,479
FILING DATE: 11-UN-1995
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726A-0007
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               140 NLWAAQRYGRELRRMSDEFEGSFK 163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
US-08-661-479-2; Sequence 2, Application US/08651479; Patent No. 5834209
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: Protein LOCATION: 1..204 OTHER INFORMATION: 0THER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 21; Conserv
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; Sequence 14, Application US/08733505A
; Patent No. 5856445
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
TITLE OF INVENTION: BCL. XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 13, Application US/08733505A
Patent No. 5856445
GENERAL INFORMATION:
APPLICANT: KORSMETER, STANLET J.
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
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                                                                                               Length 204;
                                                                                                                                                             Indels
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                                                                                            Score 109; DB 2;
Pred. No. 1.7e-09;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: HOWELL & HAFERKAMP, L.C. STREET: 7733 FORSYTH BLVD., SUITE 1400 CITY: ST. LOUIS STATE: MISSOURI
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CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          140 NLWAAQRYGRELRRMSDEFEGSFK 163
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 9654
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEPAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                         Query Match 76.8%;
Best Local Similarity 87.5%;
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 204 amino acids TYPE: amino acid
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; MOLECULE TYPE: peptide US-08-733-505A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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US-08-733-505A-13
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Sequence 12, Application US/08733505A

Patent NO. 5856445

GENERAL INFORMATION:

APPLICANT: KORSMEYER, STANLEY J.

TITLE OF INVENTION: BELL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR

NUMBER OF SEQUENCES: 60

CORRESPONDENCE ADDRESS:

STREET: 7733 FORSYTH BLVD., SUITE 1400

CITY: ST. LOUIS

STATE: MISSOURI

STATE: USA
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ZIP: 63105
COMPUTER READABLE FORM:
MEDITUR TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
FILING DATE:
                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/733,505A FILING DATE:
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35,197
35, 965458
                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOKET NUMBER: 96545
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 9654;
TELEPHONE: (314) 727-5188
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-5188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
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US-08-733-505A-12
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RESULT 15
US-09-375-257-3
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Sequence 3, Application US/08717123
Sequence 3, Application US/08717123
Sequence 3, Application US/08717123
Sequence 3, Application US/08717123
GENERAL INFORMATION:
APPLICANT: Horne, William A.
APPLICANT: Oltersdorf, Tilman
TITLE OF INVENTION: Human BAD Polypeptides, Encoding Nucleic
TITLE OF INVENTION: Acids and Methods of Use
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76.8%; Score 109; DB 2; Length 204; 87.5%; Pred. No. 1.7e-09; ative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: Campbell and Flores STREET: 4370 La Johla Village Drive, Suite 700 STATE: California COUNTRY: United States
                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/733,505A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
: 7733 FORSYTH BLVD., SUITE 1400
ST. LOUIS
MISSOURI
                                                                                                                                                                                                                                                        APPLICATION:
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 965458
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
TELEFAX: (314) 727-6092
TELEFAX: (314) 727-6092
SEQUENCE CHARACTERISTICS:
TWOTH: 204 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/717,123
FILING DATE: 20-SEP-1996
CLASSIFICATION: 435
ATTORNEY INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-ID 1929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           140 NIWAAQRYGRELRRMSDEFEGSFK 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-ID 1929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 NLWAAQEYGRELRRMSDEFVDSFK 24
                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 87.59
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-733-505A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                        63105
                                                STATE: M
COUNTRY:
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Sequence 3, Application US/09375257

GENERAL INFORMATION:
APPLICANT: Horne, William A.
APPLICANT: Oltersdorf, Tilman
TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC
TITLE OF INVENTION: ACIDS AND METHODS OF USE
FILE REFERENCE: 480140.42801
CURRENT APPLICATION NUMBER: US/09/375,257
CURRENT FILING DATE: 1999-08-16
NUMBER OF SEQ ID NOS: 15
SOTTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 204
                                                                                                                                                                                                     0
                                                                                                                                              Query Match 74.6%; Score 106; DB 2; Length 204; Best Local Similarity 83.3%; Pred. No. 5e-09; Matches 20; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74.6%; Score 106; DB 4; Length 204;
83.3%; Pred. No. 5e-09;
Live 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: September 23, 2003, 09:45:40 Job time : 32 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             140 NLWAAQRYGRELRRMTDEFEGSFK 163
                                                                                                                                                                                                                                                                                  140 NIWAAQRYGRELRRMTDEFEGSFK 163
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                                                                                                                                                                                                                                                    1 NLWAAQEYGRELRRMSDEFVDSFK 24
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 83.33
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CRGANISM: Mus musculus US-09-375-257-3
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Sequence 2, Appli
Sequence 1, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 258, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 17, Appli
Sequence 2, Appli
Sequence 284, Appli
Sequence 583, Appli
Sequence 1, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                September 23, 2003, 09:47:20; Search time 389 Seconds (without alignments) 10.335 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Published_Applications_AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

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16: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

17: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/US10B_NEW_PUB.pep:*

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18: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-894-657-1
US-09-894-657-7
US-10-209-967-2
4 US-10-066-179-2
5 US-10-059-261-258
2 US-10-059-261-258
2 US-10-059-378-3
4 US-10-066-179-3
5 US-10-174-105A-147
2 US-10-174-105A-147
2 US-10-174-1394
1 US-09-841-132-583
4 US-10-007-693-97
5 US-10-092-750-1
                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
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142
1 NLWAAQEYGRELRRMSDEFYDSFKKGL 27
                                                                                                                                                                                                                                                                                                        556269 seqs, 148893369 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                     OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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137
137
137
127
109
106
57
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47
46.5
46.5
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Perfect score:
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                                                                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Database:
                                                                                                                                                                                                                                                                                                        Searched:
                                                                                                                                                                                                                  Sequence:
                                                                                                          Run on:
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danen edanen edanen edanen	Sequence 10939, A Sequence 13669, A Sequence 46, Appl Sequence 37, Appl Sequence 75, Appl Sequence 38, Appl	Sequence 11148, A Sequence 11541, A Sequence 10793, A Sequence 18, Appl Sequence 218, App	ednen ednen ednen ednen ednen	Sequence 218, App Sequence 218, App Sequence 218, App Sequence 218, App Sequence 218, App Sequence 218, App Sequence 218, App
US-09-815-242-13424 5 US-10-092-750-241 5 US-10-136-444-8 2 US-10-342-224-110 5 US-10-342-224-110	0.05-10-150-761-12 0.05-10-156-761-12 0.05-10-156-081-13 0.05-10-234-432-3 0.05-10-234-432-3 0.05-10-234-432-3	US-09-815-242-111 US-10-156-761-11 US-09-815-242-107 US-09-854-286-18 US-09-854-286-18	2 0S 10 140 021 21 2 US 10 140 021 21 2 US 10 140 274 21 2 US 10 140 471 21 2 US 10 140 927 21 2 US 10 -140 924 21 0S -10 -140 924 21	S-10-140-926-2 S-10-141-698-2 S-10-141-704-2 S-10-141-704-2 S-10-142-421-2 S-10-142-767-2
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RESULT 1
US-09-922-378-2
Sequence 2, Application US/09922378
Patent No. US20020037869A1
GENERAL INFORMATION:
APPLICANT: Horne, William A.
TITLE OF INVENTION: HUMAN BAD POLIYPEPTIDES, ENCODING NUCLEIC
TITLE OF INVENTION: ACIDS AND METHODS OF USE
FILE REFERENCE: 480140.428D3
CURRENT APPLICATION NUMBER: US/09/922,378
CURRENT FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96.5%; Score 137; BB_9; 1
96.3%; Pred. No_4::2e-12x,
tive 0; MigMatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                            SEQ ID NO 2
LENGTH: 168
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: DX
US-09-922-378-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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ALIGNMENTS

103 NLWAADRYGRELRRMSDEFVDSFKKGL 129 1 NLWAAØEYGRELRRMSDEFVDSFKKGL~27-Sequence 1, Application US/09894657 Patent No. US20020098569A1 GENERAL INFORMATION: APPLICANT: Hillman, Jennifer L. Yue, Henry Lal, Preeti Shah, Purvi RESULT 2 US-09-894-657-1 δŏ g

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Gaps

; 0

Indels

Best Local Similarity 96.3 Matches 26; Conservative

Sep 23 11:56:18 2003

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APPLICANT: MUNGER, JOSHUA
TITLE OF INVENTION: METHODS AND COMPOSITION CONCERNING HERPESVIRUS US3 AND
TITLE OF INVENTION: METHODS AND COMPOSITION
FILE REFERENCE: ARCD:380US
CURRENT APPLICATION NUMBER: US/10/209,967
CURRENT FILING DATE: 2002-07-31
PRIOR PILING DATE: 2001-07-31
NUMBER OF SEQ ID NOS: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96.5%; Score 137; DB 9; Length 168; 96.3%; Pred, No. 1.26-12; Indels 0; Mismatches 1; Indels
        OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96.5%; Score 137; DB-127, 96.3%; Pred NO. 1.2e-12; Live 0; Mismatches 1;
                                                                                                                                                                              ATTORNEY AGENT INFORMATION:

NAME: Billings, Lucy J.

REGIGYRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0421 US

TELECOMMONICATION INFORMATION:

TELEPHONE: 650-855-0555

TELEPHONE: 650-845-4166

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:
                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/894,657
FILING DATE: 28-Jun-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/410,372
FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             103 NIWAAQRYGRELRRWSDEFVDSFKKGL 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LIBRARY: Genbank
CLONE: 1683637
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 NLWAAÓEYGRELRRMSDEFVDSFKKGL 27
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; Publication No. US20020115631A1
; GENERAL INFORMATION:
    APPLICANT: Horne, William A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/10209967; Publication No. US20030171279A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                        LENGIH: 168 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 96.3%
Watches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 96.3
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CRGANISM: Human BAD
US-10-209-967-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 5
US-10-066-179-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; / Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL PROLIFERATION
Corley, Neil C.
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL.
PROLIFERATION
                                                                                                                                                                                                                                                                   MEDIUM TYPE: Diskette
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/894,657
FILING DATE: 28-Jun-2001
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
                                                                                                              ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Dr. CITX: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: CURKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/POCKET NUMBER: PF-0421 US
TELEPHONE: 650-855-0555
TELEPRAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           103 NIWAAQRYGRELRRMSDEFVDSFKKGL 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 NIWAAQEYGRELRRMSDEFVDSFKKGL 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 09/410,372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 168 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7, Application US/09894657 Patent No. US20020098569Al GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yue, Henry
Lal, Preeti
Shah, Purvi
Corley, Neil C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                      NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LIBRARY: SYNORAB01
                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
                                                                                                                                                                                                          USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 26; Conserva
                                                                                                                                                                                                                             ZIP: 94304
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                                                                                                                                                                                                          COUNTRY:
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US-09-894-657-7
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76.8%;
87.5%;
        NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
                                                                                                                                                                                          Query Match 76.85
Best Local Similarity 87.55
Matches 21; Conservative
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Matches 20; Conservative
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Matches 20; Conservative
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ORGANISM: Mus musculus
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US-10-066-179-3
                                                                                                                        ; ORGANISM: Mus musculus US-10-209-967-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 9
US-10-066-179-3
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US-09-922-378-3
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                                                                                                     TYPE: PRT
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Sequence 258, Application US/10059261

Sequence 258, Application US/10059261

Sequence 258, Application US/20030077826A1

Sequence 258, Application No. US20030077826A1

Sequence 258, Application No. US20030077826A1

APPLICANT: EDELMAN, LENA

APPLICANT: BRIAND, JEAN-PAUL

TITLE OF INVENTION: SPECIFIC CELLES AND A MODULE ABLE TO TARGET

TITLE OF INVENTION: SPECIFIC CELLES AND A MODULE REGULATING THE APOPTOGENIC

TITLE OF INVENTION: (PTPC)

STILE REPERENCE: 03495.0216

CURRENT FILING DATE: 2002-08-29

PRIOR APPLICATION NUMBER: 60/265,594

PRIOR APPLICATION NUMBER: 60/265,594
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Publication No. US20030171279A1
GENERAL INFORMATION:
APPLICANT: MUNGER, JOSHUA
APPLICANT: ROIZMAN, BERNARD
TITLE OF INVENTION: METHODS AND COMPOSITION CONCERNING HERPESVIRUS US3 AND
TITLE OF INVENTION: BAD-INVOLVED APOPTOSIS
FILE REFERENCE: ARCD:380US
CURRENT APPLICATION WUMBER: US/10/209,967
CURRENT FILING DATE: 2002-07-31
PRIOR FILING DATE: 2001-07-31
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                                                                                                                                                                                                                                                                                                                            Length 168;
APPLICANT: Oltersdorf, Tilman
TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC
TITLE OF INVENTION: ACIDS AND METHODS OF USE
FILE REFERENCE: 480140.42861
CURRENT APPLICATION NUMBER: US/10/066,179
CURRENT FILING DATE: 2002-02-01
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
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96.3%; Pred. NO. 1.26-12;
live 0; Mismatches 1; Indels
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1 Similarity 96.0%; Pred. No. 4.6e-12;
24; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             103 NLWAAQRYGRELRRMSDEFVDSFKKGL 129
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                                                                                                                                                                                                                                                                                                     ORGANISM: Unknown Organism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 325
                                                                                                                                                                                                                                                        ) ORGANISM: Homo sapiens
US-10-066-179-2
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Matches 24; Conserv
                                                                                                                                                                                          SEQ ID NO 2
LENGTH: 168
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US-10-209-967-4
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LENGIH: 25
                                                                                                                                                                                                                                       TYPE: PRT
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APPLICANT: Horne, William A.
APPLICANT: Oltersdorf, Tilman; TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC; TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC; TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC; TITLE OF INVENTION: HUMBER: US/10/066,179
CURRENT APPLICATION NUMBER: US/10/066,179
CURRENT FILING DATE: 2002-02-01
NUMBER OF SEQ ID NOS: 15
SEQ ID NO 3
LENGTH: 204
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Length 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74.6%; Score 106; DB 9; Length 204; 83.3%; Pred. No. 5.8e-08; Live 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Horne, William A.
APPLICANT: Oldersdorf, Tilman
TITLE CANT: Oldersdorf, Tilman
TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC
TITLE OF INVENTION: ACIDS AND METHODS OF USE
FILE REFERENCE: 480140.42803
CURRENT APPLICATION NUMBER: US/09/922,378
CURRENT APPLICATION NUMBER: US/09/922,378
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
                                                        3; Indels
Score 109; DB 12;
Pred. No. 2.1e-08;
0; Mismatches 3;
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                                                                                                                                        140 NLWAAQRYGRELRRMSDEFEGSFK 163
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                                                                                                           1 NLWAAQEYGRELRRMSDEFVDSFK 24
                                                                                                                                                                                                                                                                                        Sequence 3, Application US/09922378 Patent No. US20020037869A1
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Tue Sep 23 11:56:18 2003

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Sequence 583, Application US/09841132
; Sequence 583, Application US/09841132
; Patent No. US20020061848A1
; GENERAL INFORMATION:
    APPLICANT: Bhatia, Ajay
    APPLICANT: Brobst, Peter
    TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
    TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
    FILER REFERENCE: 210121.46968
; CURRENT APPLICATION NUMBER: US/09/841,132
; CURRENT FILING DATE: 2001-04-23
; NUMBER OF SEQ ID NOS: 599
; SOFTWARE: FastSEQ for Windows Version 3.0/4.0
; SEQ ID NO 583
LENGTH: 1053
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                                                                                                                                                                                           Sequence 394, Application US/09940244

Publication No. US20030044796A1

GENERAL INFORMATION:
APPLICANT: Neri, Bruce P.
APPLICANT: Hall, Jeff G.
APPLICANT: Smith, Lloyd M.
TILLE OF INVENTION: Reactions on Dendrimers
FILE REFERENCE: FORS-06478

CURRENT APPLICATION NUMBER: US/09/940,244

CURRENT FILING DATE: 2002-05-06

NUMBER OF SEQ ID NOS: 422

SOFTWARE: Patentin Version 3.1
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162 EEFHKEMRRLADELLRLFLRAL 183
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6 QEYGRELRRMSDEFVDSFKKGL 27
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; Publication No. US20020146776A1
; GENERAL INFORMATION:
; APPLICANT: Bhatia, Ajay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: C. Trachomatis D serovar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; CTHER INFORMATION: Synthetic US-09-940-244-394
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Matches 9; Conserv
                                                                                                                                                 RESULT 12
US-09-940-244-394
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LENGIH: 350
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                                                                                               Sequence 147, Application US/10174105A

Sequence 147, Application US/10174105A

Sequence 147, Application US/10174105A

Sequence 147, Application US/10174105A

Sequence 147, Application No. US20030068652A1

GENERAL INFORMATION:
APPLICANT: CALL Signaling Technology, Inc.
APPLICANT: CALL Signaling IDSNTIFICATION OF PROPER COUPLED WITH DATABASE SEARCHING
FILE REFERENCE: CST-138 CLP3

CURRENT APPLICATION NUMBER: US/10/174, 105A

CURRENT APPLICATION NUMBER: US 09/148, 712

PRIOR APPLICATION NUMBER: US 09/535, 364

PRIOR APPLICATION NUMBER: US 09/535, 364
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| Sequence 2, Application US/10168780
| Publication No. US20030172405A1
| GENERAL INFORMATION:
| APPLICANT: TANAKA, Hiroshi
| APPLICANT: KAYANO, TOShiaki
| APPLICANT: KAYANO, Maschiro
| APPLICANT: KANO, Maschiro
| APPLICANT: KOBAYASHI, Macatomo
| APPLICANT: KOBAYASHI, Macatomo
| APPLICANT: ROBAYASHI, Macatomo
| TITLE OF INVENTION: GIBBERELLIN 3BETA-HYDROXYLASE GENES OF RICE AND USES THEREOF
| TITLE OF INVENTION: GIBBERELLIN 3BETA-HYDROXYLASE GENES OF RICE AND USES THEREOF
| TITLE OF INVENTION: GIBBERELLIN 3BETA-HYDROXYLASE GENES OF RICE AND USES THEREOF
| TITLE OF TOWN TOWNER: DO 11/361608
| PRIOR FILING DATE: 2000-12-20
| PRIOR FILING DATE: 1999-12-20
| NUMBER OF SEQ ID NOS: 8
| SOFTWARE: Patentin Ver. 2.0
| SEQ ID NO 2
| LENGTH: 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: MOD_RES; LOCATION: (8)..(8)
COTHER INFORMATION: PHOSPHORYLATION; serine at position 8 is phosphorylated US-10-174-105a-147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 57; DB 15; Length 15; Pred. No. 0.063; 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
OTHER INFORMATION: Synthetic Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 GRELRRMSDEFVDS 22
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ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best_Local Similarity
Matches 12; Conserv
                                                                                         JS-10-174-105A-147
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Έ
                                                                                                                                                                                                                                                                                                                                                          Query Match 32.7%; Score 46.5; DB 14; Length 1053; Best Local Similarity 40.7%; Pred. No. 2.3e+02; Matches 11; Conservative 7; Mismatches 6; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/10092750
; Sequence 1, Application US/10092751
; General information:
    General information:
    APPLICANT: Hammond, Philip W.
    APPLICANT: Alpin, Julia
    APPLICANT: Alpin, Julia
    APPLICANT: Wright, Martin C.
    ITLE OF INVENTION: Polypeptides Interactive with BCL-XI
    ITLE OF INVENTION: Polypeptides Interactive with BCL-XI
    FILE REFERENCE: 50036/05002
    CURRENT APPLICATION NUMBER: US/10/092,750
    CURRENT FILING DATE: 2002-03-07
    PRIOR APPLICATION NUMBER: US 60/274,526
    NUMBER OF SEQ ID NOS: 253
    SOFTWARE: FastSEQ for Windows Version 4.0
    SEQ ID NO 1
    ibnGTH: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 32.4%; Score 46; DB 15; Length 35; Best Local Similarity 55.6%; Pred. No. 6.8; Matches 10; Conservative 2; Mismatches 2; Indels
APPLICANT: Probst, Peter
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT
TITLE OF INVENTION: AND DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.515C2
CURRENT APPLICATION NUMBER: 0S/10/007,693
CURRENT APPLICATION DATE: 2001-12-05
NUMBER OF SEQ ID NOS: 157
LENGTH: 1053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: September 23, 2003, 10:03:35 Job time: 390 secs
                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Chlamydia trachomatis serovar D
US-10-007-693-97
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CORGANISM: Homo sapiens
US-10-092-750-1
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US-10-092-750-1
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September 23, 2003, 09:43:16; Search time 22 Seconds (without alignments) 57.715 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                       OM protein - protein search, using sw model
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US-09-544-664B-2 142 1 NLWRAQEYGREI.RRMSDEFVDSFKKGL 27 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 seqs, 47026705 residues Searched:

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	Q92934 homo sapien	mus n	035147 rattus norv				P32449 saccharomyc		P50506 debaryomyce		P30209 bluetongue											rickett	Q07512 petunia hyb				P42103 bacillus su	Q9k7q7 bacillus ha	P37484 bacillus su	Q58413 methanococc	P43803 haemophilus		74
SUMMARIES		ai a	BAD_HUMAN	BAD_MOUSE	BAD_RAT		MTBR_BPRH1	PPCK_THETN	AROG_YEAST	BXD1_DROME	HXK_DEBOC	AROG_CANAL	VP5_BTV2A	SYM_THEMA	PPCK_RHISN	VG13_BPMD2	RPSD_BORBU	CE05_MOUSE	IPYR_MYCPE	Y591_AQUAE	RIR1_CHLMU	RIR1_CHLTR	BIM_HUMAN	MRAW_RICPR		TNAA_AERPE	au.		YXAD_BACSU		YYBT_BACSU	SYV_METUR	SECA_HAEIN	ISC1_ARCFU	DPOA_LEIDO
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VSIS_REOVJ AP3_ARATH	YGFG_ECOLI ACP2_ENTHI	CPP2_ENTHI E2BB_RABIT	PAN1_HUMAN RMUC_PSEAE	HT31_ARATH KPC1_CAEEL
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ALIGNMENTS

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is no way modified and this statement is not removed. Gaage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain. SIMILARITY: BELONGS TO THE BCL-2 FAMILY. CAUTION: Ref.1 sequence differs from that shown due to frameshifts in position 64 and 91.
                                                                                                                                                                                                                                                                                                                                                                                                                           receptor signaling and the apoptotic pathways.
SUBUNIT: Forms heterodimers with the anti-apoptotic proteins, Bcl-x(L), Bcl-2 and Bcl-w. Also binds protein S100A10 (By similarity).
The Ser-75/Ser-99 phosphorylated form binds 14-3-3 proteins (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               phosphorylation, locates to the cytoplasm.
TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.
DOMAIN: Intact BH3 domain is required by BIK, BID, BAK, BAD AND
BAX for their pro-apoptotic activity and for their interaction
with anti-apoptotic members of the Bcl-2 family.
PTM: Phosphorylated on Ser-75 in response to survival stimuli.
Subsequent phosphorylation on Ser-99 promotes heterodimerization
with 14-3-3 proteins. This interaction then facilitates the
phosphorylation at Ser-118, a site within the BH3 domain, leading
to the release of Bcl-x(L) and the promotion of cell survival.
Ser-99 is the major site of AKT/PKB phosphorylation, Ser-118 the
                                                                                                                                                                                                                                                                            mutagenesis, and biophysical studies.";
Protein Sci. 9:2528-2534(2000).
-!- FUNCTION: Promotes cell death. Successfully competes for the binding to Bcl-x(L), Bcl-2 and Bcl-w, thereby affecting the level of heterodimerization of these proteins with BAX. Can reverse the death repressor activity of Bcl-x(L), but not that of Bcl-2 (By similarity). Appears to act as a link between growth factor
                                                                                                                                                                     MEDINE=21073561; Pubmed=11206074;
Petros A.M., Nettesheim D.G., Wang Y., Olejniczak E.T., Meadows R.P.,
Mack J., Swift K., Matayoshi E.D., Zhang H., Thompson C.B.,
                                                                                                                                                                                                                                                           "Rationale for Bcl-xL/Bad peptide complex formation from structure,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BY
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Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EIMILARITY).
PHOSPHORYLATION (BY PKA AND PKE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PHOSPHORYLATION (BY PKA AND PKB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ser-99 is the major site of AKT/PKB phosphorylation, Ser-major site of protein kinase A (CAPK) phosphorylation (by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Outer mitochondrial membrane. Upon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Phosphorylation; Polymorphism; 3D-structure.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MIM; 603167; -. 605.005737; C:cytoplasm; NAS. 60; 60:0005741; C:mitochondrial outer membrane; 160; 60:0005515; F:protein binding activity; NAS. 60; 60:0008632; P:apoptotic program; TAS. 60; 60:0006917; P:induction of apoptosis; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U66879; AAB36516.1; ALT_FRAME.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AF021792; AAB72092.1; -. AF031523; AAB88124.1; -. BC001901; AAH01901.1; -.
                                                                                                                                                      STRUCTURE BY NMR OF 103-127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genew; HGNC:936; BAD.
MIM; 603167; -.
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DOMAIN: Intact BH3 domain is required by BIK, BID, BAK, BAD AND BAX for their pro-apoptotic activity and for their interaction with anti-apoptotic members of the Bcl-2 family.

PTM: Phosphorylated on Ser-112 in response to survival stimuli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-95136361; PubMed-7834748;
Yang E., Zha J., Jockel J., Boise L.H., Thompson C.B., Korsmeyer S.J.;
Tabd, a heterodimeric partner for Bcl-XL and Bcl-2, displaces Bax and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mol. Cell 6:41-51(2000).

-!- FUNCTION: Promotes cell death. Successfully competes for the binding to Bol-x(L), Bol-2 and Bol-w, thereby affecting the level of heterodimerization of these proteins with BAX. Can reverse the death repressor activity of Bol-x(L), but not that of Bol-2. Appears to act as a link between growth factor receptor signaling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Subsequent phosphorylation on Ser-136 promotes heterodimerization with 14-3-3 proteins. This interaction then facilitates the phosphorylation at Ser-155, a site within the BH3 domain, leading to the release of Bcl-x(L) and the promotion of cell survival Ser-136 is the major site of AKT/PKB phosphorylation, Ser-155 the major site of protein kinase A (CAPK) phosphorylation.
                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=98022383; PubMed=9381178;
Del Peso L., Gonzalez-Garcia M., Page C., Herrera R., Nunez G.;
"Interleukin-3-induced phosphorylation of BAD through the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "14-3-3 proteins and survival kinases cooperate to inactivate BAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Datta S.R., Katsov A., Hu L., Petros A., Fesik S.W., Yaffe M.B., Greenberg M.E.;
                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                         01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Bcl2-antagonist of cell death (BAD) (Bcl-2 binding component
                                                                                                            Length 168;
                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PHOSPHORYLATION, AND MUTAGENESIS OF SER-112 AND SER-136.
SIMILARITY).
A -> S (in dbSNP:3729933).
                                                       121
18392 MW; 69FD8D27DDEE3241 CRC64;
                                                                                                        Score 137; DB-1;
Pred No. 8.2e-13;
0; (Mismatches 1;
                                    /FTId=VAR_015380
                                                                                                                                                                                                                                                                                                                                                                                                                                      (Bcl-xL/Bcl-2 associated death promoter).
                                                                                                                                                                                                                                                                                                                      204 AA.
                                                                                                                                                                                                          103 NIWAAQRYGRELRRMSDEFVDSFKKGL 129
                                                                                                                                                                                       27
                                                                                                                                                                              1 NLWAAGEYGRELRRMSDEFVDSFKKGL
                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20403302; PubMed=10949026;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MUTAGENESIS OF SERINE RESIDUES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BH3 domain phosphorylation."; Mol. Cell 6:41-51(2000).
                                                                                                              96.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science 278:687-689(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUE=Brain, and Thymus;
                                                                                                                                                    26; Conservative
                                                                                                                                                                                                                                                                                                                        STANDARD;
                   107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cell 80:285-291(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             promotes cell death.
                                                                           168 AA;
                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                   107
                                                                                                                                                                                                                                                                                                                                                                                                                                                      BAD OR BBC6
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                                                                                                                                                                                                                                                                                                                        BAD MOUSE
                                                                           SEQUENCE
                                                                                                               Query Match
Best Local
                    VARIANT
                                                         HELIX
                                                                                                                                                                                                                                                                                  RESULT 2
BAD_MOUSE
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ---
          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PHOSPHORILATION (BY PKA AND PKB).
S->A: NO PHOSPHORILATION.
S->A: NO PHOSPHORILATION.
S->A: NO PHOSPHORILATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hsu S.Y., Kaipia A., Zhu L., Hsueh A.J.W.; "Interference of BAD (Bcl-xL/Bcl-2-associated death promoter)-induced apoptosis in mammalian cells by 14-3-3 isoforms and Pil."; Mol. Endocrinol. 11:1858-1867(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BAD in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chórdata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDITIVE=21109372; PubMed=11161472; Hamner S., Arumae U., Yu L.-Y., Sun Y.-F., Saarma M., Lindholm D.; "Functional characterization of two splice variants of rat BAD and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=98194755; Pubmed=9535132; D'Agata V., Magro G., Travali S., Musco S., Cavallaro S.; "Cloning and expression of the programmed cell death regulator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
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PHOSPHORYLATION (BY PKA AND PKB).
PHOSPHORYLATION (BY PKA AND PKB).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               035147; 070256; 09JRX1;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Bcl2_antagonist of cell death (BAD) (Bcl-2 binding component
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 109; DB 1; Length 204;
Pred. No. 1.2e-08;
); Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [1]
SEQUENCE FROM N.A., AND MUTAGENESIS OF SER-113 AND SER-137
Contains 1 Bcl-2 homology 3 (BH3) domain. BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6C2BA910205053F7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Bcl-xL/Bcl-2 associated death promoter).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          205 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S->A: NO
BCL-X(L)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 NLWAAQEYGRELRRMSDEFVDSFK 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neurosci. Lett. 243:137-140(1998).
                                                                                                                                                                                                                                                                                                                                                                                   MGD; MGI:1096330; Bad.
InterPro: IPR000712; Bc12_BH.
PROSITE; PS01259; BH3; FALSE_NEG.
Apoptosis; Phosphorylation.
DOMAIN 147 161 BH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=98034386; PubMed=9369453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22080 MW:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76.8%;
87.5%;
                                                                                                                                                                                                                                                                                                       EMBL; L37296; AAA64465.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        112
136
155
112
1136
                                                                                                                                                                                                                                                                                                                                      A55671; A55671.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       204 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                      Q92934; 1G5J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10116;
SIMILARITY: SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the rat brain."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Ovary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOD_RES
MOD_RES
MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BAD_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 3
SO THE PETEE TERMS SO THE STATE THE PETEE THE PETEE THE SO THE STATE THE PETEE THE STATE THE STATE THE STATE THE PETEE THE STATE THE PETEE THE STATE THE STATE THE PETEE THE STATE 
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their interaction with Bcl-w in sympathetic neurons.";
Mol. Cell. Neurosci. 17:97-106(2001).
Cell. Neurosci. 18:07-12 and Bcl-w, thereby affecting the level of heterodimerization of these proteins with BaX. Can reverse the death repressor activity of Bcl-x(L), but not that of Bcl-2 (By similarity). Appears to act as a link between growth factor receptor signaling and the apoptotic pathways.
Cell. Suburi: Forms heterodimers with the anti-apoptotic proteins, Bcl-x(L), Bcl-2 and Bcl-w. Also binds protein $100Al0. The Ser-113/Ser-137 phosphorylated form binds 14-3-3 proteins.
Cell. SUBCELLUIAR LOCATION: Outer mitochondrial membrane. Upon phosphorylation, locates to the cytoplasm (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PHOSPHORYLATION (BY PKA AND PKB)
(BY SIMILARITY).
PHOSPHORYLATION (BY PKA AND PKB)
(BY SIMILARITY).
PHOSPHORYLATION (BY PKA AND PKB)
(BY SIMILARITY).
LEPRESAGTATOMROSASWTRIIQSWWDRNLGKGGSTPSQ.-> BELTYSYBFLEVRALAMEGWPLLNWFYGSFPHTLEPTPP BYAMFLRYLC (in isoform Beta).
/FTIGALSP. 000534.
S->A: NO EFFECT ON HETERODIMERIZATION
WITH 14-3-3 PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ROTEINS. NO EFFECT ON HETERODIMERIZATION ITH BCL2 NOR WITH PROTEIN P11.
DAGGR -> ERRGRK (IN REF. 1).
7AFA71DAE9CF4A81 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          abundant form.

DOMAIN: Intact BH3 domain is required by BIK, BID, BAX, BAD AND BAX for their pro-proptotic activity and for their interaction with anti-apoptotic members of the Bcl-2 family.

PTM: Phosphorylated on Ser-113 in response to survival stimuli. Subsequent phosphorylation on Ser-137 promotes heterodimerization with 14-3-3 proteins. This interaction then facilitates the phosphorylation at Ser-156, a site within the BH3 domain, leading to the release of Bcl-x(L) and the promotion of cell survival. Ser-137 is the major site of AKT/PKB phosphorylation, Ser-156 the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISOUE SPECIFICITY: Expressed in all tissues tested, including brain, liver, spleen and heart. In the brain, restricted to epithelial cells of the choroid plexus. Isoform alpha is the more
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S->A: NO HETERODIMERIZATION WITH 14-3-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            major site of protein kinase A (CAPK) phosphorylation (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              similarity).
-!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
-!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro, IPR000712, Bc12_BH.
PROSITE; PS01259; BH3; FALSE_NBG.
Apoptosis; Phosphorylation; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=Alpha;
IsoId=035147-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WITH BCL2
SDAGGR ->
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROTEINS.
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22228 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF031227; AAC15100.1; -. EMBL; AF279910; AAF91427.1; -. EMBL; AF279911; AAF91428.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; Q92934; 1G5J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29
205 A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=Beta;
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DB 1; Length 205;

Score 109;

76.8%;

g

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InterPro; IPR001258; NHL.
InterPro; IPR001315; Znf_Bbox.
InterPro; IPR01841; Znf_ring.
Pfam; PF01436; NHL; 5.
Pfam; PF00643; Zf_Bbox; 1.
Pfam; PF00097; zf_GARC4; 1.
SMART; SM00336; BBOX; 1.
SMART; SM00184; RING; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE: PS50119; ZF BBOX; 1.
PROSITE: PS00518; ZF_RING_1; 1.
PROSITE: PS50089; ZF_RING_2; 1.
Zinc-finger; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 QEYGRELRRMSDEFVDSFK 24
                                                                                                   AL133284; CAB92723.1; -. BC003154; AAH03154.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27 F
71988 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-1989 (Rel. 10, Created)
01-NOV-1995 (Rel. 32, Last sequ
16-OCT-2001 (Rel. 40, Last anno
                                                                              EMBL; U18543; AAA86474.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35.9%;
                                                                                                                                                                      HGNC:16380; TRIM32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 57.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteriophage rho-11s.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         653 AA;
                                                                                                                                                 HSSP; P29590; 1BOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REVISION TO 476.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZN_FING
ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
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MTBR_BPRH1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDILNE-22388257; PubMed-12477932;

REDILNE-22388257; PubMed-12477932;

RICHAUSDER R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RIABSER R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RIABSER R.L., Sceberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Bidtchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Bidtchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Rochards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Rabeley J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Rhitting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Rhitting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Rhitting M., Schain J.E., Jones S.J.M., Marra M.A.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J.M., Marra M.A.,

Rhaman and mouse cDNA sequences.",

Proc. Natl. Acad. Sci. U.S.A., 99:16899-1699150000 full-length

Proc. Natl. Acad. Sci. U.S.A., 99:16899-169916000 C.G.

HIV-2 AND BRAY FRIV-1 TAT PROTEIN IN VIVO.

HIRDRALL THE ACTIVATION DOMAIN OF HIV-1 TAT AND CAN ALSO INTERACT WITH THE

HIV-1 HURL ALL TAT PROTEIN IN VIVO.
                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Usage by and for commercial
                                                                                                                                                                                                                                                         013049; Q9NQP8; 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Zinc-finger protein HT2A (72 KDa Tat-interacting protein) (Tripartite motif-containing protein 32).
                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE-95297135; PubMed=7778269; Fridell R.A., Harding L.S., Bogerd H.P., Cullen B.R.; Fridell R.A., Harding L.S., Bogerd H.P., Cullen B.R.; "Identification of a novel human zinc finger protein that specifically interacts with the activation domain of lentiviral Tat
                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBCELLULAR LOCATION: Nuclear.
-!- TISSUE SPECIFICITY: SPLEEN, THYMUS, PROSTRATE, TESTIS, OVARY,
                              0;
                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: Contains 1 RING-type zinc finger.
-!- SIMILARITY: Contains 1 B box-type zinc finger.
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      Pred. No. 1.2e-08;
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                                                                                                                                                                                                                                       653 AA.
                            Mismatches
                                                                                                                       141 NLWAAQRYGRELRRMSDEFEGSFK 164
                                                                         1 NLWAAQEYGRELRRMSDEFVDSFK 24
                                                                                                                                                                                                                                          PRT;
                            ;
0
  87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Virology 209:347-357(1995).
                          21; Conservative
                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INTESTINE AND COLON.
                                                                                                                                                                                                                                                                                                                                                                                                                         (Human)
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                       HT2A_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sehra H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           proteins
                                                                                                                                                                                          RESULT 4
HT2A HUMAN
                          Matches
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entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Behrens B., Noyer-Weidner M., Pawlek B., Lauster R., Balganesh T.S.,
Trautner T.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Trautner T.A.;
Submitted (SEP-1987) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THIS ENZYME METHYLATES CYTOSINE WITHIN THE SEQUENCES
GGCC AND GAGCTC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae; Lambda-like viruses. NCBL_TaxID=10735;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Organization of multispecific DNA methyltransferases encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Modification methylase RhollsI (EC 2.1.1.73) (Cytosine-specific
methyltransferase RhollsI) (Bsu Plls) (M.RhollsI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + DNA cytosine adenosyl-L-homocysteine + DNA 5-methylcytosine.
-!- SIMILARITY: BELONGS TO THE C5-METHYLTRANSFERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                              MIM; 602290; -.
GO; GO:0005634; C:nucleus; TAS.
GO; GO:0003713; F:transcription co-activator activity; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 653,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B BCX-TYPE.
F -> I (IN REF. 1).
D83B1595CA8378FD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 51; DB 1;
Pred. No. 11;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               503 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RING-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POLY-ALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               temperate Bacillus subtilis phages.";
EMBO J. 6:1137-1142(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=87246516; PubMed=3109889;
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NP_BIND
SEQUENCE
                                            Query Match
Best Local
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                                                                         Matches
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    Noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                              ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- PATHWAY: Rate-limiting gluconeogenic enzyme.
-1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-1- SIMILARITY: Belongs to the phosphoenolpyruvate carboxykinase [ATP]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ProDom; PD004723; PEPCK_ATP; 1.
IIGRFAMS; TIGR00224; PCKA; 1.
PROSITE; PS00532; PEPCK_ATP; 1.
Gluconeogenesis; Lyase; Decarboxylase; ATP-binding; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- CATALYTIC ACTIVITY: ATP + oxaloacetate = ADP + phosphoenolpyruvate
                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-MB4 / JCM 11007;
MEDLINE-21992816; PubMed-11997336;
Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
Chen Y., Xue Y., Li W., Hang L., Dong X., Ma Y., Ling L.,
Tan H., Chen R., Wang J., Yu J., Yang H.;
"A complete sequence of T. tengcongensis genome.";
Genome Res. 12:689-700(2002).
                                                                                                                                                                                                                                                                                              ÷
                                                                                                                                                                                                                                                               35.6%; Score 50.5; DB 1; Length 503; 50.0%; Pred. No. 9.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Phosphoenolpyruvate carboxykinase [ATP] (EC 4.1.1.49) (PEP carboxykinase) (Phosphoenolpyruvate carboxykinase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria, Firmicutes, Clostridia, Thermoanaerobacteriales, Thermoanaerobacteriaceae, Thermoanaerobacter.
                                                                                                                                                                                                                                                                                            Indels
                                                                         HSSP, ACELLY, M.RhollsI.

REBASE; 2835; M.RhollsI.

RICEPTO; IPRO01525; C5_DNA_meth.

Pfam; PF00145; DNA_methlase; 1.

RPRINTS; PR00105; C5_METTRFRASE.

R TICRFAMS; TIGRO0675; Gam; 1.

R PROSITE; PS00094; C5_MTASE_1; 1.

RROSITE; PS00095; C5_MTASE_2; 1.

RM Transferase; Methyltransferase; Restriction system.

TOWN TRANSFERSE TOWN TRANSFERSE.

RM TRANSFERSE TOWN TRANSFERSE.
                                                                                                                                                                                                                                   AAAFB8FE01B8129E CRC64;
                                                                                                                                                                                                                                                                                              .,
                                                                                                                                                                                                                                                                                                                                                                                                                            521 AA.
modified and this statement is not removed.
                                                                                                                                                                                                                                                                                           5; Mismatches
              entities requires a license agreement (gor send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                         Thermoanaerobacter tengcongensis.
                                                                                                                                                                                                                                                                                                                       3 WAAQE-YGRELRRMSDEFVD 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HAMAP; MF_00453; -; 1.
InterPro; IPR001272; PBPCK_ATP.
Pfam; PF01293; PEPCK_ATP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE013131; AAM24977.1; -.
                                                                                                                                                                                                                                57129 MW;
                                                         EMBL; X05242; CAA28869.1; -.
                                                                                                                                                                                                                                                                                           10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=119072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                           PPCK_THETN
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                                                                                                                                                                                                                                                                                                                                                                                             RESULT 6
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Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: STEREOSPECIFIC CONDENSATION OF PHOSPHOENOLPYRUVAIE (PEP)
AND D-ERYTHROSE-4-PHOSPHATE (E4P) GIVING RISE TO 3-DEOXY-D-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SECURNCE FROM N.A. MEDLINE=92225349; PubMed=1348717; Kuenzler M., Paravicini G., Egli C., Irniger S., Braus G.H.; Kuenzler M., primary structure and regulation of the ARO4 gene, encoding the tyrosine-inhibited 3-deoxy-D-arabino-heptulosonate-7-phosphate synthase from Saccharomyces cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Doignon F., Biteau N., Aigle M., Crouzet M.; "The complete sequence of a 6794 bp segment located on the right arm of chromosome II of Saccharomyces cerevisiae. Finding of a putative dUTPase in a yeast."

Yeast 9:1131-1137(1993).
                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1994 (Rel. 28, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Phospho-2-dehydro-3-deoxyheptonate aldolase, tyrosine-inhibited
(EC 4.1.2.15) (Phospho-2-keto-3-deoxyheptonate aldolase) (DAHP
synthetase) (3-deoxy-D-arabino-heptulosonate 7-phosphate synthase).
ARO4 OR YBR249C OR YBR1701.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                               ij
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ENZYME REGULATION: INHIBITED BY TYROSINE.
                                                                                                   Length 521;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                first step.
-!- INDUCTION: By amino acid starvation.
-!- SIMILARITY: BELONGS TO CLASS-I DAHP SYNTHETASE FAMILY.
                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (NOV-1993) to the EMBL/GenBank/DDBJ databases.
ATP (BY SIMILARITY).
1783A3320B106341 CRC64;
                                                                                                                                                               .
ω
                                                                                                   DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (DAHP).
                                                                                             Score 50.5; DB Pred. No. 9.9; 9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                            370 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                       481 NTWKDKEEYDKTAKRLAORFIENFOK 506
                                                                                                                                                                                                                           1 NLWA-AQEYGRELRRMSDEFVDSFKK 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ARABINO-HEPTULOSONATE-7-PHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=94078675; PubMed=8256522;
234 A'
58771 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1993 (Rel. 27, Created)
                                                                                             Match 35.6%;
Local Similarity 30.8%;
les 8; Conservative 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gene 113:67-74(1992),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REVISIONS TO 205-207.
227
521 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-S288c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=S288C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kuenzler M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AROG_YEAST
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CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HXK_DEBOC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RC SEQUENCE FKON N.A.

RC STRAIN=Berkeley;

REDINE-2019606; PubMed=10731132;

REDINE-2019606; PubMed=10731132;

Redinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

Ramanatides P.G., Scherer S.E., Holt R.A., Henkins R.A., Galle R.F.,

Ramanatides P.G., Scherer S.E., Holt R.A., Henkins R.A., Galle R.F.,

Rananatides P.G., Scherer S.E., Richards S., Ashburner M., Henderson S.N.,

Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Burtion G.G., Wortunan J.R., Yandell M.D., Barshow Co., Ch. Baldwin D.,

RA Bardon R.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

Ballew R.M., Davle C., Barter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Ballew R.M., Basu A. Baxendle J., Bayraktaroglu L., Beasley E.M.,

Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

Burtis K.C., Busan D.A., Buller H., Cadieu E., Center A., Chandra I.,

Burtis K.C., Busan D.A., Buller H., Cadieu E., Center A., Chandra I.,

Burtis K.C., Busan D.A., Bayler B.M., Davies P.,

Burbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

RA Goson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunko B.C.,

Burbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischman R.A.,

Glodek A., Gong F., Gorrell J. H., Gu Z., Guan P., Harris M.,

Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Fouck J.,

Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

Jalali M., Kalush F., Morntosh M., Wobarry C., Morris J., Moshrefi A.,

Jalazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Resee M.G.,

RA Mount S.M., Welson K.A., Nixon K., Pollard J., Puri V., Resee M.G.,

RA Reinert K., Remington K.S., Nonski M., Stupski M.P., Smith T.,

Shue B.C., Siden Kiamos I., Simpson M., Stupski M.P., Smith T.,

Shies E., Spradling A.C., Furrer E., Venter E., Shen H.,

Shies E., Spradling A.C., Furrer E., Venter E., Shen E.,

Shies E., Spradling A.C., Furrer E., Shen E.,

Shue B.C., Stuper E., Spradling A.S., Shorter E
                                                                                                                                                                                                                                                                        ô
EMBL; X61107; CAA43419.1; -.
EMBL; L20296; AAA65607.1; -.
EMBL; Z36118; CAA85212.1; -.
PIR; S38185; S38185.
HSSP; P00886; 1QR7.
GOS; S00000453; ARO4.
GO; GO:0003849; R:2-dehydro-3-deoxyphosphoheptonate aldolase . . .; IDA. InterPro; IPR006219; AroFGH.
InterPro; IPR006218; DAHP1/KDSA.
                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila,
                                                                                                                                             Pfam; PF00793; DAHP_Synth_1; 1.
Probom; PD005060; AroFGH; 1.
TIGRFAMS; TIGR00034; aroFGH; 1.
Aromatic amino acid biosynthesis; Lyase; Multigene family.
SEQUENCE 370 AA; 39749 MW; S94ED48F24175979 CRC64;
                                                                                                                                                                                                                                          Score 50; DB 1; Length 370;
                                                                                                                                                                                                                                                                       4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         O9VEB3: 095U84:
16-OCT-2001 (Rel. 40, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Brix domain containing protein 1 homolog.
                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 320 AA.
                                                                                                                                                                                                                                                       Pred. No. 8.1;
                                                                                                                                                                                                                                                                       4; Mismatches
                                                                                                                                                                                                                                                                                                    1 NLWAAQEYGRELRRMSDE 18
                                                                                                                                                                                                                                                                                                                        35.2%;
55.6%;
                                                                                                                                                                                                                                                                       10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                     Best_Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                BXD1 DROME
                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CG7993
                                                                                                                                                                                                                                                                                                                                                                                               BXD1_DROME
     g
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Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., "The genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                     Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M., George R.A., Guarin H., Kronmiller B., Pacleb J.M., Park S., Wan K.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                            Rubin G.M., Celniker S.E.;
"A Drosophila full-length cDNA resource.";
Genome Bloi. 3:RESEARCH0080.1-RESEARCH0080.8(2002).
-!- SUBCELLULAR LOCATION: Nuclear; nucleolar (By similarity).
-!- SIMILARITY: Contains 1 Brix domain.
-!- CAUTION: Ref.1 sequence differs from that shown due to erroneous gene model prediction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukarýotá, Fungi, Ascomycota; Saccharomycotiná, Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Debaryomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Debaryomyces occidentalis (Yeast) (Schwanniomyces occidentalis).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ñ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34.9%; Score 49.5; DB 1; Length 320; 43.5%; Pred. No. 8.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            188 188 I -> T (IN REF. 1).
320 AA; 36509 MW; EE96936DD68B3703 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Hexokinase (EC 2.7.1.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       478 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE003721; AAF55514.1; ALT_SEQ.
EMBL; AV058248; AAL13477.1; -
FlyBase; FBGN0038585, CG7993.
InterPro; IPF007109; Brix.
Pfam; PF04427; Brix; 1.
Hypothetical protein; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 WAAQEYGRELRRMSDEFVDSFKK 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                              STRAIN=Berkeley;
MEDLINE=22426066; PubMed=12537569;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-ATCC 2322 / CBS 819;
MEDLINE-95339407; PubMed-7614556;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sest Local Similarity
                                                                                                                                                                                                                         [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=27300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HXK_DEBOC
P50506:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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VP5_BTV2A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
                                                                                                                                                                                                                                                                                                                                                     RESULT 11
δŽ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of the ARO4 gene encoding a second DAHP synthase.";

Curr. Genet. 29:441-445(1996).

-!- FUNCTION: STEREOSPECIFIC CONDENSATION OF PHOSPHOENOLPPRUVATE (PEP)

AND D-ENYTHROSE-4-PHOSPHATE (E4P) GIVING RISE TO 3-DEOXY-D-

ARABINO-HEPTULOSONATE-7-PHOSPHATE (DAHP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PARTIAL SEQUENCE FROM N.A.
MEDLINE=96207468; PubMed=8625423;
Pereira S.A., Livi G.P.;
"Aromatic amino-acid biosynthesis in Candida albicans: identification
                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEBS-2003 (Rel. 41, Last annotation update)
Phospho-2-dehydro-3-deoxyheptonate aldolase, tyrosine-inhibited
(EC 4.1.2.15) (Phospho-2-**etco-3-deoxyheptonate aldolase) (DAHP
synthetase) (3-deoxy-D-arabino-heptulosonate 7-phosphate synthase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENZYME REGULATION: INHIBITED BY TYROSINE (BY SIMILARITY).
PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
                                                                                                                                                                                                                                                         Transferase; Kinase; Glycolysis; Allosteric enzyme; ATP-binding. BINDING 111 111 111 GLGCOSE-BINDING (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; mitosporic Saccharomycetales; Candida.
                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATALYTIC ACTIVITY: 2-dehydro-3-deoxy-D-arabino-heptonate
phosphate + phosphate = phosphoenolpyruvate + D-erythrose
phosphate + H(2)0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: BELONGS TO CLASS-I DAHP SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                   34.5%; Score 49; DB 1; Length 478; 42.1%; Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-AFCC 11651 / B792;
Sousa S., Pereira S.A., Livi G.P.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                      080D5F9134478ABA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             370 AA.
                                                                                                                                                                                                                                                                                                                                                                5; Mismatches
                                                                                                                                                                                                                                                                                                                                                    Pred. No.
                                                                                                                                                                                Pfan: PF03727; hexokinase2; 1. Pfan: PF03727; hexokinase2; 1. Pfan: PF00349; hexokinase; 1. PR1NTS; PR00475; HEXOKINASE. ProDom; PD001109; Hexokinase; 1. PROSITE; PS00378; HEXOKINASES; 1.
                                                                                                                                       PIR; S57203; S57203.
HSSP; Q26609; 1BDG.
InterPro; IPR001312; Hexokinase.
                                                                                                                                                                                                                                                                                                                                                                                                            | ||:::| |: :|||38 GETLRKITDHFISELEKGL 56
                                                                                                                                                                                                                                                                                                                                                                                         9. GRELRRASDEFVDSFKKGL 27
                                                                                                                                                                                                                                                                                                      478 AA; 53066 MW;
                                                                                                                            EMBL; S78714; AAB34892.1; -.
                                                                                                                                                                                                                                                                                                                                                  42.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Candida albicans (Yeast).
                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                 Local Similarity
ses 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=5476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           first step.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AROG_CANAL
                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AROG_CANAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 10
QΫ́
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -:- EUNCTION: THE VES PROTEIN IS ONE OF THE TWO PROTEINS (WITH VP2)
WHICH CONSTITUTE THE THE VEST PARTICLE OUTER CAPSID.
-!- SIMILARITY: BELONGS TO THE REQVIRUSES VP5 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDINE-9020938; PubMed=2157314; Hirasawa I., Roy P.; PubMed=2157314; Mithe nucleotide sequence of VP5 of a strain of bluetongue virus of serotype 2 isolated in the USA reveals its close relationship with a virus of serotype 1 isolated in Australia."; Virus Res. 15:107-112(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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                                                                                                                                                                                                                                                                     Pram; PF00793; DAHP_Synth_1; 1.
ProDom; PD005060; AroFGH; 1.
TIGRFAMS; TIGR00034; aroFGH; 1.
Aromatic amino acid biosynthesis; Lyase; Multigene family.
SEQUENCE 370 AA; 40291 MW; 11E5E324C8D7B6DB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         526 AA; 58953 MW; DE50D6013B983A04 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 48; DB 1;
Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bluetongue virus (serotype 2 / isolate USA). Viruses; dsRNA viruses; Reoviridae; Orbivirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Outer capsid protein VP5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     526 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 AAQEYGRELRRMSDEFVDSFKKGL 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                InterPro; IPRO06219; AroFGH.
InterPro; IPRO06218; DAHP1/KDSA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; A43486; P5XRBU.
InterPro; IPR000145; Orbi_VP5.
Pfam; PF00901; Orbi_VP5; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74 ALEYGKRLKKLADELKD 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                               33.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X62283; CAA44172.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 47.1%;
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 AQEYGRELRRMSDEFVD
                                                                                                                                                     EMBL; U53216; AAB48240.1;
HSSP; P00886; 1QR7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10907;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- FUNCTION: Is required not only for elongation of protein synthesis but also for the initiation of all mRNA translation through initiator tRNA(fMet) aminoacylation (By similarity).
-!- CATALYTY: ATP + L-methionine + tRNA(Met) = AMP + dipbosphate + L-methionyl-tRNA(Met).
-!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
-!- SUBUNIT: HOMOdimer (By similarity).
                                                                                                                                                                                                                                                                                                 STRAIN=MSBB / DSM 3109;
MEDLINE=99287316; PubMed=10360571;
Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
Haft D.H., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
Fividence for lateral gene transfer between Archaea and Bacteria from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family. MetG subfamily 2A.
-i- SIMILARITY: Contains 1 tRNA-binding domain.
                                                    15-011-1999 (Rel. 38, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Methionyl-tRNA synthetase (EC 6.1.1.10) (Methionine--tRNA ligase)
                                                                                                                                            Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
                                                                                                                                                                                                                                 Guipaud O., Marguet E., Noll K.M., de la Tour C.B., Forterre P.;
                                                                                                                                                                                                                                              "Both DNA gyrase and reverse gyrase are present in the hyperthermophilic bacterium Thermotoga maritima."; Proc. Natl. Acad. Sci. U.S.A. 94:10606-10611(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIGRFAMS; TIGR00398; metG; 1.
TIGRFAMS; TIGR00399; metG_C_term; 1.
PROSITE; PS00178; AA_TRNA_LIGASE_1; FALSE_NEG.
PROSITE; PS50886; TRBD; 1.
             629 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   genome sequence of Thermotoga maritima."; Nature 399:323-329(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00133; tRNA-Synt_1; 1.
Pfam; PF01588; tRNA_bind; 1.
PIRSF; PIRSF001528; MetRS_dimerising;
PRINTS; PR01041; TRNASINTHMET.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -:- SUBCELLULAR LOCATION: Cytoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HAMAP; MF_01228; fused; 1.
InterPro; IPR004495; MetG_Cterm.
InterPro; IPR001300; tRNA-synt_1a.
InterPro; IPR001412; tRNA-synt_I.
InterPro; IPR002304; tRNA-synt_met.
InterPro; IPR002547; tRNA-synt_met.
              PRT;
                                                                                                                                                                                                    STRAIN=MSB8 / DSM 3109;
MEDLINE=98021416; PubMed=9380682;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE001768; AAD36162.1; -. PIR; E72297; E72297. HSSP; P23395; 1A8H.
                                        (Rel. 38, Created)
(Rel. 38, Last sequ
(Rel. 41, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U76417; AAB87143.1; -.
             STANDARD;
                                                                                                                 METG OR METS OR TM1085.
                                                                                                                              Thermotoga maritima
                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                           NCBI_TaxID=2336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IGR; TM1085;
                                         5-JUL-1999
             SYM THEMA
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                                                                                                                                                                                                                                                                                                                    ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=92079905; PubMed=1720862; MEDLINE=92079905; PubMed=1720862; Oesternas M., Finan T.M., Stanley J.; Oesternas M., Finan T.M., Stanley J.; Site-directed mutagenesis and DNA sequence of pckA of Rhizobium NGR234, encoding phosphoenolpyruvate carboxykinase: gluconeogenesis and host-dependent symbiotic phenotype."; Mol. Gen. Genet. 230:257-269(1991).
-!- CATALYTIC ACTIVITY: ATP + oxaloacetate = ADP + phosphoenolpyruvate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- PATHWAY: Rate-limiting gluconeogenic enzyme.
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the phosphoenolpyruvate carboxykinase [ATP]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                    Gaps
tRNA-binding; Metal-binding; Zinc; Complete proteome. 10 20 "HIGH" REGION. 97 301 "KMSKS" REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rhizobiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Phosphoenolpyruvate carboxykinase [ATP] (EC 4.1.1.49) (PEP carboxykinase) (Phosphoenolpyruvate carboxylase) (PEPCK).
                                                                                                                                                                                                                                                                 33.8%; Score 48; DB 1; Length 629; 37.5%; Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                    9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobia Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
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B2CED7FA54326B1E CRC64;
                                                                                                                                                                                                               BOE0759F7C78ACEC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HAMAP; MF_00453; -; 1.
InterPro: IPR001272; PEFCK_ATP.
Pfam; PF01293; PEPCK_ATP; 1.
ProDom; PD004723; PEFCK_ATP; 1.
TIGRFAMS; TIGR00224; POKA; 1.
PROSITE; PS00532; PEPCK_ATP; 1.
Gluconeogenesis; Lyase; Decarboxylase; ATP-binding.
                                                                                         ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  537 AA.
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41.7%; Pred. No. 28;
Live 5; Mismatches
                                                                                                                                                                                                                                                                                                                    6; Mismatches
                                                                           TRNA-BINDING
                                                                                                                                                                                                                                                                                                                                                                                              | |||: |:: : || : ||:
LQAAQQAGKDPQEFCDELAEKFKR 78
                                                                                                                                                                                                                                                                                                                                                                 2 LWAAQEYGRELRRMSDEFVDSFKK 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATP
                                                                                                                                                                                                                    73004 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rhizobium sp. (strain NGR234)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X63291; CAA44925.1; -. HSSP; P22259; 1AQ2.
                                                                                                                                                                                                                                                                                                                  9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                              301
629
125
128
146
300
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                                                                                                                                                                                                                    629 AA;
                                                                                                                                                                                                                                                                                         Similarity
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RNA-binding;
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SEQUENCE
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                                                                                             METAL
METAL
METAL
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                                                                                                                                                                                                                                                                                                                    Matches
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STRAIN=297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fraser C.M., Casjons S., Huang W.M., Sutton G.G., Clayton R.A.,
Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE=98300335; PubMed=9636706; Ford M.E., Sarkis G.J., Belanger A.E., Hendrix R.W., Hatfull G.F.; "Genome structure of mycobacteriophage D29: implications for phage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia
                                                                                                                                                                           no RNA stage; Caudovirales; Siphoviridae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33.5%; Score 47.5; DB 1; Length 595; 45.5%; Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      interiro, ipr005021; Phage_termin.
Pfam; PF03354; Phage_terminase; 1.
SEQUENCE 595 AA; 66397 MW; AFD123ED5371E263 CRC64;
                                                                                                                                                                                                                                                                    J. Mol. Biol. 279:143-164(1998).
-!- SIMILARITY: BELONGS TO THE PHAGE TERMINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thesis (1994), National Taiwan University, Taiwan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Borrelia burgdorferi (Lyme disease spirochete).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0CT-1996 (Rel. 34, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
                                                                                                     (Rel. 37, Created)
(Rel. 37, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      631 AA.
                                                                                 595 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RNA polymerase sigma factor rpoD (Sigma-70) RPOD OR BB0712.
             25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 NLWAAQEYGRELRRMSDEFVDS 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-ATCC 35210 / B31;
MEDLINE=98065943; PubMed=9403685;
3 WAA-QEYGRELRRMSDEFVDSFKK
                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF022214; AAC18453.1; -. PIR; B72801; B72801.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 89-631 FROM N.A. STRAIN=ATCC 35210 / B31;
Pan M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                STANDARD;
                                                                                                                                                              Mycobacteriophage D29.
Viruses; dsDNA viruses,
NCBI_TaxID=28369;
                                                                                                                                        Gene 13 protein (GP13).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=139;
                                                                               VG13_BPMD2
O64206;
                                                                                                        15-DEC-1998
                                                                                                                  15-DEC-1998
                                                                                                                              28-FEB-2003
                                                                                                                                                                                                                                                            evolution."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                         RESULT 14
VG13_BPMD2
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licensedisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                               Pan M., Yeh J., Tsai C.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THE SIGMA FACTOR IS AN INITIATION FACTOR THAT PROMOTES
ATTACHMENT OF THE RNA POLYMERASE TO SPECIFIC INITIATION SITES AND
THEN IS RELEASED. THIS IS THE PRIMARY SIGMA-FACTOR OF THIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000943; Sigma_70.
Pfam; PF03979; sigma70_r1_1; 1.
Pfam; PF044642; sigma70_r1_2; 1.
Pfam; PF04545; sigma70_r2; 1.
Pfam; PF045545; sigma70_r3; 1.
Pfam; PF045545; sigma70_r4; 1.
PROSITE; PS00715; SIGMA70_r4; 1.
PROSITE; PS00716; SIGMA70_2; 1.
Transcription regulation; Sigma factor; DNA-directed RNA polymerase;
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     Hanson M.
Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M. van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J., Utterback T., Watthey L., McDonald L., Artiach P., Bowman C., Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B., Smith H.O., Venter J.C., "Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       132 POLYMERASE CORE BINDING (POTENTIAL).
508 H-T-H MOTIF (BY SIMILARITY).
73642 MW; BD565AB7D8F44796 CRC64;
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Job time: 26 secs
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Pred. No.
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50.0%;
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                                                                                                                                                                                                                            Nature 390:580-586(1997).
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September 23, 2003, 09:43:16; Search time 96 Seconds (without alignments) 72.577 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                            US-09-544-664B-2
142
1 NLWAAQEYGRELRRMSDEFVDSFKKGL 27
                                                                                                                                                                                                                                                                                                                                   830525 seqs, 258052604 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                            OM protein - protein search, using sw model
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2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
1: sp_nhc:*
10: sp_phage:*
10: sp_phage:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_virus:*
17: sp_virus:*
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19: sp_virus:*
14: sp_unclassified:*
15: sp_viris:*
16: sp_viris:*
17: sp_viris:*
18: sp_viris:*
18: sp_viris:*
19: sp_viris:*
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Gapop 10.0 , Gapext 0.5
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_rvirus:*
sp_bacteriap:*
sp_archeap:*

	Description	09i9n2 brachydanio	Q8h4m3 oryza sativ	Q8r8yl thermoanaer	Q81mf2 oryza sativ	064692 arabidopsis	Q8tvx8 methanopyru	Q9hzq3 pseudomonas	28n955 homo sapien	Q8xxs6 ralstonia s	Q8f5r1 leptospira	Q8eh69 shewanella	9u111 drosophila	29w5b6 drosophila	295u84 drosophila	Q8kdc3 chlorobium	Ogail5 streptomyce
SUMMARIES		Q9I9N2	Q8H4M3	8R8Y1	Q8LMF2	064692	Q8TVX8	Q9HZQ3) 526N8()		Q8F5R1	98Ен69		29W5B6		Q8KDC3	
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	% Query Match	59.2	38.0	37.3	36.6	35.9	35.9	35.9	35.2	35.2	35.2	35.2	35.2	35.2	34.9	34.5	34.5
	Score	84	54	53	52	. 21	51	51	20	20	20	20	50	20	49.5	49	49
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2 LWAAQEYGRELRRMSDEFVDSFKK 25

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606 AA.

PRT;

PRELIMINARY;

Q8H4M3 Q8H4M3;

RESULT 2 Q8H4M3 ID Q8H4M

Q8pyk0 methanosarc Q9ruk9 deinococcus Q8thm7 methanosarc O17342 caenorhabdi Q9hk10 thermoplasm Q87b15 thermoplasm Q87b17 clostridium Q97b17 clostridium Q9dbu0 potato mop- Q8vjs3 mycobacteri Q10843 mycobacteri Q9hy62 pseudomonas Q9fq05 atrichum an Q8ppy8 xanthomonas Q9fq05 atrichum an Q8bad6 bluetongue Q8bad7 bluetongue Q8bad6 bluetongue Q8bad7 bluetongue Q8bad7 bluetongue Q8bad7 bluetongue Q8bad8 staphylococ Q8w4z1 brassica ol Q9sxj6 arabidopsis Q94jy6 arabidopsis Q95t19 brassica ca	6 AA. ce update) tion update) rio). Vertebrata; Euteleostomi; Ostariophysi; Cypriniformes; osis regulators identified in B5107ECB CRC64; DB 13; Length 146;	4; Indels 0 ; Gaps 0 ;
34.5 378 17 Q8PYK0 34.5 564 16 Q9RUK9 34.5 1350 9 17 Q9HKL0 34.5 1690 17 Q9HKL0 34.2 1713 17 Q97B15 34.2 1303 12 Q9GBUG 33.8 223 16 Q9CBUG 33.8 223 16 Q9CBUG 33.8 228 10 Q9CBUG 33.8 295 16 Q9HKC5 33.8 295 16 Q9HC5 33.8 295 16 Q9HC5 33.8 357 16 Q9FUG5 33.8 357 16 Q9FUG5 33.8 373 10 Q9FUG5 33.8 233 17 Q9FUG3 33.5 233 17 Q2GUG 33.5 233 17 Q2GUG 33.5 234 16 Q8CAPC 33.5 239 10 Q8WAZ1 33.5 239 10 Q8WAZ1 33.5 309 10 Q9CAZ1 33.5 311 10 Q9CAZ1 33.5 311 10 Q9CAZ1	INARY; PRT; 146 Lrel. 15, Created) Lrel. 22, Last sequence trel. 22, Last annotatively contata; Craniata; Clebrafish) (Danio rery Created) Clebrafish) (Danio rery Created) Clebrafish) (Danio are contata; Created) Clebrafish) (Danio annotata; Created) Clebrafish) (Danio annotata; Created) PubMed=10917738; 3., The mammalian apoptore of the contata annotata; Created) F66962.2;	vative 5; Mismatc
11 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	RESULT 1 Q919N2 D919N2 DT 01-0CT-2000 (TrEMBLY DT 01-0CT-2001 (TrEMBLY DT 01-0CT-2002 (TREMBLY DE Bad. GN BY BAD. GN BAD. GN BAD. GN	les 15;

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Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBL_TaxID=3702;
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                                                                                                                                        STRAINSON.

STRAINSON.

McCombie W.R., de la Bastide M., Spiegel L., Preston R., Ferraro K.,

Kuit K., Nascimento L., Zutavern T., Balija V., Bell M., Baker J.,

Santos L., Miller B., Katzenberger F., Muller S., King L., Yang C.,

Dike S., O'Shaughnessy A., Palmer L., Dedhia N.;

"Genomic sequence for Oryza sativa, Nipponbare strain, clone

OJ1325DOS, from chromosome IO, complete sequence.";

Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AC115686; AAM74351.1;
Oryza sativa (japonica cultivar-group).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-cv. Columbia;
Rounsley S.D., Kaul S., Lin X., Ketchum K.A., Crosby M.L.,
Brandon R.C., Sykes S.M., Mason T.M., Kerlavage A.R., Adams M.D.,
Somerville C.R., Venter J.C.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=99218843; PubMed=10200325;
Thomas S.G., Phillips A.L., Hedden P.;
"Molecular cloning and functional expression of gibberellin 2-oxidases, multifunctional enzymes involved in gibberellin deactivation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
0
                                                                                                                                                                                                                                                                                                                                                                                                         36.6%; Score 52; DB 10; Length 889;
40.0%; Pred. No. 79;
live 6; Mismatches 9; Indels
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                                                                                                                                                                                                                                                                                                                                             Hypothetical protein.
SEQUENCE 889 AA; 101583 MW; C47D8715883D6376 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF03171; 20G-FeII_Oxy; 1. SEQUENCE 335 AA; 38216 MW; 181F6EAA1EE1C331 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
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EMBL; AC004077; AAM14908.1; --
EMBL; AJ132437; CAB41009.1; --
InterPro; IPR0055123; 20G-FeII_Oxy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  335 AA
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136 AVEEYIKEMKRMSSKFLEMVEEEL 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Putative GA4 protein. T31E10.11 OR GA20X3.
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Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                         SEQUENCE FROM N.A.
                                                                                    NCBI_TaxID=39947;
                                                                                                                                                                                                                                                                                                                              Gramene; 08LMF2;
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SEQUENCE FROM N.A.

REDIINE=21992816; PubMed=11997336;

RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,

RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,

RA Tan H., Chen R., Wang J., Yu J., Yang H.;

RT Tan H., Chen R., Wang J., Yu J., Yang H.;

RT Genome Res. 12:689-700(2002).

BR Genome Res. 12:689-700(2002).

BR Genome Res. 12:689-700(2002).

RY Hypothetical protein; Complete protecome.

KW Hypothetical protein; Complete protecome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                 Oryza Sativa (japonica cultivar-group).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

NCBI_TAXID=39947;
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                                                                                                                                                                                                                                          STRAIN—cv. Nipponbare;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7, BAC
clone:OJ1116_CO08.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AP004002; BAC20651.1; -
SEQUENCE 606 AA; 68758 MW; D453B0DEF5AB2D94 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                         DB 10; Length 606; 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thermoanaerobacter tengcongensis.
Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
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Hypothetical protein TTE1854.
                01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) 0J1116_C08.8 protein. 0J1116_C08.8
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Last annotation update)
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NCBI_TaxID=119072;
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                                                                                                                                                                                                                                                                                                                                                                                                       Score 54; DB 1
Pred. No. 26;
8; Mismatches
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   Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 WAAQEYGRELRRMSDEFVDSFKKGL
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                                                                                                                                                                                                                                                                                                                                                                                                         38.0%;
40.0%;
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(TrEMBLrel, 23,
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 40.0
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best_Local Similarity 42.9
Matches 9; Conservative
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                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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01-JUN-2002
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Q8R8Y1

RESULT 3

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Q8LMF2;

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RESULT 4 Q8LMF2

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TISSUE-Brain;

RA Anehori K., Ishibashi T., Chiba Y., Fujimori K., Hiraoka S.,

RA Anai H., Watanabe S., Ishida S., Ono Y., Hotuta T., Watanabe M.,

RA Sugiyama T., Irie R., Otsuki T., Sato H., Ota T., Wakamatsu A.,

RA Ishii S., Yamanoto J., Isono Y., Rawai-Hio Y., Saito K., Nishikawa T.,

RA Kimura K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,

RA Wagatsuma M., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,

RA Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;

RY WEDO human cDNA sequencing project.";

RY Submitted (JuL-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AK095662; BACU4601.1; -.

KW HYPOTHARICAL protein.

SQ SEQUENCE 173 AA; 21285 MW; OEBFF3BFD96FE775 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Raistonia solanacearum (Pseudomonas solanacearum).
Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales;
Raistoniaceae, Raistonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 35.2%; Score 50; DB 4; Length 173; Local Similarity 47.6%; Pred. No. 24; No. 24; Aismatches 7; Indels Les 10; Conservative 4; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2002 (TIEMBLrel. 20, Created)
01-MAR-2002 (TIEMBLrel. 20, Last sequence update)
01-MAR-2003 (TIEMBLRel. 23, Last annotation update)
Probable APP-binding ABC transporter protein.
RSC2037 OR RS03602.
                                                                                                                                                                                                                                                                                           01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
  5.
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  5; Mismatches
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EMBL; AL646067; CAD15739.1; -.

InterPro; IPR003593; AAA_ATPase.

InterPro; IRR003439; ABC_transporter.
                                                                                                          611 LTRAESYGPLRDLERLADEFYDA 633
                                                   22
                                                                                                                                                                                                                                       PRT;
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MEDLINE=21681879; Pubmed=11823852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36 KEGGREERRKEERWIDGRKKG 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 QEYGRELRRMSDEFVDSFKKG 26
                                                      2 LWAAQEYG--RELRRMSDEFVDS
                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein FLJ38343.
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  11; Conservative
                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                Q8N955;
                                                                                                                                                                                                                                          Q8N955
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  Matches
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Q8N955
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STRAIN=ATCC 15692 / PAO1;

MEDLINE-20437337; PubMed=10984043;

MEDLINE-20437337; PubMed=10984043;

Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Hickey M.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;

"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                     Methanopyrus kandleri.
Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                             Slesarev A.I., Mezhevaya K.V., Matarova K.S., Polushin N.N., Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L., Natale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O., Malykh A.G., Koonin E.V., Kozyavkin S.A.; "The complete genome of hyperthermophile Methanopyrus kandleri AV19 and monophyly of archaeal methanogens."; Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 35.9%; Score 51; DB 17; Length 722; Best Local Similarity 42.9%; Pred. No. 88; Matches 9; Conservative 7; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1248 AA; 138499 MW; C3D3DBFEE6736C7A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         722 AA; 81933 MW; 7FA609E9868A997E CRC64;
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                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 1248 AA.
                                                   722 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  opportunistic pathogen.";
Nature 406:959-964(2000).
EMBL; AE004720; AAG60332.1; -.
InterPro; IPR003672; Cobn/Mg_chltase.
InterPro; IPR000408; Reg_chr_condens.
Pfam; PF02514; cobn Mg_chel; 1.
PROSITE; PS00626; RCCl_2; 1.
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                                                                                                          Created)
                                                                                                  01-07N-2002 (TrEMBLrel. 21, Created 01-07N-2002 (TrEMBLrel. 21, Last se 01-0CT-2002 (TrEMBLrel. 22, Last an Predicted ArPase of the AAA+ class.
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635 AREHGKELRRKEEEYRNRVRK 655
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-AV19 / DSM 6324 / JCM 9639;
MEDLINE=21927647; PubMed=11930014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 AQEYGRELRRMSDEFVDSFKK 25
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                                                   PRELIMINARY;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=2320;
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                                                                                                                                                                                                                                                                                              Methanopyrus
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                                                   Q8TVX8
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RESULT 6
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                           Q8TVX8
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Length 363;

SEQUENCE

DR KW SQ

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MEDLINE-20196006; PubMed-10731132; Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Papagiannakis G., Spanos L., Bolshakov V., Siden-Kiamos I., Louis "Sequencing the distal X chromosome of Drosophila melanogaster."; Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
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Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases
                                                              39874 MW; D59DE879EA9BFCB6 CRC64;
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Last annotation update)
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Last annotation update)
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Pred. No. 56;
5; Mismatches 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                               371 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
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                                                                                                                    35.2%; Score ilarity 45.0%; Pred. Conservative 5; Mis
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69 AAKEYALKLKKLHDELSDEF 88
                                                                                                                                                                                                                                        4 AAQEYGRELRRMSDEFVDSF 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIGREAMS; TIGRO0420; trmU; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CG3021 protein (LD29918p).
EG:BACR7A4.8 OR CG3021.
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Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EG:BACR7A4.8 protein.
EG:BACR7A4.8 OR CG3021.
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                                                                                         Query Match
Best Local Similarity
9; Conserve
                                                                363 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             371 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                Complete proteome. SEQUENCE 363 AA;
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  TIGE; SO1361; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=7227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               09U1L1
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MEDLINE-22297686, PubMed=12368813;
MEDLINE-22297686, PubMed=12368813;
MEDLINE-22297686, PubMed=12368813;
Medleberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,
Read T.D., Eisen J.A., Scott J., Beanan M., Brinkac L., Daugherty S.,
Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S.,
DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F.,
Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M.,
Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C.,
Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A.,
Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.;
Genome sequence of the dissimilatory metal ion-reducing bacterium
Shewanella oneidensis.";
                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales; Alteromonadaceae; Shewanella.
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JI-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Phospho-2-dehydro-3-deoxyheptonate aldolase, tyr-sensitive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN-56601 / Serovar lai;
                                                                                                                                                    Length 230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35.2%; Score 50; DB 16; Length 330; 39.3%; Pred. No. 51;
                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AE011338; AAN48805.1; -. Lyase; Complete proteome. SEQUENCE 330 AA; 36561 MW; 88B495C834E497C8 CRC64;
                                                                                         7C3FDA1E7A19A2A4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
DTDP-glucose 4,6-dehydratase (EC 4.2.1.46).
RFBB3 OR LA1606.
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                                                                                                                                                                                                             3;
                                                                                                                                               Score 50; DB 16;
Pred. No. 34;
1; Mismatches 3;
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ProDom; PD000006; ABC_transporter; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
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EMBL; AE015580; AAN54426.1; -.
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                                                                                      25231 MW;
                                                                                                                                                 35.2%;
71.4%;
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                                                                                                                                                                                                                                                                                                        6 QEYGRELRRMSDEF 19
                                                                                                                                               Query Match 35.2
Best Local Similarity 71.4
Matches 10; Conservative
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                                SMART; SM00382; AAA; 1.
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                                                                                         230 AA;
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                                                           Complete proteome
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Query Match

Best Loc Matches

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Q8EH69 RESULT 11 Q8EH69

Louis C.;

Gaps

10;

Indels

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Balton G.G., Northang J.R., Yandell M.D., Zhang G., Chen L.M., Randon R.C., Rosers Y.-L. G., Blacks R. C., Mondon R.C., Rosers Y.-L. G., Blacks R. C., Chompon M., Randon R.C., Rosers Y.-L. G., Mandon R.C., Randon R. C., Randon R.C., Randon R. C., Banca P. W., Beenso P. W., Beenson P. W., Beetson P. W., Beetson
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ENBLS AROS8248; AAL13477.1; -

Flybase; FBGN0038585; CG7993.
STRAIN-Berkeley;
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
Yu C., Lewis S.E., Rubin G.M., Celniker S.;
Submitted (Aug-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AR003419; AAF45578.3;
EMBL; AY051773; AAK93197.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34.9%; Score 49.5; DB 5; Length 320; 43.5%; Pred. No. 58; tive 6; Mismatches 4; Indels 3
                                                                                                                                                                                                                                                Score 50; DB 5; Length 389;
Pred. No. 61;
                                                                                                                                                                                                                                                                                   Indels
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320 AA; 36509 MW; EE98936DD68B3703 CRC64;
                                                                                                                                              ElyBase: FBG00040337; ES:BACR7A4.8.
InterPro: IPR004506; TrmU.
Pfam; PF03054; trNA_Me_trans; 1.
TIGRFAMS; TIGRO0420; trmU; 1.
SEQUENCE 389 AA, 43350 MW; 20C9405FFCC9FAE2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein CT1131.
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                                                                                                                                                                                                                                                                                                                                                 57 WACROLGVELROVNYVREYWTAVFSOFLDDYQMGL 91
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9; Mismatches
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149 WAQTE---ELRRLRNLFIDTFQR 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly).
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Best Local Similarity
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Q8KDC3
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Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;

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                                                                         SEQUENCE FROM N.A.

A BISEN J.A., Nelson K.E., Paulson I.T., Heidelberg J.F., Wu M.,

Bisen J.A., Deboy R., Gwinn M.L., Nelson W.C., Haft D.H.,

A Hickey E.K., Peterson J.D., Durkin A.S., Kolonay J.L., Yang F.,

Hickey E.K., Peterson J.D., Durkin A.S., Kolonay J.L., Yang F.,

A Holt I., Umayam L.A., Mason T., Brenner M., Shea T.P., Parksey D.,

Nierman W.C., Feddblyum T.V., Hansen C.L., Craven M.B., Radune D.,

Vanathevan J.C., Tettelin H., White O., Gruber T.M., Ketchum K.A.,

Vanter J.C., Tettelin H., Bryant D.A., Fraser C.M.,

"The complete genome sequence of Chlorobium tepidum T.S., a

photosynthetic, anaerobic, green-sulfur bacterium.",

Broc. Natl. Acad. Sci. U.S.A. 99:9509-9514(2002).
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34.5%; Score 49; DB 16; Length 214;

Best Local Similarity 37.0%; Pred. No. 43;

Matches 10; Conservative 8; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002785; DUF83.

TIGREAMS; TIGR00372; TIGR00372; 1.

Hypothetical protein; Complete proteome.

SEQUENCE 214 AA; 24004 MW; 56D389219D60B6AD CRC64;
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                   Chlorobium.
NCBI_TaxID=1097;
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Search completed: September 23, 2003, 09:45:06 Job time : 101 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

September 15, 2003, 17:16:01; Search time 38.1857 Seconds (without alignments) 112.231 Million cell updates/sec Run on:

US-09-544-664-3 145 1 NLWAAQRYGRELRRMSDEFEGSFKGLP/27) Title: Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

1107863 seqs, 158726573 residues Searched:

1107863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

A_Geneseq_19Jun03:*

| SIDSI/gcgdata/geneseqp_embl/AA1991_DAT:*
| SIDSI/gcgdata/geneseqp_embl/AA1991_DAT:*
| SIDSI/gcgdata/geneseqp_embl/AA1992_DAT:*
| SIDSI/gcgdata/geneseqp_embl/AA1992_DAT:*
| SIDSI/gcgdata/geneseqp_embl/AA1993_DAT:*
| SIDSI/gcgdata/geneseqp_embl/AA1995_DAT:*
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| SIDSI/gcgdata/geneseqcyembl/AA2003_DAT:*
| SIDSI/gcgdata/geneseqcyembl/AA2003_DAT:* | SIDS1/gcgdata/geneseqp_emb1/Aa1982_DAT:*
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| SIDS1/gcgdata/geneseqp_emb1/Aa1984_DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description) 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1								69 Longer murine BAD
El	AAB370	AAB703	AAR951	AAW613	AAW61316	AAW613	AAW613	AAW588	AAB703
DB	21	22	17	19	13	13	19	19	22
% Query Match Length DB ID	27	162	204	204	204	204	204	204	204
% Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
Score	145	145	145	145	145	145	145	145	145
Result	П	2	m	4	Ŋ	φ	7	φ	σ
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WPI; 2000-679325/66

Murine BAD protein BAd-DTTR apoptosis Bc12 polypeptide B Bc6 protein for Human Bc1-xL/Bc1-7 Human Bc1-xL/Bc1-7 Human BAD mutant a Human BAD protein Human BAD protein Human BAD protein Human BAD protein Human Bad peptide PTPC-interacting T Wutant Bc12 compet Human Bc12 compet Human Bc12 compet Human Bad peptide Mutant Bc12 compet	Ead Bad Bad T Bad T Bol T Bol Bad Bad T Bol Bad
24 ABR39082 22 AAU00220 21 AAB37001 21 AAB37002 21 AAB37055 18 AAB37055 19 AAB37055 22 AAB37055 22 AAB3572 22 AAB3572 22 AAB3577 22 AAB787 23 AAU78627 23 AAU78610 23 AAU78610	23 AAU7861 23 AAU7861 23 AAU7862 23 ABG7849 23 ABG7849 23 AAU7861 23 AAU7861 23 AAU7862 23 AAU7862
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44 113 114 116 116 116 117 118 118 118 118 118 118 118 118 118	. W W W W W & 4 4 4 4 4 4

ALIGNMENTS

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Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective; cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad; apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate; colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma; melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;
                                                                                                                                                                                                                                                                                                                                                            :2
                                                                                                                                                                                                                                                                                                                                                            Ľ
                                                                                              Bcl2 polypeptide BH3 domain peptide #3.
                                                                                                                                                                                                                                                                                                                                                           Wang J, Zhang Z, Shan S,
                           AA
                        AAB37003 standard; peptide; 27
                                                                                                                                                                                                                                                                                                                                  (UYJE-) UNIV JEFFERSON THOMAS
                                                                                                                                                                                  stroke; myocardial infarction
                                                                                                                                                                                                                                                                                                           07-APR-1999; 99US-0128202.
                                                                                                                                                                                                                                                                                  06-APR-2000; 2000WO-US09352
                                                                       (first entry)
                                                                                                                                                                                                                                  WO200059526-Al.
                                                                                                                                                                                                          Homo sapiens
                                                                       28-FEB-2001
                                                                                                                                                                                                                                                          12-OCT-2000.
                                                                                                                                                                                                                                                                                                                                                           Huang Z,
                                                AAB37003;
RESULT 1
             AAB37003
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The invention relates to a peptide conjugate having the formula:

(R.X)n-peptide where n = 1-10; X = C=0, when the R-X group is attached
to the N-terminus of the peptide, or a side chain of the peptide where
the functional group of the side chain is NE2 or OH; or X = O or NH;
when the R-X group is attached to the C-terminus of the peptide, or a
side chain of the peptide, where the side chain functional group is COOH
or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally
monosubstituted with a 1-5C straight or branched chain alkyl group,
phenyl optionally monosubstituted with a 1-5C straight or branched chain
alkyl group, or benzyl. The peptides AAB37001-B37058 represent analogues
of the peptide portion of the conjugate. The peptides represent analogues
of a BC1-2 superfamily polypeptide corresponding to amino acids 72-97 of
the BH3 domain of the cell death agonist Bad. The peptide conjugate is
useful for modulating apoptosis in the cells of a subject, or for
reversing B cell lymphoma/leukemia 2 (BC1-2)-mediated blockage of
apoptosis in cancer cells. It is also useful for inhibiting BC1-2
function. In particular, the peptide conjugate is useful for treating a
subject afflicted with a cancer characterized by cancer cells that
express BC1-2. The cancer includes prostate, colorectal, gastric,
non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis; immunostimulant; neuroprotective; nootropic; antiischaemic; vulnerary; cytostatic; antiviral; antiarthritc; antiinflammatory; wound healing; immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer; immunodeficiency disease; neurodegenerative disease; viral infection; ischaemic cell death; reperfusion cell death; arthritis; infertility; lymphoproliferative condition; inflammation; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide conjugate is also useful for treating disorders characterized by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                  New peptide conjugates for modulating apoptosis or for inhibiting cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for treating neurodegenerative disorders, stroke, or cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 increased apoptosis, e.g. neurodegenerative disorders, acquired immunodeficiency syndrome (AIDS), stroke or myocardial infarction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ·;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shorter murine BAD mutant amino acid sequence SEQ ID NO:3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 145; DB 21;
100.0%; Pred. No. 2.6e-15;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 NLWAAQRYGRELRRMSDEFEGSFKGLP 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB70370 standard; protein; 162 AA.
                                                                                                      Claim 18; Page 17; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAY-2000; 2000WO-US11864.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0136783.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-MAY-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200110888-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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The present invention describes an isolated or synthetic polypeptide

(I) comprising a less than full length amino acid sequence of a mutant

Ball acid. 2 associated cell death regulator polypeptide (BAD) or its

fragment, which contains amino acid substitutions at Seril8 of a human

Expansion of a murine BAD. (I) has immunostimulant, neuroprotective,

BAD (shorter murine BAD). (I) has immunostimulant, neuroprotective,

nootropic, antifichaemic, vulnerary, cytostatic, antiviral,

antiarthritic, antiniflammatory and immunosuppressive activities, and

can be used as an apoptosis inducer or inhibitor. BAD polypeptides and

polynucleotides can be used for screening candidate compounds and drugs

for activity that promote cell survival or apoptosis. Other uses include

inducing or inhibiting apoptosis in a cell. Candidate compounds

identified and (mutant) BAD polypeptides are useful in treating

immunodeficiency diseases, neurodegenerative diseases, ischaemic cell

death, reperfusion cell death, wound healing, cancer, viral infections,

autoimmune diseases. The present sequence represents a specifically

claimed shorter murine BAD mutant amino acid sequence from the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Epitope; murine; bcl-x(L)/bcl-2 associated death promoter; Bad; stroke; polypeptide; bcl-x; cell death; regulate; BH1; BH2; apoptotic cell death; cytokine deprivation; IL-3 dependent cell line; immunodeficiency; AIDS; neurodegenerative disease; senescence; ischaemia; neoplasia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                         New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide, useful for screening for candidate compounds which induce or inhibit apoptosis, comprises amino acid substitutions at Ser118, Ser155 or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 162;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "BH1 conserved amino acids"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "BH2 conserved amino acids"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bcl-x(L)/bcl-2 associated death promoter protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 100.0%; Score 145; DB 22; Similarity 100.0%; Pred. No. 1.9e-14; 27; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 NLWAAQRYGRELRRMSDEFEGSFKGLP 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "PEST sequence'
                                                                                                                                                                                                   Claim 7; Page 148-149; 157pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA.
(APOP-) APOPTOSIS TECHNOLOGY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR95168 standard; Protein; 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                       WPI; 2001-138734/14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     162 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
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Best Local S:
Matches 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                     Zhou X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Region
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ID AAR9
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Korsmeyer SJ;

NAME OF THE PROPERTY OF THE PR

31-OCT-1995; 31-OCT-1994;

09-MAY-1996.

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The present invention describes mutant bab (BLLTAL/BLLT associated cell death regulator) proteins, having an amino and other than Ser at position 112 and/or 136, relative to the murine BAD 204 as sequence. The position 112 and/or 136, relative to the murine BAD 204 as sequence. The fragments of mutant BAD protein. Also described are: (1) fragments of mutant BAD with a heterologous polypeptide that concrases intracellular delivery. Mutant BAD proteins are used to treat or prevent diseases associated with reduced apoptosis, e.g. cancer, viral infection, lymphoproliferation, arthritis, infertility, infertion, lymphoproliferation, arthritis, infertility, infertion and autoimmune disease. Polynucleotide sequences encoding mutant BAD proteins can be used similarly by gene therapy or to produce transgenic animals for use as disease models or in drug screening. BAD creaming the specified Ser are used to screen for enhancers of inhibitors of serine-phosphatase. Inhibitors are potentially useful intendent of excessive apoptotic status of cells is determined by measuring relative amounts of phosphorylated and non-phosphorylated bab, by usual immunoassays. Mutant BAD proteins have greater death-promoting activity than wild-type BAD which can become phosphorylated on the specified Ser, forming a product that does not beterodiments with BCL-2 or BCL-XL but instead binds to 14-3-3 family but the cytosol, thus promoting cell survival. The mutants with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Murine, mouse, BCL-XL/BCL-2 associated cell death regulator; BAD protein, serine substituted mutant; apoptosis; cancer; viral infection.
                                                                                                                                                                                                                        present invention describes mutant BAD (BCL-XL/BCL-2 associated cell
                                                                       New mutant BAD polypeptide with phosphorylatable serine replaced -
useful for, e.g. treating reduced apoptosis such as in cancer or
viral infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mutant BCL-XL/BCL-2 associated cell death regulator #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 145; DB 19;
100.0%; Pred. No. 2.4e-14;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            140 NIWAAQRYGRELRRMSDEFEGSFKGLP 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 NLWAAQRYGRELRRMSDEFEGSFKGLP 27
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                                                                                                                                                                          Claim 1; Fig 10; 95pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UNIW ) UNIV WASHINGTON
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WPI; 1998-261422/23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          204 AA;
                           N-PSDB; AAV27833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Korsmeyer SJ;
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Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW61316;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 5
AAW61316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents the murine bcl-x(L)/bcl-2 associated death promoter (Bad) gene. Bad is a 22.1 kD protein which interacts with bcl-2 and bcl-x proteins and regulates cell death. It has homology to the bcl-2-related family clustered in the BH1 and BH2 domain. Bad has been found to hybridise to bcl-x(L) and bcl-2 in yeast two-hybrid assays and in vivo in mammalian cells. Overexpressed Bad counters the death inhibitory activity of bcl-x(L), but is much less effective at countering the death inhibitory activity of bcl-x(L). Bad expression can accelerate apoptotic cell death induced by cytckine deprivation in an IL-3 dependent cell line expressing bcl-x(L). Bad competes with Bax for binding to bcl-x(L). Bad may be used to identify agents which inhibit its binding to bcl-x(L) to form heterodimers. Such agents may be used to treat neurodegenerative diseases, immunodeficiency diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein; serine substituted mutant; apoptosis; cancer; viral infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                  Polynucleotide encoding bcl-x(L)/bcl-2 associated death promoter useful to treat neoplasia and apoptosis and to identify agents inhibiting its binding to bcl-2 or bcl-x(L) to form heteromultimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 145; DB 17; Length 204; 100.0%; Pred. No. 2.4e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Murine BCL-XL/BCL-2 associated cell death regulator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        140 NIWAAQRYGRELRRMSDEFEGSFKGLP 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 NLWAAQRYGRELRRMSDEFEGSFKGLP 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      e.g. AIDS, senescence or ischaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW61315 standard; Protein; 204 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           llarity 100.0%; Por Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 3; Fig 1; 130pp; English
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                                                                                                94US-0333565.
                                              95WO-US14246
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Matches 27; Conserv
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Seguence

Query Match

WO9817682-A1

Mus sp

30-APR-1998

07-0CT-1998

AAW61315;

RESULT 4 AAW61315

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17-0CT-1997; 18-OCT-1996; Korsmeyer SJ

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Gaps

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Length 204; Indels 4

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Matches
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                                                                                            The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell death regulator) proteins, having an amino acid other than Ser at position 112 and/or 136, relative to the murine BAD 204 aa sequence. The present sequence represents a mutant BAD protein. Also described are: (1) I fragments of mutant BAD protein able to decrease cell viability; (2) increases intracellular delivery. Mutant BAD proteins are used to treat or prevent diseases associated with reduced apoptosis, e.g. cancer, viral infection, lymphoproliferation, arthritis, infertility, mutant BAD proteins can be used similarly by gene therapy or to produce transgenic animals for use as disease models or in drug screening. BAD proteins phosphorylated at specified Ser are used to screen for enhancers and inhibitors of serime-phosphatase. Inhibitors are potentially useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein; serine substituted mutant; apoptosis; cancer; viral infection.
                                                                                                                                                                                                                                                                                                        phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have greater death-promoting activity than wild-type BAD which can become phosphorylated on the specified Ser, forming a product that does not heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family proteins in the cytosol, thus promoting cell survival. The mutants with Ser substituted cannot bind 14-3-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                     in treatment of excessive apoptosis such as AIDS, neurodegeneration, aging or ischaemic cell death. The apoptotic status of cells is determined by measuring relative amounts of phosphorylated and non-
                   New mutant BAD polypeptide with phosphorylatable serine replaced useful for, e.g. treating reduced apoptosis such as in cancer or viral infection
                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 145; DB 19; Length 204; 100.0%; Pred. No. 2.4e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mutant BCL-XL/BCL-2 associated cell death regulator #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     140 NIWAAQRYGRELRRMSDEFEGSFKGLP 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 NLWAAQRYGRELRRMSDEFEGSFKGLP 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW61317 standard; Protein; 204 AA.
                                                                        Claim 7; Page 59; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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N-PSDB; AAV27835.
                                                                                                                                                                                                                                                                                                                                                                                              204 AA;
N-PSDB; AAV27834.
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Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 6
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The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell death regulator) proteins, having an amino acid other than Ser at position 112 and/or 136, relative to the murine BAD 204 as sequence. The position 12 and/or 136, relative to the murine BAD 204 as sequence. The present sequence represents a mutant BAD protein. Also described are: (1) fragments of mutant BAD protein able to decrease cell viability; (2) increases intracellular delivery. Mutant BAD proteins are used to treat or prevent diseases associated with reduced apoptosis, e.g. cancer, viral infection, lymphoproliferation, arthritis, infertility, infertility, infertility infarmation and autoimmune disease. Polynucleotide sequences encoding mutant BAD proteins can be used similarly by gene therapy or to produce transgenic animals for use as disease models or in drug screening. BAD proteins phosphorylated at specified Ser are used to screen for enhancers and inhibitors of serine-phosphatase. Inhibitors are potentially useful in treatment of excessive apoptosis such as AIDS, neurodegeneration, aging or ischaemic cell death. The apoptotic status of cells is determined by measuring relative amounts of phosphorylated and non-phosphorylated and the specified Ser, forming a product that does not phosphorylated on the specified Ser, forming a product that does not proteins in the cytosol, thus promoting cell survival. The mutants with cell ser substituted cannot bind 14-3-3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
New mutant BAD polypeptide with phosphorylatable serine replaced useful for, e.g. treating reduced apoptosis such as in cancer or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 145; DB 19; 100.0%; Pred. No. 2.4e-14;
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                                                                                                                                                  Claim 7; Page 60; 95pp; English
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les 27; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-261422/23.
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                                                                       viral infection
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                                                                                                                                  death regulator) proteins, having an amino acid other than Ser at position 112 and/or 136, relative to the murine BAD 204 as sequence. The present sequence represents a mutant BAD protein. Also described are: (1) fragments of mutant BAD protein to decrease cell viability; (2) fusion proteins of mutant BAD with a heterologous polypeptide that increases intracellular delivery. Mutant BAD proteins are used to treat or prevent diseases associated with reduced apoptosis, e.g. cancer, viral infection, lymphoproliferation, arthritis, infertility, viral infection, lymphoproliferation, arthritis, infertility, mutant BAD proteins can be used similarly by gene therapy or to produce transgenic animals for use as disease models or in drug screening. BAD proteins phosphorylated at specified Ser are used to screen for enhancers and inhibitors of serine-phosphatase. Inhibitors are potentially useful
                                                                                                                    present invention describes mutant BAD (BCL-XL/BCL-2 associated cell
                                                                                                                                                                                                                                                                                                                                                                                       in treatment of excessive apoptosis such as AIDS, neurodegeneration, aging or ischaemic cell death. The apoptotic status of cells is determined by measuring relative amounts of phosphorylated and non-phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have greater death-promoting activity than wild-type BAD which can become phosphorylated on the specified Ser, forming a product that does not heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family proteins in the cytosol, thus promoting cell survival. The mutants with Ser substituted cannot bind 14-3-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BAD protein, Bcl-XL/Bcl-2 associated cell death regulator; 14-3-3; serine phosphorylation; post-translational modification; apoptosis; signal transduction regulator; phosphoserine phosphatase; senescence; immunodeficiency disease; neurodegenerative disease; infertility; cancer, viral infection; lymphoproliferative condition; arthritis; inflammation; autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
New mutant BAD polypeptide with phosphorylatable serine replaced useful for, e.g. treating reduced apoptosis such as in cancer or viral infection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 145; DB 19;
Pred. No. 2.4e-14;
Mismatches 0;
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                                                                              Claim 7; Page 60-61; 95pp; English.
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Best Local Similarity
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This sequence represents a novel serine-phosphorylated protein, BAD

(Bc1-X1/Bc1-2 associated cell death regulator). The serine residue is
phosporylated in a post-translational modification and allows binding

to the 14-3-3 protein which is a signal transduction regulator.

Modulators of phosphorylated BAD, which act through inhibition/activation

of a phosphoserine phosphatase, are useful for preventing/treating

increased/decreased apoptosis in a cell. The increased apoptosis may

result from immunodeficiency diseases, senescence, neurodegenerative

disease, isohaemic cell death, repertusion cell death, infertility and

wound-healing. Decreased apoptosis may result from cancer, viral

infection, lymphoproliferative conditions, arthritis, infertility.

inflammation and autoimmune diseases. Measuring the amount of

thosphorylated compared to unphosphorylated BAD polypeptide and/or total

EAD in a cell is useful for determining the apoptotic state of a cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis; immunostimulant; neuroprotective; nootropic; antiischaemic; vulnerary; cytostatic; antiviral; antiarthritic; antiinflammatory; wound healing; immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer; immunodeficiency disease; neurodegenerative disease; viral infection; ischaemic cell death; reperfusion cell death; arthritis; infection; lymphoproliferative condition; inflammation; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide, useful for screening for candidate compounds which induce or inhibit apoptosis, comprises amino acid substitutions at Serl18, Serl55 or Serl13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
            Serine-phosphorylated Bcl-X-1/Bcl-2 Associated cell Death regulator polypeptide - useful for modulation of apoptosis associated with, e.g. cancer and immunodeficiency diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Longer murine BAD mutant amino acid sequence SEQ ID NO:2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 145; DB 19; 100.0%; Pred. No. 2.4e-14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 140 NLWAAQRYGRELRRMSDEFEGSFKGLP 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 NLWAAQRYGRELRRMSDEFEGSFKGLP 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB70369 standard; protein; 204 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (APOP-) APOPTOSIS TECHNOLOGY INC.
                                                                                            Claim 3; Fig 8; 61pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAY-2000; 2000WO-US11864.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0136783.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 100.
nes 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-138734/14
                                                                                                                                                                                                                                                                                                                                                                                                                          204 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200110888-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-FEB-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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Matches
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Region
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                            The present invention describes an isolated or synthetic polypeptide

(I) comprising a less than full length amino acid sequence of a mutant

BC1-XL/BC1-2 associated cell death regulator polypeptide (BAD) or its

fragment, which contains amino acid substitutions at Seril8 of a human

BAD, SeriS5 of a mutine BAD (longer murine BAD) or Seril3 of a murine

BAD (shorter murine BAD). (I) has immunostimulant, neuroprotective,

nootropic, antischaemic, vulnerary, cytostatic, antiviral,

antiarthritic, antiinflammatory and immunosuppressive activities, and

can be used as an apoptosis inducer or inhibitor. BAD polypeptides and

con be used as an apoptosis in a cell. Candidate compounds and drugs

for activity that promote cell survival or apoptosis. Other uses include

inducing or inhibiting apoptosis in a cell. Candidate compounds

identified and (mutant) BAD polypeptides are useful in treating

immunodeficiency diseases, neurodegenerative diseases, ischaemic cell

death, reperfusion cell death, wound healing, cancer, viral infections,

claimed longer murine BAD mutant amino acid sequence from the present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes a method (M1) for inducing apoptosis in a cell infected with herpes simplex virus (HSV), which comprises administering to the cell, a composition having an agent that inhibits phosphorylation of pro-apoptotic polypeptide BAD by HSV US3. Also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Inducing apoptosis in a cell infected with herpes simplex virus, HSV, by administering to the cell, a composition comprising an agent that inhibits phosphorylation of pro-apoptotic polypeptide BAD by HSV US3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BAD; herpes simplex virus; HSV; US3; herpes virus; apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                              Length 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               Score 145; DB 22;
Pred. No. 2.4e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 NLWAAQRYGRELRRMSDEFEGSFKGLP 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 15; Page 168; 192pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABR39082 standard; Protein; 204 AA
Claim 4; Page 148; 157pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Murine BAD protein SEQ ID NO:4.
                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-JUL-2002; 2002WO-US24177.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-JUL-2001; 2001US-308929P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-MAY-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.0
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Munger J, Roizman B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UYCH-) UNIV CHICAGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-248168/24.
N-PSDB; ABZ81201.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              virucide; infection
                                                                                                                                                                                                                                                                                                                                                                                              204 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-FEB-2003.
                                                                                                                                                                                                                                                                                                                                                           invention.
                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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ABR39082
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modifying fusion protein comprising Bad gene sequence fused via a short
linker to diphtheria toxin translocation domain (DTTR). The
functional apoptosis-modifying fusion protein is capable of binding a
target cell and integrating into or crossing a cellular membrane of the
described is a method (MZ) for treating a patient infected with HSV, by administering to the patient, a composition comprising a peptide comprising a sequence of 4-100 continuous amino acids of a 168 residue amino acid sequence (see ABR39081), where the peptide comprises ser112, ser135, or their combinations. BAD has virucide activity. MI is useful for inducing apoptosis in a cell infected with HSV, where the cell is in a human. MZ is useful for treating a patient infected with HSV. The present sequence represents murine BAD, which is used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diphtheria toxin receptor binding domain; DTR; neoplasm; tumour; hyper-proliferation; Alzheimer's disease; neurodegenerative disorder; transient ischaemic neuronal injury; stroke; spinal cord injury;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                Length 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse; Bad-DTTR; apoptosis; cancer; spinal muscular atrophy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 145; DB 24; 100.0%; Pred. No. 2.4e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bad-DTTR apoptosis-modifying fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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/note= "10x histidine tag"
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(USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 NLWAAQRYGRELRRMSDEFEGSFKGLP 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chimeric - Mus sp.
Chimeric - Corynebacterium diptheriae.
Chimeric - Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU00220 standard; Protein; 567 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Youle RJ, Liu X, Collier RJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-AUG-2000; 2000WO-US22293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                            1 Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Huntington's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-218343/22
                                                                                                                                                                                                                                                                                                                                              204 AA;
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                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
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target cell. The apoptosis-modifying fusion protein comprises at least two domains: the DTR domain, which targets the fusion protein to the target cell and the BCl-XL domain, which modifies an apoptotic response of the target cell. The fusion protein is useful for modifying (inhibiting or enhancing) apoptosis in a target cell, such as neuron, lymphocyte, cancer, neoplasm, macrophage, epithelial, stem, tumour or hyper-proliferative cell or an adipocyte. It is also useful for reducing apoptosis in a subject after transient ischaemic neuronal injury, especially spinal cord injury. The fusion protein may be used to treat various diseases and injury. The fusion protein may be used to treat to apoptotic cellular response, including neurodegenerative disorders such as Albeiment's disease, including neurodegenerative disorders attophy, stroke episodes and unrequiated cell growth as in tumours and effectively throughout the body and targeted to selective tissue and
                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a peptide conjugate having the formula: (R-X)n\text{-peptide} where n=1\text{-}10; X=C=0, when the R-X group is attached to the N-terminus of the peptide, or a side chain of the peptide where the functional group of the side chain of the peptide, or N=0 or NH, when the R-X group is attached to the C-terminus of the peptide, or a side chain of the peptide, where the side chain functional group is COOH
                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective; cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad; apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate; colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma; melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS; stroke; myocardial infarction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New peptide conjugates for modulating apoptosis or for inhibiting cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for treating neurodegenerative disorders, stroke, or cancer
                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                              Length 567;
                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 145; DB 22; 100.0%; Pred. No. 7.4e-14;
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                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bcl2 polypeptide BH3 domain peptide #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Huang Z, Wang J, Zhang Z, Shan S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB37001 standard; peptide; 26 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                    27; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                       567 AA;
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or CONHZ; and R = 2-18C alkyl or alkoxy, 2-14C alkylenyl containing one or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally monosubstituted with a 1-5C straight or branched chain alkyl group, competitions alkyl group, or benzyl. The peptides AAB37001-B37058 represent examples of the peptide portion of the conjugate. The peptides represent analogues of a Bcl-2 superiamily polypeptide corresponding to amino acids 72-97 of the BH3 domain of the cell death agonist Bad. The peptide conjugate is useful for modulating apoptosis in the cells of a subject, or for useful for modulating apoptosis in the cells of a subject, or for apoptosis in cancer cells. It is also useful for inhibiting Bcl-2 function. In particular, the peptide conjugate is useful for treating a subject affilicted with a cancer characterized by cancer cells that express Bcl-2. The cancer includes prostate, colorectal, gastric, non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide conjugate is also useful for treating disorders characterized by increased apoptosis, e.g. neurodegenerative disorders, acquired immunodeficiency syndrome (AIDS), stroke or myocardial infarction.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a peptide conjugate having the formula: (R-X)n-peptide where n=1-10; X=C=0, when the R-X group is attached to the N-terminus of the peptide, or a side chain of the peptide where
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective; cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad; apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate; colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma; melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS; stroke; myocardial infarction.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 21;
3e-14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                         95.2%; Score 138; 100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 NEWAAQRYGRELRRMSDEFEGSFKGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 18; Page 17; 74pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                    26 AA;
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when the R-X group is attached to the C-terminus of the peptide, or a side chain of the peptide, where the side chain functional group is COOH or COOH2; and R = 2.18C alkyl or alkoxy, 2.14C alkylenyl containing one or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally monosubstituted with a 1-5C straight or branched chain alkyl group, or benzyl. The peptides ABB37001-B37058 represent examples of alkyl group, or benzyl. The peptides ABB37001-B37058 represent analogues of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of the BH3 domain of the conjugate. The peptides represent analogues of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of the BH3 domain of the cell death agonist Bad. The peptide conjugate is useful for modulating apoptosis in the cells of a subject, or for reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of apoptosis in cancer cells. It is also useful for inhibiting Bcl-2 function. In particular, the peptide conjugate is useful for treating a subject afflicted with a cancer characterized by cancer cells that cancer cancer includes prostate, colorectal, gastric, or corresponding remain or thyroid cancers, neuroblastoma, melanoma, or acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide conjugate is also useful for treating disorders characterized by
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective; cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad; apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate; colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma; melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS; stroke; myocardial infarction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New peptide conjugates for modulating apoptosis or for inhibiting B
the functional group of the side chain is NH2 or OH; or X = 0 or NH,
                                                                                                                                                                                                                                                                                                                                                                                                                       increased apoptosis, e.g. neurodegenerative disorders, acquired immunodeficiency syndrome (AIDS), stroke or myocardial infarction.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95.2%; Score 138; DB 21; 100.0%; Pred. No. 3e-14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB37056 standard; peptide; 27 AA.
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Best Local Similarity
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The invention relates to a peptide conjugate having the formula:

(R-X)n-peptide where n = 1-10; X = C=0, when the R-X group is attached

to the N-terminus of the peptide, or a side chain of the peptide where

the functional group of the side chain is NH2 or NH; or X = O or NH,

when the R-X group is attached to the C-terminus of the peptide, or a

conditional group of the side chain functional group is conditionally or alkoy, 2-14C alkylenyl containing one

conducted with a 1-5C straight or branched chain alkyl group,

conductionally monosubstituted with a 1-5C straight or branched chain

contwo double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally

contwo double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally

contwo double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally

contwo benzyl. The peptides AAB37001-B37058 represent examples

contwo benzyl. The peptide corresponding to amino acids 72-97 of

alkyl group, or benzyl. The peptide corresponding to amino acids 72-97 of

contained by the cell death agonist Bad. The peptide conjugate is

contained to modulating apoptosis in the cells of a subject, or for

constitution. In particular, the peptide conjugate is useful for treating a

confunction. In particular, the peptide conjugate is useful for treating a

confunction. In particular, the peptide conjugate is useful for treating a

cute or chronic lymphocytic and non-lymphocytic leukemia. The peptide

conjugate is also useful for treating disorders characterized by

increased apoptosis, e.g. neurodegenerative disorders, acquired

immunodeficiency syndrome (AIDS), stroke or myocardial infarction.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95.2%; Score 138; DB 21; Length 27;
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live 0; Mismatches
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Matches 26; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    · Sequence
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The invention relates to a peptide conjugate having the formula:

(R-X)n-peptide where n = 1-10; X = C=0, when the R-X group is attached

to the N-terminus of the peptide, or a side chain of the peptide where

to the functional group of the side chain is NH2 or NH; or X = O or NH,

when the R-X group is attached to the C-terminus of the peptide, or a

conside chain of the peptide, where the side chain functional group is CODH

con two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally

con convexituted with a 1-5c straight or branched chain alkyl group,

con two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally

con two double bonds, cyclobutyl, cyclopentyl, cyclohexyl or branched

colored alkyl group, or benzyl. The peptides Anb37001-B37058 represent analogues

colored BB1-2 superfamily polypeptide orresponding to amino acids 72-97 of

colored BB1 domain of the cell death agonist Bad. The peptide conjugate is

colored bonds of the cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of

apoptosis in cancer cells. It is also useful for inhibiting BC-2

conjugate is also useful for treating disorders characterized by

conjugate is also useful for treating disorders characterized by

conjugate is also useful for treating disorders characterized by

conjugate is also useful for treating disorders cancer informed infanction.

conjugate is also useful for treating disorders cancers acquired

immunodeficiency syndrome (AIDS), stroke or myocardial infarction.
                                  Claim 18; Page 19; 74pp; English.
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28 AA; Sequence

Gaps 0; 95.2%; Score 138; DB 21; Length 28; 100.0%; Pred. No. 3.2e-14; Live 0; Mismatches 0; Indels Query Match
Best Local Similarity 100.0
Matches 26; Conservative

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1 NLWAAQRYGRELRRMSDEFEGSFKGL 26

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Search completed: September 15, 2003, 17:22:13 Job time : 38.1857 secs

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September 15, 2003, 17:22:21; Search time 14.0786 Seconds (without alignments) 81.144 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-544-664-3 145 1 NIWAAQRYGRELRRWSDEFEGSFKGLP 27 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

328717 seqs, 42310858 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08 Maximum Match 100% Listing first 45 summaries

Issued_Patents_AA:*

Database:

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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5: /cgn2_6/ptodata/1/iaa/FG_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/FG_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	ID	-08-333-565-	8-661-479-	-08-733-505A	-08-733-505A	8-733-505A-1	-08-733-5	-08-717-123-	-09-375-257-	3-665-617	-08-717-123-	3-985-335-	-08-982-332-,	-09-410-372-	-09-410-372	-09-375-257-	-08-333-565-1	-661	-08	-08-733	33.	-08-733	-08-333	-661	-08-733-505A-3	-08-706-741B-	S-08-924-695A-6	-074-57
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o¥	Query Match I	100.0	100.0	100.0	100.0	100.0	100.0	97.9	97.9	83.1	83.1	83.1	83.1	83.1	83.1	83.1	77.9	77.9	70.3	70.3	70.3	70.3	59.3	59.3	42.1			-
	Score	145	145	145	145	145	145	142	142	120.5	120.5	120.5	120.5	120.5	120.5	120.5	113	113	102	102	102	102	98	86	61	19	19	53
	Result No.	 H H	2	\$ m	3	'n	Q	7	ω	σ	10	11	12	13	14	12	16	17	18	19	20	21	22	23	24	25	26	27

Sequence 3, Appli Sequence 1, Appli	Sequence 40, Appl Sequence 18296, A		4656	2011	Sequence 30979, A	Sequence 19594, A		Seguence 31458, A	Sequence 23807, A	Sequence 5164, Ap	Sequence 2, Appli	Sequence 4, Appli	Sequence 2, Appli	Sequence 2, Appli
US-09-388-774-3 US-09-546-153-1	US-08-867-087B-40 US-09-252-991A-18296	US-09-651-656-27 US-09-650-855-27	US-09-328-352-4656	US-09-252-991A-31348	US-09-252-991A-30979	US-09-252-991A-19594	US-09-252-991A-32466	US-09-252-991A-31458	US-09-252-991A-23807	US-09-328-352-5164	US-09-235-103-2	US-09-235-103-4	US-08-464-340A-2	PCT-US94-08449A-2
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36.6 36.6	35.2	33.8	33.4	32.1	31.7	31.7	31.4	31.4	31.0	31.0	31.0	31.0	31.0	31.0
55 53 53	51 50.5	0 4 0	48.5	46.5	46	46	45.5	45.5	45	45	45	45	45	45
28	30 31	32	34	35	36	37	38	36	40	41	42	43	44	45

ALIGNMENTS

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, LUCATION: 1..204; OTHER INFORMATION: /note= "Deduced amino acid sequence ; OTHER INFORMATION: of mouse BAD."
US-08-333-565-2
                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/33,565
FILING DATE: 31-CCT-1994
CLASSIFICATION: 435
ATTORNET/AGENT INFORMATION:
NAME: SMith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726A-000700
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2440
TELEPHONE: (415) 326-2422
INFORMATION FOR SSQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single
                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                           ZIP: 94301
RESULT 1
US-08-333-565-2
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ö Gaps ó Query Match 100.0%; Score 145; DB 1; Length 204; Best Local Similarity 100.0%; Pred. No. 1.4e-14; Matches 27; Conservative 0; Mismatches 0; Indels 0

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RESULT 4
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Septent No. 5856445
GENERAL INFORMATION:
APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Deduced amino acid sequence of mouse BAD."
                                                                                                                                                                                                            APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
TITLE OF INVENTION: REGULATOR
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTATIONS

ZIP: 94301

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DARM:

APPLICATION NUMBER: US/08/661,479

FILING DATE: 11-JUN 1995

CLASSIFICATION NUMBER: US/08/661,479

FILING DATE: 31-OCT-1994

ATTORNEY/AGENT INFORMATION:

NAME: Smith, William M

REGISTARION NUMBER: 30,223

REFERENCE/DOCKET NUMBER: 15726A-000700

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 326-2440

TELEPHONE: (415) 326-2420

TELEPHONE: (415) 326-2420

TELEPHONE: (415) 326-2420

TELEPHONE: (415) 326-2420

TELEPHONE: CARRACTERISTICS:
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1 NLWAAQRYGRELRRMSDEFEGSFKGLP 27
                                                                                                                                         Sequence 2, Application US/08661479
Patent No. 5834209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 204 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; CTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: CUS-08-661-479-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Protein LOCATION: 1..204
                                                                                                                                                                                                                                                                                                                                                                   CITY: Palo Alto
STATE: California
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US-08-733-505A-1
                                                                                                  RESULT 2
US-08-661-479-2
                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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Sequence 12, Application US/08733505A
Patient No. 5856445
GENERAL INFORMATION:
APPLICANT: KORSMEYER, STANLEY J.
APPLICANT: RORSMEYER, SERINE SUBSTITUTED MUTANIS OF
TITLE OF INVENTION:
BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
                                                                                                                                                                                                     OPERATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 145; DB 2; Best Local Similarity 100.0%; Pred. No. 1.4e-14; Matches 27; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: HOWELL & HAFERKAMP, L.C. STREET: 7733 FORSYTH BLVD., SUITE 1400 CITY: ST. LOUIS STATE: MISSOURI COUNTRY: USA
ADDRESSEE: HOWELL & HARBKRAUL, ..... STREET: 7733 FORSYTH BLVD., SUITE 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      140 NLWAAQRYGRELRRMSDEFEGSFKGLP 166
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NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REPERENCE/DOCKET NUMBER: 965458
TELEPHONE: (314) 727-5188
TELEPHONE: (314) 727-6092
INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 965458
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEPHONE: (314) 727-6092
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION: 530
              STREET: 7/33 CITY: ST. LOUIS
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                                                                                         COUNTRY: US
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TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR NUMBER OF SEQUENCES: 60 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Horne, William A.
APPLICANT: Oltersdorf, Tilman
TITLE OF INVENTION: Human BAD Polypeptides, Encoding Nucleic
TITLE OF INVENTION: Acids and Methods of Use
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 145; DB 2; Length 204; 100.0%; Pred. No. 1.4e-14;
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APPLICATION NUMBER: US/08/717,123
FILING DATE: 20-SEP-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                 ADDRESSEE: HOWELL & HAFBEKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      140 NLWAAQRYGRELRRMSDEFEGSFKGLP 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 NLWAAQRYGRELRRMSDEFEGSFKGLP 27
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5965703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 95
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35,197
                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.(
Matches 27; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-733-505A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
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ZIP: 63105
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. Journal
GENERAL INFORMATION:
APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
TITLE OF INVENTION: 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
100.0%; Score 145; DB 2;
Best Local Similarity 100.0%; Pred. No. 1.4e-14;
Matches 27; Conservative 0; Mismatches 0;
                                                                                                                                                                            100.0%; Score 145; DB 2;
100.0%; Pred. No. 1.4e-14;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       140 NIWAAQRYGRELRRWSDEFEGSFKGLP 166
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                                                                                                                                                                                                                                                                  1 NLWAAQRYGRELRRMSDEFEGSFKGLP 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 6
US-08-733-505A-14
; Sequence 14, Application US/08733505A
; Patent No. 5856445
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, STANLEY J.
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 13, Application US/08733505A Patent No. 5856445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 9654
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 204 amino acids
amino acid
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                     27; Conservative
                                                                                       ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-733-505A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
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                                                                                                                                                                              Query Match
Best Local Similarity
Matches 27; Conserv
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US-08-733-505A-13
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GENERAL INFORMATION:
APPLICANT: Horne, William A.
APPLICANT: Oldersdorf, Tilman
TITLE OF INVENTION: Human BAD Polypeptides, Encoding Nucleic
TITLE OF INVENTION: Acids and Methods of Use
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 168;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/717,123
FILLING DATE: 20-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
                                                                                                                                                                                                                                                                                                                                               .2e-11;
2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 120.5; DB 2;
Pred. No. 6.3e-11;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                     Query Match 83.1%; Score 120.5; Best Local Similarity 89.3%; Pred. No. 6.2e Matches 25; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    103 NLWAAQRYGRELRRMSDEFVDSFKKGLP 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-ID 1929
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-949
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                         1 NLWAAQRYGRELRRMSDEFEGSF-KGLP 27
ATTORNEY/ACENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION UNBER: 31,794
REFERENCE/DOCKET NUMBER: CL-8
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LINGTH: 166 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-717-123-2; Sequence 2, Application US/08717123; Patent No. 5965703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83.1%;
89.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                168 amino acids
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COUNTRY: United States
ZIP: 92122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 89.3
Matches 25; Conservative
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                                                                                                                                                                                                                                    single
                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: sin
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                                                                                                                                                                                                                                                                                                  US-08-665-617-2
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Patent No. 5663316

GENERAL INFORMATION:
APPLICANT: Widong, Yin
TILE OF INVENTION: Gene and Protein for Regulation of Cell Death
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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GENERAL INFORMATION:

APPLICANT: Horne, William A.

APPLICANT: Oltersdorf, Tilman

TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC

TITLE OF INVENTION: ACIDS AND METHODS OF USE

FILE REFERENCE: 480140.480140.480180.4805

CURRENT APPLICATION NUMBER: US/09/375,257

CURRENT FILING DATE: 1999-08-16

NUMBER OF SEQ ID NOS: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97.9%; Score 142; DB 4; Length 204; 96.3%; Pred. No. 4.1e-14; tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                Score 142; DB 2; Length 204;
Pred. No. 4.1e-14;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ...UNKESSEE: Saliwanchik & Saliwanchik STREET: 2421 N.W. 41st Street, Suite A-1 CITY: Gainesville STATE: Florida COUNTRY: USA ZIP: 32606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     140 NIWAAQRYGRELRRMIDEFEGSFKGLP 166
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       P-ID 1929
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APPLICATION NUMBER: US/08/665,617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 32606
COMPUTER READABLE FORM:
MEDUJUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/09375257 Patent No. 6504022
                       TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                      97.9%;
96.3%;
       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                  Query Match
Best Local Similarity 96.35
Matches 26; Conservative
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Best Local Similarity 96.3
Matches 26; Conservative
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CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Mus musculus US-09-375-257-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Fas.
SEQ ID NO 3
LENGTH: 204
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US-08-665-617-2
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US-09-375-257-3
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us-09-544-664-3.rai

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Length 168;
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APPLICANT: Yue, Henry
APPLICANT: Lal, Preeti
APPLICANT: Shah, Purvi
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
TITLE OF INVENTION: PROLIFERATION
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 120.5; DB 3;
Pred. No. 6.3e-11;
0; Mismatches 2;
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/410,372
FILING DATE:
                                                                                                                                                                     MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASLSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,335
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                       ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          103 NIWAAQRYGRELRRMSDEFVDSFKKGLP 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        PF-0421 US
                                                                                                                                                                                                                                                                                                                                                            RILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-04
TELECOMUNICATION INFORMATION:
TELEPHONE: 650-855-055
TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/09410372; Patent No. 6281334; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83.1%;
89.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 89.33
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
CORRESPONDENCE ADDRESS:
                               STREET: 31/4 ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IMMEDIATE SOURCE:
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                                                                                                           USA
                                                                                                       COUNTRY: US
ZIP: 94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94304
                                                             CITY: Palo
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; CLONE: 7
US-08-985-335-7
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                                                                                                                                                               APPLICANT: Yue, Henry
APPLICANT: Lal, Preeti
APPLICANT: Shab, Purvi
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: PROLIFERATION
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Yue, Henry
APPLICANT: Lal, Preeti
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: PROLIFERATION
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,335
FILING DATE: Filed Herewith
APPLICATION NUMBER: US/08/985,335
FILING DATE: FILED Herewith
APPLICATION NUMBER: US/08/985,335
FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE,DOCKET NUMBER: BF-0421 US
TELEPHONEL SOCKET NUMBER: BF-0421 US
TELEPHONEL SOCKET NUMBER: DF-0421 US
                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc
STREET: 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   103 NLWAAQRYGRELRRMSDEFVDSFKKGLP 130
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Patent No. 6080847
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
                                                                             Sequence 1, Application US/08985335
Patent No. 6080847
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
APPLICANT: Lal, preeti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIBRARY: SYNORAB01
CLONE: 358673
                                                                                                                                                                                                                                                                                                                                                                STREET: 3174 Por
CITY: Palo Alto
STATE: CA
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Matches 25; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-985-335-1
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                                                               US-08-985-335-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Tue, Henry
APPLICANT: Lal, Preeti
APPLICANT: Lal, Preeti
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/410,372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Dr. CITY: Palo Alto STATE: OA STATE: USA ZIP: 94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         103 NLWAAQRYGRELRRMSDEFVDSFKKGLP 130
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/985,335
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy U.
REGISTRATION NUMBER: 36,749
REGISTRATION INFORMATION:
TELEPRENCE/DOCKET NUMBER: PF-0421 US
TELEPRONE: 650-845-4166
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 NLWAAQRYGRELRRMSDEFEGSF-KGLP 27
                                                                                                                                   PF-0421 US
              ATORNEY AGENT INFORMATION:
ATORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0421
TELEPHONE: 650-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7, Application US/09410372 Patent No. 6281334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
TOPOLOGY: linear
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                         IMMEDIATE SOURCE:
LIBRARY: SYNORAB01
CLONE: 358673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
US-09-410-372-7
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Gaps
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; GENERAL INFORMATION:
; APPLICANT: Horne, William A.
; APPLICANT: Oltersdorf, Tilman
; TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC
; TITLE OF INVENTION: ACIDS AND METHODS OF USE
; TILE REPERENCE: 480140.42811
; CURRENT APPLICATION NUMBER: US/09/375,257
; NUMBER OF SEQ ID NOS: 15
; SOFTHER FEASTSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ξ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83.1%; Score 120.5; DB 4; Length 168; 89.3%; Pred. No. 6.3e-11; ive 0; Mismatches 2; Indels 1.
                                                                                                                                               DB 3; Length 168;
                                                                                                                                                                                           Indels
                                                                                                                                           83.1%; Score 120.5; DB 3 ilarity 89.3%; Pred. No. 6.3e-11; Conservative 0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: September 15, 2003, 17:45:05 Job time : 14.0786 secs
                                                                                                                                                                                                                                                                  103 NIWAAORYGRELRRMSDEFVDSFKKGLP 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    103 NLWAAQRYGRELRRMSDEFVDSFKKGLP 130
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                                                                                                                                                                                                                                        1 NLWAAQRYGRELRRMSDEFEGSF-KGLP 27
                                                                                                                                                                                                                                                                                                                                                                             US-09-375-257-2
; Sequence 2, Application US/09375257
; Patent No. 6504022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 89.3
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens
US-09-375-257-2
; TOPOLOGY: linear; 
; IMMEDIATE SOURCE: 
; LIBRARY: GenBank 
; CLONE: 1683637 
US-09-410-372-7
                                                                                                                                             Query Match
Best Local Similarity
Watches 25; Conserv
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(without alignments)
184.034 Million cell updates/sec
                                                                                                                                                                                             September 15, 2003, 17:25:56; Search time 21.4071 Seconds
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(cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
(cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
(cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
(cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
(cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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(cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
(cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
(cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
(cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
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(cgn2_6/ptodata/1/pubpaa/US00_NEW_PUB.pep:*
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/cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Published_Applications_AA:*
.: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                       27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   541936 seqs, 145912426 residues
                                                                                                                                                                                                                                                                                                                                                         145
1 NEWAAQRYGRELRRMSDEFEGSFKGLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                              OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                         BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 length: 0
length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                            Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Minimum DB s
Maximum DB s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Database :
                                                                                                                                                                                                                                                                                                                                                                                             Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                                                                                                      Run on:
                                                                                                                                                                                                                                                                                                                        Title:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

7 5 5 2	Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 62, Appl
US-10-114 US-10-325 US-10-92 US-10-92 US-09-72 US-09-72 US-09-925 US-10-15	5 US-10-166-357- 5 US-10-166-372- 5 US-10-184-722- 5 US-10-251-385-
00001111111111111111111111111111111111	
3311.0 3311.0	29.7 29.7 29.7
444444444 44444444444 44444444444 444444	4 4 4 4 3 3 3 3
11111111111111111111111111111111111111	2444 2444 7447

ALIGNMENTS

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Gaps
                                      Sequence 3, Application US/09922378

Sequence 3, Application US/09922378

Sequence 3, Application US/09922378

GENERAL INFORMATION:

APPLICANT: Horne, William A.

APPLICANT: Horne, William A.

TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC;

TITLE OF INVENTION NUMBER: US/09/922,378

CURRENT APPLICATION NUMBER: US/09/922,378

NUMBER OF SEQ ID NOS: 15

SEQ ID NO 3

LENGTH: 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
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Pred. No. 2.5e-13;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Horne, William A. APPLICANT: Oltersdorf, Tilman TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC TITLE OF INVENTION: ACIDS AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        140 NIWAAQRYGRELRRMIDEFEGSFKGLP 166
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; Publication No. US20020115631A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97.9%;
96.3%;
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Best Local Similarity 96.3
Matches 26, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; GENERAL INFORMATION:
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US-10-066-179-3
RESULT 1
US-09-922-378-3
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US-09-894-657-1
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; Sequence 2, Application US/09922378
; Patent No. US20020030869A1
; GENERAL INFORMATION:
    APPLICANT: Horne, William A.
    APPLICANT: Oltersdorf, Tilman
; TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC
; TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC
; TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC
; TITLE OF INVENTION: ALIDS AND METHODS OF USE
; CURRENT APPLICATION NUMBER: US/09/922,378
; CURRENT PILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 168;
                                                                                                                                                                                                                                          Query Match 97.9%; Score 142; DB 14; Length 204; Best Local Similarity 96.3%; Pred. No. 2.5e-13; Matches 26; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL PROLIFERATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83.1%; Score 120.5; DB 9
89.3%; Pred: No. 3.2e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      103 NLWAAQRYGRELRRMSDEFVDSFKKGLP 130
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                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 480140.428C1
CURRENT APPLICATION NUMBER: US/10/066,179
CURRENT FILING DATE: 2002-02.
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 204
                                                                                                                                                                                                                                                                                                                                   1 NLWAAQRYGRELRRMSDEFEGSFKGLP 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/09894657 Patent No. US20020098569Al GENERAL INFORMATION: APPLICANT: Hillman, Jennifer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Corley, Neil C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yue, Henry
Lal, Preeti
Shah, Purvi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 83.1
Best Local Similarity 89.3
Matches 25, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                          TYPE: PRT
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGIH: 168
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US-09-922-378-2
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COLIEY, Neil C.
TITLE OF INVENTION: PROLIFERATION
PROLIFERATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASKSEQ for Windows Version 2.0
SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/894,657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
                                                                     FILING DATE: 28-Jun-2001
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 09/410,372
FILING DATE: - GUNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: BILLINGS. Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0421 US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPRAN: 650-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENX: 650-845-4166
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: <URKDOWN>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0421 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/894,657
FILING DATE: 28-Jun-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/410,372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   103 NIWAAQRYGRELRRMSDEFVDSFKKGLP 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 NLWAAQRYGRELRRMSDEFEGSF-KGLP 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 168 amino acids TYPE: amino acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/09894657; Patent No. US20020098569Al; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94304
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIBRARY: SYNORAB01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yue, Henry
Lal, Preeti
Shah, Purvi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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Best Local Similarity 89.3
Matches 25; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: li
IMMEDIATE SOURCE:
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US-09-894-657-7
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ZIP: 94304
COMPUTER READABLE FORM:
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                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
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APPLICANT: BRIAND, JEAN-PAUL
TITLE OF INVENTION: CHIMERIC MOLECULES CONTAINING A MODULE ABLE TO TARGET
TITLE OF INVENTION: SPECIFIC CELLS AND A MODULE REGULATING THE APOPTOGENIC
TITLE OF INVENTION: FUNCTION OF THE PERMEABILITY TRANSITION PORE COMPLEX
TITLE OF INVENTION: (PPPC)
FILE REPERENCE: 03495.0216
CURRENT APPLICATION NUMBER: US/10/059,261
CURRENT FILING DATE: 2002-08-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                 1;
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APPLICANT: Horne, William A.; APPLICANT: Oltersdorf, Tilman; TITLE OF INVENTION: ACIDS AND METHODS OF USE; FILE REFERENCE: 480140.428C1; CURRENT APPLICATION NUMBER: US/10/066,179; CURRENT FILING DATE: 2002-02-01; NUMBER OF SEQ ID NOS: 15; SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 83.1%; Score 120.5; DB 14; Length 168; Best Local Similarity 89.3%; Pred. No. 3.2e-10; Matches 25; Conservative 0; Mismatches 2; Indels 1;
                                                                                                                                                                                                                                                                     Length 168;
                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                 Score 120.5; DB 9;
Pred. No. 3.2e-10;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       103 NLWAAQRYGRELRRMSDEFVDSFKKGLP 130
                                                                                                                                                                                                                                                                                                                                                                                   103 NLWAAQRYGRELRRMSDEFYDSFKKGLP 130
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                                                                                                                                                                                                                                                                                                                                                          1 NLWAAQRYGRELRRMSDEFEGSF-KGLP 27
                                                                                                                                                      LIBRARY: GenBank
CLONE: 1683637
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 258, Application US/10059261 Publication No. US20030077826A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/265,594
                    SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                   83.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2001-02-02
NUMBER OF SEQ ID NOS: 325
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 258
LENGTH: 25
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Unknown Organism
                                                                                                               TOPOLOGY: linear
                                                                                                                                                                                                                                                                   Query Match 83.1
Best Local Similarity 89.3
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: EDELMAN, LENA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                 IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-059-261-258
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                                                                                                                                                                                                                          US-09-894-657-7
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DEFICANT: Call Signating Technology, Inc.

APPLICANT: Call Signating Technology, Inc.

APPLICANT: Call Signating Technology, Inc.

APPLICANT: CAMB, Michael J.

APPLICANT: COMB, Michael J.

APPLICANT: COMB, Michael J.

APPLICANT: Tan, YI

TITLE OF INVENTION: POSITIVE IDENTIFICATION OF PHOSPHO-PROTEINS USING MOTIF-SPECIT

TITLE OF INVENTION: CONTEXT-INDEPENDENT ANTIBODIES COUPLED WITH DATABASE SEARCHI

FILE REFERENCE: CST-138 CIP3

CURRENT APPLICATION NUMBER: US 09/148,712

PRIOR APPLICATION NUMBER: US 09/148,712

PRIOR APPLICATION NUMBER: US 09/535,364

PRIOR FILING DATE: 1998-09-04

PRIOR PPLICATION NUMBER: US 09/535,364

PRIOR PRIOR FILING DATE: 2000-03-24

NUMBER OF SEQ ID NOS: 193

SEQ ID NO 147

LENGTH: 15
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; OTHER INFORMATION: PHOSPHORYLATION; serine at position 8 is phosphorylated
US-10-174-105A-147
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; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: TOX peptide
US-10-059-261-258
                                                                                                                                                                       0
                                                                                                                Length 25;
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Guegler, Karl J.
Patterson, Chandra
TITLE OF INVENTION: GROWTH-ASSOCIATED TRYPSIN-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 49.0%; Score 71; DB 15; I Best Local Similarity 100.0%; Pred. No. 0.00058; Matches 14; Conservative 0; Mismatches 0;
                                                                                                             Query Match 78.6%; Score 114; DB 15; Best Local Similarity 91.7%; Pred. No. 4.1e-10; Matches 22; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                             1 NIWAAQRYGRELRRMSDEFVDSFK 24
                                                                                                                                                                                                                             1 NLWAAQRYGRELRRMSDEFEGSFK 24
                                                                                                                                                                                                                                                                                                                                                                                            US-10-174-105A-147; Sequence 147, Application US/10174105A; Publication No. US20030068652A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Synthetic Peptide FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/09828423
Patent No. US20020099178A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
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LOCATION: (8)..(8
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Sequence 1077, Application US/10238075
Publication No. US20030148324A1
GENERAL INFORMATION:
APPLICANTION:
TITLE OF INVENTION: Polynucleotides which are of nature B2/D+ A- and which are is:
TITLE OF INVENTION: E.coli, and biological uses of these polynucleotides and of the contraction of the contra
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21;
                                                                                                                           US-10-092-750-1
; Sequence 1, Application US/10092750
; Publication No. US20030032157A1
; GENERAL INFORMATION:
; APPLICANT: Hammond, Philip W.
; APPLICANT: Wright, Martin C.
; TILLE OF INVENTION: Polypeptides Interactive with BCL-X1
; TILLE REFERENCE: 50036/050002
; CURRENT APPLICATION NUMBER: US/10/092,750
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: US 60/274,526
; PRIOR FILING DATE: 2001-03-08
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Publication No. US20030032157A1
GENERAL INFORMATION:
APPLICANT: Hammond, Philip W.
APPLICANT: Alphin, Julia
APPLICANT: Wright, Martin C.
TITLE OF INVENTION: Polypeptides Interactive with BCL-X1
FILE REFERENCE: 50036/050002
CURRENT FILING DATE: 2002-03-07
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SOFTWARE: FastSEQ for Windows Version 4.0
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SOFTWARE: FastSEQ for Windows Version 4.0
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      108 ERWGGDLRRMRDEADG 123
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Matches 10; Conservative
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US-10-092-750-241
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Best Local Similarity
Matches 10; Conserva
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US-10-238-075-1077
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LENGTH: 138
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Word Perfect 6.1/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/828,423
FILING DATE: 05-Apr-2001
CLASSIFICATION: <URROwn>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 34.5%; Score 50; DB 15; Best Local Similarity 56.2%; Pred. No. 12; Matches 9; Conservative 4; Mismatches 3
                                                                                                                                                                                                                                                                                                                                    FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REFRENCE/DOCKET NUMBER: PF-0505 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36.6%; Score 53; DB 33.3%; Pred. No. 20; tive 5; Mismatches
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APPLICANT: IKEDA, HARUO
APPLICANT: IKEDA, HARUO
APPLICANT: IKEDA, HARUO
APPLICANT: HORIKAWA, JUN
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: BARAKI, YOSHIYUKI
APPLICANT: BARTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLINUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT PILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR PILING DATE: 2001-05-30
PRIOR FILING DATE: 2010-05-30
PRIOR PILING DATE: 2010-05-30
PRIOR PILING DATE: 2010-05-30
PRIOR PILING DATE: 2010-08-02
NUMBER OF SEQ ID NOS: 15109
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                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 09/388,774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LIBRARY: GENEBANK
CLONE: 9133985
SEQUENCE DESCRIPTION: SEQ ID NO: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9145, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptomyces avermitilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 946 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 650-845-4166
TELEX: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 QRYGRELRRMSDEFEG 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 33.33
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IMMEDIATE SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 10
US-10-156-761-9145
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Search completed: September 15, 2003, 17:47:52 Job time : 21.4071 secs
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US-09-984-198-153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RY: USA
94304-1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wu, Frank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Palo Alto
                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 650-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ß
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STATE:
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                                                                                                                                                                                                RESULT 15
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Patent No. US20020091243A1
GENERAL INFORMATION:
APPLICANT: Gatanaga, T.
APPLICANT: Granger, G.A.
TITLE OF INVENTION: Factor Receptor Releasing Enzyme Activity, and Methods TITLE OF INVENTION: of Use Thereof
NUMBER OF SEQUENCES: 154
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                        Length 682;
                                                                                                                                                                                                                                                    Query Match 31.7%; Score 46; DB 12; Length 68
Best Local Similarity 40.0%; Pred. No. 1.6e+02;
Matches 10; Conservative 5; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/752,639
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22000-20577.21
              CURRENT APPLICATION NUMBER: US/10/238,075
CURRENT FILING DATE: 2002-09-10
PRIOR APPLICATION NUMBER: 0003145
PRIOR FILING DATE: 2000-03-10
NUMBER OF SEQ ID NOS: 1576
SEQ ID NO 1077
                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US99/10793
                                                                                                                                                                                                                                                                                                                                  2 LWAAQRYGRELRRMSDEFEGSFKGL 26
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APPLICATION NUMBER: 09/081,385
FILING DATE:
APPLICATION NUMBER: 08/964,747
FILING DATE: 05-NOV-1997
APPLICATION NUMBER: 60/030,761
FILING DATE: 06-NOV-1996
ATTORNET/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELERX: 650-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 153:
SEQUENCE CHARACTERISTICS:
LENGTH: 852 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Wu, Frank
REGISTRATION NUMBER: 41,386
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                                                                                                                                                                        TYPE: PRT
ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
FILE REFERENCE: BLANDINE
                                                                                                                                                                                                                US-10-238-075-1077
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US-09-752-639-153
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APPLICANT: Gatanaga, T.
APPLICANT: Granger, G.A.
TITLE OF INVENTION: Factors Altering Tumor Necrosis
TITLE OF INVENTION: Factor Receptor Releasing Enzyme Activity, and Methods
TITLE OF INVENTION: of Use Thereof
NUMBER OF SEQUENCES: 154
CORRESPONDENCE ADDRESS:
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                                                Gaps
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      Length 852
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                                                Indels
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Score 45.5; DB 9;
Pred. No. 2.4e+02;
5; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 NLWAA-----QRY-GRELRRMSDEFEGSFKGLP 27
                                                                                           1 NLWAA----QRY-GRELRRMSDEFEGSFKGLP 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/984,198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22000-20577.21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US99/10793
FILING DATE:
APPLICATION NUMBER: 09/081,385
FILING DATE:
APPLICATION NUMBER: 08/964,747
FILING DATE: 05-NOV-1997
APPLICATION NUMBER: 60/030,761
FILING DATE: 06-NOV-1996
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                            Sequence 153, Application US/09984198 Patent No. US20020106679A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: MORRISON & FOERSTER STREET: 755 PAGE MILL ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 41,386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       153:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 22
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-494-0792
TELEFAX: 650-494-0792
    31.4%;
35.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 852 amino acids
TYPE: amino acid
    Query Match
Best Local Similarity 35.39
Matches 12; Conservative
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GenCore version 5.1.6
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OM protein - protein search, using sw model

September 15, 2003, 17:18:16; Search time 12.15 Seconds Run on:

(without alignments)
213.708 Million cell updates/sec

US-09-544-664-3

145 1 NLWAAQRYGRELRRMSDEFEGSFKGLP 27 score: Sequence: Perfect

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 seqs, 96168682 residues Searched: 283308 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000

Minimum DB : Maximum DB :

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database:

PIR_76:*
1: pirl:*
2: pir2:*
3: pir3:*
1: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	Description	now -	inter-alpha-trypsi	-inhib	ŏ	pha-t	2-dehydro-3-deoxy-	floral homeotic pr	ne/putre	thre	endonuclease VIII		hypothetical prote	endonuclease VIII,	conserved hypothet	Ig kappa chain - h	annexin P35 - maiz	transforming prote	oxidoreductase, so	threonine synthase	hypothetical prote		oxoglutarate dehyd			Ψ	cal p	probable polyamine	proteina	hypothetical prote
SUMMARIES	ID	567	557	4	D70760	IYHUZ	S38185	A42095	C84338	A96753	A64807	A85572	C90721	AD0590	E83517	S40376	T02975	C36365	F72289	T08545	B81287	G82308	F82668	B96695	T02961	A44308	T09486	S	9831	480
	DB	1		7																										
	Length	204	946	946	223	946	370	232	374	516	263	263	263	263	453	134	314	206	220	526	779	597	967	5138	314	435	1140	399	497	1164
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	Score	4	Ø	9	53	53	52	51	50	20	49	49	49	49	49	48.5	•	48	48	48	47.5	47	47	47	Ġ	46.5	ø	46	46	46
	ult No.		7	m	4	ιO	w	7	ထ	σι	10	13	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

DNA-directed RNA p	hypothetical prote	conserved hypothet	probable transfera	neuropeptide Pol-R	probable transmemb	Antho-RFamide neur	hypothetical prote	NADH dehydrogenase	chlorocruorin chai	conserved hypothet	conserved hypothet	potassium channel	sodium ion pumb ox	oxaloacetate decar	oxaloacetate decar
A81393	C75420	G69510	E81148	S43852	E83337	A39172	C71473	G83314	859899	F83201	H95406	JG5920	B44465	AB0509	AE0909
N	N	7	7	7	7	7	N	C 3	~	7	~	~	N	(7	7
1378	194	261	263	287	328	334	562	902	165	295	346	513	591	591	591
31.7	31.4	31.4	31.4	31.4	31.4	31.4	31,4	31.4	31.0	31.0	31.0	31.0	31.0	31.0	31.0
46	45.5	45.5	45.5	45.5	45.5	45.5	45.5	45.5	45	45	45	45	45	45	45

ALIGNMENTS

RESULT 1

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inter-alpha-trypsin inhibitor heavy chain 2 - golden hamster
(5.5pecies: Mesocricetus auratus (golden hamster)
(5.5pecies: Mesocricetus auratus (golden hamster)
(5.5pecies: Mesocricetus auratus (golden hamster)
(5.5ate: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 20-Jun-2000
(5.6cession: JC5575; PC4485
(7.8ccession: JC5575; PC4485
(7.8ccession: JC5575; PC4485
(7.8ccession: JC5577; PC4485
(7.8ccession: JC5577; PC4485
(7.8ccession: JC5574; MUD:97420688; PMID:9276673
(7.8ccession: JC5575
(7.8ccession: JC5574
(7.8ccession: JC5575
(7.8ccession: JC5574
(7.8ccessio
                                                                                                                                                                      C, Accession: A55671
R; Yang, E.; Zha, J.; Jockel, J.; Boise, L.H.; Thompson, C.B.; Korsmeyer, S.J.
Cell 80, 285-221, 1995
A; Title: Bad, a heterodimeric partner for Bcl-x-L and Bcl-2, displaces Bax and promot A; Reference number: A55671; WUID:95136361; PMID:7834748
A; Accession: A55671
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A;Residues: 55-64;140-146;151-156;424-447;500-528;577-605 <NA2>
C;Comment: In the plasma three inter-alpha-trypsin inhibitor heavy chains 1, 2 and 3
that the complexes play important role for panceatic cancer.
C;Superfamily: inter-alpha-trypsin inhibitor complex component II
F;261-264,717-916/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ô
bad protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-204 < YAN>
A; Cross-references: GB:L37296; NID:g639778; PIDN:AAA64465.1; PID:g639779
C; Reywords: heterodimer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary: not compared with conceptual translation
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42.1%; Score 61; DB 2; Length 946; 37.0%; Pred. No. 1;

Query Match Best Local Similarity

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precursor of one

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us-09-544-664-3.rpr

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A; Accession: S09064
A; Accession: S09064
A; Accession: S09064
A; Residues: 265, 'RR', 268-284, 'D', 286-946 <SCH>
A; Residues: 265, 'RR', 268-284, 'D', 286-946 <SCH>
A; Residues: 265, 'RR', 268-284, 'D', 286-946 <SCH>
A; Note: this sequence has been revised in reference S00346
B; Salier, J.P.; Diarra Mehrpour, M.; Sesboue, R.; Bourguignon, J.; Benarous, R.; Ohku Proc. Natl. Acad. Sci. U.S.A. 84, 8272-8276, 1987
A; Title: Isolation and characterization of CDNAs encoding the heavy chain of human in A; Reference number: A39967; MUID:88068576; PMID:2446322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A, Accession: S00632
A; Molecule type: mRNA
A; Residues: 384-673, A',675-704, 'S',706-728, 'D',730, 'A',732-766 <SA2>
A, Cross references: GB:M33033; NID:9186589; PIDN:AAA59195.1; PID:9186590
R; Enghild, J.J.; Thogersen, I.B.; Pizzo, S.V.; Salvesen, G.
B, Enghild, J.J.; Thogersen, I.B.; Pizzo, S.V.; Salvesen, G.
A; Fitle: Analysis of inter-alpha-trypsin inhibitor and a novel trypsin inhibitor, pre
A; Reference number: A92736; MUID:89380192; PMID:2476436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A.Molecule type: protein
A.Residues: 55-74 <ERG>
R.Malki, N.; Balduyck, M.; Maes, P.; Capon, C.; Mizon, C.; Han, K.K.; Tartar, A.; Fou Biol. Chem. Hoppe-Seyler 373, 1009-1018, 1992
A.Title: The heavy chains of human plasma inter-alpha-trypsin inhibitor: their isolat A.Reference number: S28928; MUID:93039735; PMID:1384548
                                                                                                                                                                                                                                               A)Cross-references: EMBL:X07173
A)Experimental source: liver
A)Note: part of this sequence, including the amino end of the mature protein, was con saing occurs at the carboxyl as well as the amino end to produce the mature protein A)Note: due to a double frameshift, the nucleic acid sequence of codons 363-372 is in A)Note: in one clone, a T is lacking from codon 716; this clone could code for a prot R,Schreitmueller, T.; Hochstrasser, K.; Reisinger, P.W.M.; Wachter, E.; Gebhard, W. Biol. Chem. Hoppe-Seyler 368, 963-970, 1987
A)Title: cDNA cloning of human inter-alpha-trypsin inhibitor discloses three differen A; Reference number: S09064; MUID:88024442; PMID:3663330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 384-673, 'A',675-704,'S',706-728,'D',730,'A',732-865 <SAL>
A; Residues: 384-673, 'A',675-704,'S',706-728,'D',730,'A',732-865 <SAL>
A; Cross-references: GB:M18193; GB:J03013; NID:g338222; PIDN:AAA60558.1; PID:9553647
A; Experimental source: liver
R; Salier, J.P.; Diarra-Mehrpour, M.; Sesbouee, R.; Bourguignon, J.; Martin, J.P.
Biol. Chem. Hoppe-Seyler 369(Suppl.), 15-18, 1988
A; Title: Human inter-alpha-trypsin inhibitor. Isolation and characterization of heavy
A; Reference number: S00632; MJD:89076497; PMID:2462430
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Biochemistry 33, 7423-7429, 1994
A;Title: TSG-6, an arthritis-associated hyaluronan binding protein, forms a stable co
A;Reference number: A53642; MUID:94271799; PMID:7516184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Comment: Inter-alpha-trypsin inhibitor is a complex of three proteins, each derivin C;Comment: This protein is a heterodimer of heavy and light chains.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;282,283/Modified site: gamma-carboxyglutamic acid (Glu) #stafus predicted F;421,422,423/Binding site: calcium (Asp, Gly, Asp) #status predicted
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C,Superfamily: inter-alpha-trypsin inhibitor complex component II
DNA and derived amino acid sequence of 346; MUID:88152237; PMID:2450046
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    A;Title: Complementary DNA a
A;Reference number: S00346;
A;Accession: S00346
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                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-946 <GEB>
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                                                                                                                                                                                                                                                                                                                                                                                                               inter-alpha-inhibitor H2 chain - mouse
C; Species: Mus musculus (house mouse)
C; Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 20-Aug-1999
C; Accession: S54354
R; Chan, P:: Risler, J.L.; Raguenez, G.; Salier, J.P.
Biochem. J: 306, 505-512, 1995
A; Title: The three heavy-chain precursors for the inter-alpha-inhibitor family in mouse:
A; Reference number: S54353; MUID:95194326; PMID:7534067
A; Status: preliminary; nucleic acid sequence not shown
A; Molecule type: mRNA
A; Residues: 1-946 <CHA>
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A; Accession: D70760
A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Residues: 1-223 <COL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein Rv2014 - Mycobacterium tuberculosis (strain H37RV)
C; Species: Mycobacterium tuberculosis
C; Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C; Accession: D70760
R; Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hanlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:X70392; NID:g695633; PIDN:CAA49842.1; PID:g695634 C;Superfamily: inter-alpha-fronsin inhibitor commine comments of the comments of th
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58.8%; Pred. No. 3.4;
iive 1; Mismatches
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                                                                                                       1 NLWAAQRYGRELRRMSDEFEGSFKGLP 27
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Ring, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Ja Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Reference number: A42095; MUID:92154682; PMID:1346756
A) Accession: A42095
A) Accession: A42095
A) Status: preliminary
A) Molecula
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A;Introp. 131. 106/2; 139/3; 153/3; 168/3
A;Introp. 112E18.30
C;Superfamily: transcription factor squa; serum response factor DNA-binding domain hc C;Keywords: DNA binding; nucleus; transcription regulation
F;2-57/Domain: serum response factor DNA-binding domain homology <SRF>
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Plant Mol. Biol. 26, 465-472, 1994
A.Fille: Genetic complementation of a floral homeotic mutation, apetala3, with an Ara
A.; Reference number: $52633; MUID:95036018; PMID:7948893
A; Accession: $52633
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submitted to the Protein Sequence Database, March 2000
                                                                                                                                                                                                                                                                                      A42093 homeotic protein APETALA3 (AP3) - Arabidopsis thaliana Floral homeotic protein APETALA3; MADS-box regulatory protein AP3 (Species: Arabidopsis thaliana (mouse-ear cress) (Species: Arabidopsis thaliana (mouse-ear cress) (Species: A4-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000 (Spacession: A42095; S52633; T47593 (Spack, T.; Brockman, L.L.; Meyerowitz, E.M. Cell 68, 683-697, 1992 (Arabidopsis thaliana encodes a MADS box A;Title: The homeotic gene APETALA3 of Arabidopsis thaliana encodes a MADS box
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C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: C84338
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A,Residues: 1-232 <JAC>
A,Cross-references: GB:M86357; NID:g166607; PIDN:AAA32740.1; PID:g166608
A;Experimental source: petals, stamens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Note: sequence extracted from NCBI backbone (NCBIN:82520, NCBIP:82521)
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A;Experimental source: cultivar Columbia; BAC clone T12E18
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A;Residues: 1-63 <OKA>
A;Cross-references: GB:D21125
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A;Accession: T47593
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A; Status: preliminary
A; Molecule type: DNA
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A; Reference number: JN0322; MUID:92225349; PMID:1348717
A; Reference number: JN0322; MUID:92225349; PMID:1348717
A; Accession: JN0322
A; Accession: JN0322
A; Accession: JN0322
A; Molecule type: DNA
A; Residues: 1-204,208-370 (KUE>
A; Residues: 1-204,208-370 (KUE>
A; Residues: 1-204,208-370 (KUE>
A; Residues: 1-204,208-370 (KUE>
A; Reference number: A8851; MUID:93374850; PMID:8366040
A; Reference number: A88651; MUID:93374850; PMID:8366040
A; Reference number: A88651; MUID:93374850; PMID:8366040
A; Residues: JS2-370 (KUE>
A; Residues: JS2-370 (KUE>
A; Residues: SS2-370 (KUE>
A; Residues: SS
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A.Residues: 1-370 (ALJ)
A.Cross references: EMEL:236118; NID:9536664; PIDN:CAA85212.1; PID:9536665; MIPS:YBR2496
B.A.Aigle, M.; Baclet, M.C.; Barthe, C.; Biteau, N.; Crouzet, M.; Doignon, F.
submitted to the Protein Sequence Database, August 1994
A.Reference number: S45940
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A;Residues: 1-370 <AIG>
A;Cross-references: EMBL:Z36118; NID:g536664; PIDN:CAA85212.1; PID:g536665; MIPS:YBR249G
R;Kuenzler, M.; Paravicini, G.; Egli, C.M.; Irniger, S.; Braus, G.H.
Gene 113, 67-74, 1992
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Score 53; DB 1; Length 946;
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                                                  Pred. No. 15;
5; Mismatches
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Pred. No. 8
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    36.6%;
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Best Local Similarity 47.69
Query Match
Best Local Similarity 33.33
Matches 9; Conservative
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Length 232;

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1 NLWAAQRYGRELRRMSDEFEG 21

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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-263 <STO>
A; Cross-references: GB: AE005174; NID: g12513625; PIDN: AAG55037.1; GSPDB: GN00145; UWGP:
A; Experimental source: strain 0157:H7, substrain EDL933
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C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 17-May-2002
                                                                                                                                                                                                                                                                                                       hypothetical protein nei [imported] - Escherichia coli (strain 0157:H7, substrain EDL C'Species: Escherichia coli (c'Species: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 17-May-2002 (C'Accession: A8572  
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May Iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda Nature 409, 529-533, 2001
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A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and A;Reference number: A99629; MUID:21156231; PMID:11258796
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C;Superfamily: formamidopyrimidine-DNA glycosidase
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                            Score 49; DB 2
Pred. No. 16;
3; Mismatches
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Pred. No. ]
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nilarity 47.4%;
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: A96753
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hutter, J.L.; Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lucos, J.S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lucos, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Ventrer, J.C.; Davis, R.W.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Residues: 1-516 <STO>
A;Coss-references: GB:AE005173; NID:95903070; PIDN:AAD55628.1; GSPDB:GN00141
C;Genetics:
A;Map position: 1
A;Map position: 1
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A;Residues: 1-263 <BLAT>
A;Cross-references: GB:AE000174; GB:U00096; NID:g1786920; PIDN:AAC73808.1; PID:g1786932;
A;Experimental source: strain K-12, substrain MG1655
C;Genetics:
A;Gene: nei
A;Map position: 16 min
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Description: DNA N-glycosylase with an apurinic lyase activity; recognizes and removes C; Superfamily: formamidopyrimidine-DNA glycosidase C; Keywords: DNA repair; glycosidase; hydrolase; lyase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Accession: A64807
R; Blattner, F.R.; Plunkett III, G; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A; Title: The complete genome sequence of Escherichia coli K-12.
A; Reference number: A64720; MUID:97426617; PMID:9278503
A; Accession: A64807
A; Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                ö
                            GB:AE004437; NID:q10581314; PIDN:AAG20071.1; GSPDB:GN00138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   endonuclease VIII (EC 3.2...) - Escherichia coli (strain K-12)
C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C;Accession: A64807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Pred. No. 23;
7; Mismatches 7; Indels
                                                                                                                                Length 374;
                                                                                                                                                                                Indels
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                                                                                                                              DB 2;
16;
                                                                                                                                                                                Mismatches
                                                                                                                              Score 50;
Pred. No.
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76.9%;
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Best Local Similarity
Matches 10; Conserv
A; Residues: 1-374 <STO>
                            A; Cross-references:
C; Genetics:
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                                                                         A; Gene: potA2
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R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th. T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gacra, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serow A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AD0590
A;Accession: AD0590
A;Accession: AD0590
A;Residues: 1-263 cPAR>
A;Residues: 1-263 cPAR>
A;Residues: 1-263 cPAR>
C;Genetics:
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A;Experimental source: strain PAO1
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Cybate: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
Cybate: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
CyAccession: 540376
Riklein, R.; Jaenichen, R.; Zachau, H.G.
Bur. J. Immunol. 23, 3248-3271, 1993
A; Title: Expressed human immunoglobulin chi genes and their hypermutation.
A; Reference number: $40312; MUID:94080891; PMID:8258341
A; Accession: $40376
C,Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 49; DB 2; Length 263;
Pred. No. 16;
3; Mismatches 7; Indels
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Pred. No. 28;
4; Mismatches 2
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A;Residues: 1-134 <KLE>
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4 GPEIRRAADNLEAAIKGKP 22
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55.6%;
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Best Local Similarity 55.64
Matches 10; Conservative
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Best Local Similarity
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Search completed: September 15, 2003, 17:27:01 Job time : 13.15 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model
Run on: September 15, 2003, 17:16:55; Search time 6.36429 Seconds (without alignments)
199.507 Million cell updates/sec
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Title: US-09-544-664-3
Perfect score: 145
Sequence: 1 NLWAAQRYGRELRRMSDEFEGSFKGLP 27
Scoring table: BLOSUM62

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: 127863 seqs, 47026705 residues Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	Q61337 mus musculu	035147 rattus norv			Q61703 mus musculu			P35632 arabidopsis	_								Q9i4u3 pseudomonas		Q9x0n8 thermotoga		Q9s7b5 arabidopsis	043521 homo sapien		P10419 anthopleura	Q9dcd2 mus musculu					calliacti	loise	hcs7	9p869 kluy
SUMMARIES		QI	BAD_MOUSE	BAD_RAT	BAD_HUMAN	ITH2_MESAU	ITH2_MOUSE	ITH2_HUMAN	AROG_YEAST	AP3_ARATH	CEO5_MOUSE	MATK_LEDPA	MATK_RHOFR	MATK_RHOTS	END8_ECO57	END8_ECOLI	END8_SALTI	END8_SALTY	RMUC_PSEAE	RAS3_RHIRA	6PGL_THEMA	THRC_SOLTU	THRC_ARATH	BIM_HUMAN	FMR2_ANTEL	FMR1_ANTEL	XAB2_MOUSE	XAB2_RAT	SEC6_DROME	RPOB_CAMJE	PRFA_POLPE		Ų	ᅰ	SNF4_KLULA
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Q9uix4 homo sapien	Q03030 salmonella	P13187 klebsiella	Q13049 homo sapien	P05886 simian immu	Q18823 caenorhabdi	Q9p0jo h nadh-ubiq	P33602 escherichia	P33900 salmonella	O54918 mus musculu	O88498 rattus norv	P27757 simian immu
KCG1_HUMAN	DCOA_SALTY .	DCOA_KLEPN	HT2A_HUMAN	ENV_SIVAT	LML1_CAEEL	NB6M_HUMAN	NUOG_ECOLI	NUOG_SALTY	BIM_MOUSE	BIM_RAT	ENV_SIVA1
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513	290	595	653	865	1535	143	907	202	196	196	768
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ALIGNMENTS

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SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hsu S.Y., Kaipia A., Zhu L., Hsueh A.J.W.;
"Interference of BAD (Bcl-xL/Bcl-2-associated death promoter)-induced apoptosis in mammalian cells by 14-3-3 isoforms and Pll.";
Mol. Endocrinol. 11:1858-1867(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D'Agata V., Magro G., Travali S., Musco S., Cavallaro S.; "Cloning and expression of the programmed cell death regulator BAD in
                                                                                                                                                                                                                                                                                                                                                      S->A: NO PHOSPHORYLATION, S->A: NO PHOSPHORYLATION; INTERACTS WITH
Ser-136 is the major site of AKT/PKB phosphorylation, Ser-155 the
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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PKB).
PKB).
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16-OCT-2001 (Rel. 40, Last sequence update)
18-FEB-2003 (Rel. 41, Last annotation update)
BCl2-antagonist of cell death (BAD) (BCl-2 binding component 6) (BCl-xL/BCl-2 associated death promoter).
                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 145; DB 1; Length 204; 100.0%; Pred. No. 1.4e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE PROM N.A., AND MUTAGENESIS OF SER-113 AND SER-137
           major site of protein kinase A (CAPK) phosphorylation. SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain. SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
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PKA AND I
PKA AND I
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MEDLINE=98194755; PubMed=9535132;
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MEDLINE=98034386; PubMed=9369453;
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InterPro; IPR000712; Bc12_BH.
PROSITE; PS01259; BH3; FALSE_NEG.
Apoptosis; Phosphorylation.
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27; Conservative
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112
1155
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136
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                                                                                                                                                                                                              HSSP; 092934; 1G5J
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035147; 070256;
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136
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BAD_RAT
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Hamner S., Arumae U., Yu L.-Y., Sun Y.-F., Saarma M., Lindholm D.;
"Functional characterization of two splice variants of rat BAD and
their interaction with Bol-w in sympathetic neurons.";

Their interaction with Bol-w in sympathetic neurons.";

Mol. Cell. Neurosci. 17:97-106(2001).

Cell. Neurosci. 17:97-106(2001).

Dinding to Bol-x(L), Bol-2 and Bol-w, thereby affecting the level of heterodimerization of these proteins with BAX. Can reverse the death repressor activity of Bol-x(L), but not that of Bol-2 (By similarity). Appears to act as a link between growth factor receptor signaling and the apoptotic pathways.

C. -: SUBUNIT: Forms heterodimers with the anti-apoptotic proteins, Bol-x(L), Bol-2 and Bol-w. Also binds protein Sl00Al0. The Ser-113/Ser-137 phosphorylated form binds l4-3-3 proteins.

C. -: SUBCELLULAR LOCATION: Outer mitochondrial membrane. Upon phosphorylation, locates to the cytoplasm (By similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=05147-2; Sequence=VSP_000534;

-i-TISSUE SPECIFICITY: Expressed in all tissues tested, including brain, liver, spleen and heart. In the brain, restricted to epithelial cells of the choroid plexus. Isoform alpha is the more abundant form.

-i-DOMAIN: Intact BH3 domain is required by BIK, BID, BAK, BAD AND BAX for their pro-apoptotic activity and for their interaction with anti-apoptoric members of the Bcl-2 family.

-i-PTW: Phosphorylated on Ser-133 in response to survival stimuli.

Subsequent phosphorylation on Ser-137 promotes heterodimerization with 14-3-3 proteins. This interaction then facilitates the phosphorylation at Ser-136 a site within the BH3 domain, leading to the release of Bcl-x(L) and the promotion of cell survival.

Ser-137 is the major site of AKT/PKB phosphorylation, Ser-156 the major site of protein kinase A (CAPK) phosphorylation (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LPRPKSAGTATQMRQSASWTRIIQSWWDRNLGKGGSTPSQ
-> EELTYSVEFLPVRAIAMEGWPLLWSFQSFPHTLPPTPP
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PHOSPHORYLATION (BY PKA AND PKB)
(BY SIMILARITY).
PHOSPHORYLATION (BY PKA AND PKB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BH3.
PHOSPHORYLATION (BY PKA AND PKB)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Phosphorylation; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Event-Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=035147-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; Q92934; 1G5J.
InterPro; IPR000712; BC12_BH.
PROSITE; PS01259; BH3; FALSE_NEG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     162
113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=Alpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=Beta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Apoptosis;
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S->A: NO HETERODIMERIZATION WITH 14-3-3 PROTEINS. NO EFFECT ON HETERODIMERIZATION WITH BCLZ NOR WITH PROTEIN P11.

SDAGGR -> ERRGRK (IN REF. 1). 7AFA71DAE9CF4A81 CRC64;

34 SI 22228 MW;

29 205 AA;

/FIId-VSP_000534. S->A: NO EFFECT ON HETERODIMERIZATION WITH 14-3-3 PROTEINS.

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SEQUENCE
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A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

R Alausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshlyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Robak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Villalon D.K., Muzny D.W., Scdergen B.J., Lu X., Gibbs R.A.,

Richards S., Muzny D.W., Scdergen B.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

R Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

R Rodriguez A.C., Grimwood J.S., Schwuck Y., Smailus D.E.,

R Rodriguez A.C., Grimwood J.S., Schwuck R.M.,

R Rodriguez A.C., Grimwood J.S., Marra M.A.;

R Generation and initial analysis of more than 15,000 full-length

RT Human and mouse CDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yin D.X., Li Z., Huang B., Chen S., Zhou H.;
"A human protein that interacts with Bcl-2 and have homology to mouse
                                                                                                                                                                                                                                         01-NOV-1997 (Rel. 35, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last amoutation update)
BCl2-antagonist of cell death (BAD) (Bcl-2 binding component 6) (Bcl-XL/Bcl-2 associated death promoter) (BCL2-like 8 protein).
BAD OR BBC6 OR BCL2L8.
                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ottilie S., Diaz J.-L., Horne W., Chang J., Wang Y., Wilson G., Chang S., Weeks S., Fritz L.C., Oltersdorf T.; "Dimerization properties of human BAD."; J. Biol. Chem. 272:30866-30872(1997).
                                                     ;
                  Length 205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=97083574; PubMed=8929532; Wang H.-G., Rapp U.R., Reed J.C.; "Bc1-2 targets the protein kinase Raf-1 to mitochondria."; Cell 87:629-638(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [3]
SEQUENCE FROM N.A.
Takayama S., Reed J.C.;
Takayama S., Reed J.C.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND PHOSPHORYLATION BY RAF-1.
                                                        ö
                                   1.4e-14;
                  100.0%; Score 145; DB 1;
100.0%; Pred. No. 1.4e-14;
ive 0; Mismatches 0;
                                                                                                                                                                                                                  168 AA.
                                                                                                               141 NIWAAQRYGRELRRMSDEFEGSFKGLP 167
                                                                                        1 NLWAAQRYGRELRRMSDEFEGSFKGLP 27
                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Bone marrow;
MEDLINE=98049554; PubMed=9388232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=22388257; PubMed=12477932;
                                                        27; Conservative
                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                    092934; 014803;
01-NOV-1997 (Re.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Lung
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                                                        Matches
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                                                                                                                                                 Tractionale for Bcl-xL/Bad peptide complex formation from structure,

"Rationale for Bcl-xL/Bad peptide complex formation from structure,

"Rationale for Bcl-xL/Bad peptide complex formation from structure,

"Rationale for Bcl-sA(2000).

"The following for Bcl-xL/Bad Bcl-w, thereby affecting the level

"The following to Bcl-x(L), Bcl-2 and Bcl-w, thereby affecting the level

"The following for Bcl-x(L), Bcl-2 and Bcl-w, thereby affecting the level

"The following for School and Bcl-w, thereby affecting the level

"The following following following following factor

"The following following following and the apoptotic pathways.

"The following form binds 14-3-3 proteins (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 c. SIMILARITY.).

C. SIMILARITY.).

C. SIGCELLIDIAR LOCATION: Outer mitochondrial membrane. Upon phosphorylation, locates to the cytoplasm.

C. TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.

C. DOMAIN: Intact BH3 domain is required by BIK, BID, BAK, BAD AND RAX for their pro-apoptotic activity and for their interaction with anti-apoptotic members of the BBL-2 family.

C. PTM: Phosphorylated on Ser-75 in response to survival stimuli.

Subsequent phosphorylation on Ser-99 promotes heterodimerization to hosphorylation at Ser-18, a site within the BH3 domain, leading to the release of BGL-x(L) and the promotion of cell survival.

Ser-99 is the major site of AKT/PKB phosphorylation, Ser-118 the major site of protein kinase A (CAPK) phosphorylation (by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              similarity).
-!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
-!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
-!- CAUTION: Ref.1 sequence differs from that shown due to frameshifts in position 64 and 91.
                                                                               Meadows R.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PHOSPHORYLATION (BY PKA AND PKB)
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STRUCTURE BY NMR OF 103-127.
MEDLINE-21073561; PubMed-11206074;
Petros A.M., Nettesheim D.G., Wang Y., Olejniczak E.T., Mea
Mack J., Swift K., Matayoshi E.D., Zhang H., Thompson C.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Apoptosis; Phosphorylation; Polymorphism; 3D-structure.
DOMAIN 110 124 BH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY).
A -> S (in dbSNP:3729933).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18392 MW; 69FD8D27DDEE3241 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0005737; C:cytoplasm; NAS.
GO; GO:0005741; C:mitochondrial outer membrane; NAS.
GO; GO:0005115; P:protedin binding activity; NAS.
GO; GO:0008632; P:apoptotic program; TAS.
GO; GO:0006917; P:induction of apoptosis; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000712; Bc12_BH.
PROSITE; PS01259; BH3; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF021792; AAB72092.1; EMBL; AF031523; AAB88124.1; EMBL; BC001901; AAH01901.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83.1%;
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MIM; 603167; -.
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ITH2_MOUSE
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CARBOHYD
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the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDINE-97420688; pubmed-9276673;
Nakatani T., Suzuki Y., Yamamoto T., Sinohara H.;
"Molecular cloning and sequencing of cDNAs encoding three heavy-chain precursors of the inter-alpha-trypsin inhibitor in Syrian hamster: implications for the evolution of the inter-alpha-trypsin inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT: I-ALPHA-I PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN, BIKUNIN. INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2 AND BIKUNIN, INTER-ALPHA-INHIBITOR (I-ALPHA-I) OF H2 AND BIKUNIN, AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN, AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN. PTM: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN 4-SULFATE BRIDGE TO THE THEIR C-TERMINAL ASPARTATE (BY
                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yamamoto T., Yamamoto K., Sinohara H.;
"Inter-alpha-trypsin inhibitor and its related proteins in Syrian hamster urine and plasma.";
J. Biochem. 120:145-152(1995).
-!- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN, INCLUDING THOSE ON CELL SURFACES IN TISSUES TO RECULATE THE LOCALIZATION, SYNTHESIE AND DEGRADATION OF HYALURONAN WHICH ARE ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY
                                                                                                                                                                                                                                               15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Inter-alpha-trypsin inhibitor heavy chain H2 precursor (ITI heavy chain H2) (Inter-alpha-inhibitor heavy chain 2) (HC2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 55-64; 140-146; 151-156; 424-447; 500-528 AND 577-605,
                                                                                                                                                                                                                                                                                                                                                                  Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Cricetinae,
                     -
                     Indels
Pred. No. 5.5e-11;
                                                                                                                                                                                        946 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ITIH FAMILY.
                     Mismatches
                                                                            103 NIWAAQRYGRELRRMSDEFVDSFKKGLP 130
                                                      27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: BELONGS TO THE ITIH FAM: SIMILARITY: Contains 1 VWFA domain.
                                                                                                                                                                                                                                                                                                                                           Mesocricetus auratus (Golden hamster).
                                                      1 NLWAAQRYGRELRRMSDEFEGSF-KGLP
                                                                                                                                                                                          PRT;
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89.3%;
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InterPro; IPR002035; VWF_A.
Pfam; PP00092; vwa; 1.
SMART; SM00609; VIT; 1.
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                     Conservative
                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                             15-JUL-1998 (Rel. 36,
15-JUL-1998 (Rel. 36,
28-FEB-2003 (Rel. 41,
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chain family
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10036;
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                     Matches
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                                                                                                                                                            INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PEDLINE-55184/60; TISSUE-Liver;

MEDLINE-95194326; PubMed-7534067;

Chan P., Risler J.-L., Raquenez G., Salier J.-P.;

Chan P., Risler J.-L., Raquenez G., Salier J.-P.;

"The three heavy-chain precursors for the inter-alpha-inhibitor
"The in mouse: new members of the multicopper oxidase protein group
with differential transcription in liver and brain.";

Biochem. J. 306:505-512(1995).

-: FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A
BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN,
INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE
LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE
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BIKUNIN. INTER-ALPHA-INHIBITOR (1-ALPHA-I) IS COMPOSED OF H1, H2
AND BIKUNIN, INTER-ALPHA-LIKE INHIBITOR (1-ALPHA-LI) OF H2 AND
BIKUNIN, AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN.
-!- TISSUE SPECIFICITY: EXPRESSED IN BOTH LIVER AND BRAIN.
-!- PTM: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN
4-SULFATE BRIDGE TO THE THEIR C-TERMINAL ASPARTATE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Inter-alpha-trypsin inhibitor heavy chain H2 precursor (ITI heavy
chain H2) (Inter-alpha-inhibitor heavy chain 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chordata, Craniata, Vertebrata, Euteleostomi, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                         (POTENTIAL).
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                                                     Serine protease inhibitor; Repeat; Signal; Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 946;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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10 V -> Y (IN REF. 2).
595 E -> I (IN REF. 2).
106580 MW; CA8BF565458E7B2E CRC64;
                                                                                                                                                                                                                                                                         (GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                                                                                 CHONDROITIN 4-SULFATE,
                                                                                                                                                                                                                                                                                                                              (GLCNAC. . .)
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                                                                                                                                                                                                                                                                                                                                                          (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42.1%; Score 61; DB 1; 37.0%; Pred. No. 0.34;
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578
SMART; SM00327; VWA; 1.
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Mammalia; Eutheria;
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Best Local Similarity
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                           PROSITE; PS50234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
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                                                                                   Glycoprotein.
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MEDLINE=89076497; PubMed=2462430;
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                                                                                                                                                                                BY SIMILARITY.
INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN
as its content is in no
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P19823; Q14659; Q15484;
O1-FEB-1991 (Rel. 17, Created)
O1-FEB-1991 (Rel. 17, Last sequence update)
O1-FEB-1993 (Rel. 42, Last amnotation update)
Inter-alpha-trypsin initiation heavy chain H2 precursor (ITI heavy chain H2) (Inter-alpha-inhibitor heavy chain B2) (Inter-alpha-trypsin inhibitor complex component II) (Serum-derived hyaluronan-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIINE=88068576; PubMed=2446322; Salier J.-P., Diarra-Mehrpour M., Sesboue R., Bourguignon J., Salier J.-P., Ohkubo I., Kurachi S., Kurachi K., Martin J.P.; Isolation and characterization of CDNAs encoding the heavy chain of human inter-alpha-trypsin inhibitor (I alpha TI): unambiguous evidence for multipolypeptide chain structure of I alpha TI."; Proc. Natl. Acad. Sci. U.S.A. 84:8272-8276(1987).
                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-88152237; PubMed-2450046; Gebhard W., Schreitmueller T., Hochstrasser K., Wachter E.; "Complementary DNA and derived amino acid sequence of the precursor of one of the three protein components of the inter-alpha-trypsin
                                                                                                                                                                                                                                                         N-LINKED (GLCNAC. . .) (POTENTIAL).
CHONDROITIN 4-SULFATE, CROSS-LINK SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                    N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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                                                                                                                                     PROSITE; PS50234; WWFA, 1. Serine protease inhibitor; Repeat; Signal; Multigene family;
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non-profit institutions as long
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                                                                                                                                                                                                                                                                                                                                                                           212 NVWIIEPQGMRFLHVPDTFEGHFQGVP 23,8
                                                                                                                                                                                                                                                                                                                                                       1 NEWAAQRYGRELRRMSDEFEGSFKGLP 27
                                                                                                                                                                                                                                                                                                              Score 60;
                                                                                                                                                                       POTENTIAL
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                                                                                                                                                                                                                                                                                                                         Pred.
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                                                 EMBL; X70392; CRA49842.1; -. PIR, S54354.
MGD; MGI:96619; Itih2.
InterPro; IPR006587; VIT.
InterPro; IPR002035; VWF_A.
Pfam; PF00092; VW3; 1.
SMART; SM00609; VW1; 1.
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37.08;
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                                                                                                                                                                                                                                                                                                                                  10; Conservative
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Best Local Similarity
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CARBOHYD
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Malki N., Balduyck M., Maes P., Capon C., Mizon C., Han K.K.,
Tartar A., Fournet B., Mizon J.;
"The heavy chains of human plasma inter-alpha-trypsin inhibitor: their
isolation, their identification by electrophoresis and partial
sequencing. Differential reactivity with concanavalin A.";
Biol. Chem. Hoppe-Seyler 373:1009-1018(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pizzo S.V., Hefta S.A., "Presence of the protein-glycosaminoglycan-protein covalent cross-link in the inter-alpha-inhibitor-related proteinase inhibitor heavy chain 2/bikunin.";
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                                                          "Human inter-alpha-trypsin inhibitor. Isolation and characterization of heavy (H) chain cDNA clones coding for a 383 amino-acid sequence of the H chain.";
                                                                                                                                                                                                                                                                                                                                                                                                                           Gebhard W.;
"cDNA cloning of human inter-alpha-trypsin inhibitor discloses three
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MEDLINE-94229087; PubMed=7513643;
Morelle W., Capon C., Balduyck M., Sautiere P., Kouach M.,
Michalski C., Fournet B., Mizon J.;
"Chondroitin sulphate covalently cross-links the three polypeptide chains of inter-alpha-trypsin inhibitor.";
Eur. J. Biochem. 221:881-888(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 699-702, AND COVALENT LINKAGE WITH CHONDROITIN SULFATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein (SHAP) is the heavy
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                                                                                                                                                                                                                                                                                                                                                                                          Schreitmueller T., Hochstrasser K., Resinger P.W.M., Wachter E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-89380192; PubMed=2476436; Enghild J.J., Thoegersen I.B., Pizzo S.V., Salvesen G.; Enghild J.J., Thoegersen I.B., Pizzo S.V., Salvesen G.; Analysis of inter-alpha-trypsin inhibitor and a novel trypsin inhibitor, pre-alpha-trypsin inhibitor, from human plasma. Polypeptide chain stoichiometry and assembly by glycan."; J. Biol. Chem. 264:15975-15981(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-98087700; PubMed-9425062;
Olsen E.H.N., Rahbek-Nielsen H., Thoegersen I.B., Roepstorff
Enghild J.J.;
Salier J.-P., Diarra-Mehrpour M., Sesboue R., Bourguignon J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYDRAIE LINKAGE SITES THR-691.
MEDLINE=93232026; Pubmed=7682553;
Enghild J.J., Salvesen G., Thoegersen I.B., Valnickova Z., Pizzo S.V., Hefta S.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 55-74; 116-127; 224-246; 295-307 AND 365-385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYDRATE-LINKAGE SITES, AND MASS SPECTROMETRY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chain of the inter alpha-trypsin inhibitor."; J. Biol. Chem. 268:26725-26730(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biol. Chem. Hoppe-Seyler 368:963-970(1987).
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                                                                                                                                                                                             Biol. Chem. Hoppe-Seyler 369:15-18(1988).
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serum-derived hyaluronan-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biol. Chem. 268:8711-8716(1993).
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                                                                                                                                                                                                                                                                                                                                                  MEDLINE=88024442; PubMed=3663330;
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                                                                                                                                                                                                                                                                         PARTIAL SEQUENCE FROM N.A.
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SEQUENCE OF 55-64.
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                                    Martin J.P.;
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us-09-544-664-3.rsp

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                            AROG_YEAST
                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN
H2.
identification of glycans and disulfide bridges in heavy chains 1 and
                                                                                            -!- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN, INCLUDING THOSE ON CELL. SURFACES IN TISSUES TO REGULATE THE LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES.
-!- SUBUNIT: I-ALPHA-I PLAAMA PROTEAGE INHIBITORS ARE ASSEMBLED FROM ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN, BIKUNIN, INTER-ALPHA-IINEBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2 AND BIKUNIN, INTER-ALPHA-IINEBITOR (P-ALPHA-I) OF H2 AND BIKUNIN, AND PRE-ALPHA-IINERON (P-ALPHA-I) OF H3 AND BIKUNIN, INTER-ALPHA-IINERON (P-ALPHA-I) OF H3 AND BIKUNIN, AND PRE-ALPHA-IINERON (P-ALPHA-II) OF H3 AND BIKUNIN, AND PRE-ALPHA-IINERON (P-ALPHA-IINERON (P-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHONDROITIN 4-SULFATE, CROSS-LINK SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /FTId=CAR_000140.
O-LINKED (GALNAC. . .) (PARTIAL).
/FTId=CAR_000214.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Serine protease inhibitor; Repeat; Signal; Multigene family; Gamma-carboxyglutamic acid; Glycoprotein.

SIGNAL 1 18 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MASS SPECTROMETRY: MW=76508; METHOD=MALDY; RANGE=55-702. SIMILARITY: BELONGS TO THE ITTH FAMILY. SIMILARITY: Contains 1 WWFA domain.
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P -> A (IN REF. 2 AND 3),
F -> S (IN REF. 2 AND 3),
N -> D (IN REF. 2 AND 3),
V -> A (IN REF. 2 AND 3),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60; G0:0005211; F:plasma glycoprotein; TAS.
InterPro; IPR006587; VIT.
InterPro; IPR002035; VWF_A.
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EMBL; M18193; AAA60558.1; --
EMBL; M33033; AAA59195.1; --
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                                                                    Biochemistry 37:408-416(1998)
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SMART; SM00609; VIT; 1.
SMART; SM00327; VWA; 1.
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DB 1; Length 946;

36.6%; Score 53;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Doignon F., Biteau N., Aigle M., Crouzet M.;
"The complete sequence of a 6794 bp segment located on the right arm of chromosome II of Saccharomyces cerevisiae. Finding of a putative
                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                               Phospho-2-dehydro-3-deoxyheptonate aldolase, tyrosine-inhibited (EC 4.1.2.15) (Phospho-2-*Acto-3-deoxyheptonate aldolase) (DAHP synthetase) (3-deoxy-D-arabino-heptulosonate 7-phosphate synthase). ARO4 OR YBR249C OR YBR1701,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycetes;
                             Ö,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              first step.
-!- INDUCTION: By amino acid starvation.
-!- SIMILARITY: BELONGS TO CLASS-I DAHP SYNTHETASE FAMILY.
                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (NOV-1993) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomycetales; Saccharomycetaceae; Saccharomyces. NCBL_TaxID=4932;
                             13;
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                                                                                                                                                                                                                                                                                           370 AA
Pred. No. 5.4;
                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
                             Mismatches
                                                                                                                            ::| : | ::| 212 DVWVIEPQGLRFLHVPDTFEGHFDGVP 238
                                                                                      1 NLWAAQRYGRELRRMSDEFEGSFKGLP 27
                                                                                                                                                                                                                                                                                                PRT;
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MEDLINE=92225349; PubMed=1348717;
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  33.3%;
                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 dUTPase in a yeast.";
Yeast 9:1131-1137(1993).
                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                      (Rel. 27, (Rel. 28, 1) (Rel. 41, 1)
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App or Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Puruganan M.D., Suddith J.I.;
"Molecular population genetics of floral homeotic loci: departures from the equilibrium neutral model at the APETALA3 and PISTILLATA genes of Arabidopsis thaliana.";
Genetics 151:839-848(1999).
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SEQUENCE FROM N.A.
STRAIN=cv. Landsberg erecta;
MEDLINE=95036018; PubMed=7948893;
Okamoto H., Yano A., Shiraishi H., Okada K., Shimura Y.;
"Genetic complementation of a floral homeotic mutation, apetala3, with an Arabidopsis thaliana gene homologous to DEFICIENS of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND VARIANTS.
STRAIN-GV. Bla-1, CV. Bretagny, CV. Bs-1, CV. Bu-0, CV. Bu-2,
CV. Chi-1, CV. CO-1, CV. Columbia, CV. Corsacalla-1, CV. Cvi-0,
CV. Gr-3, CV. Jl-1, CV. Kas-1, CV. Kent, CV. Landsberg erecta,
CV. Li-3, CV. Li-8, and CV. Lisse;
MEDLINE-99126449; PubMed-9927474;
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PRT, 232 AA.
P35632; Q39003; Q8LB79; Q9S7Q3; Q9SQ14; Q9SQ15; Q9SQ16; Q9SQ17;
Q9SQ18; Q9SQ19; Q9SQ21; Q9SQ21; Q9SX13;
Q1-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
                             SGD; SO000453; ARO4.
GO; GO:0003849; F:2-dehydro-3-deoxyphosphoheptonate aldolase .
InterPro; IPR006219; AroFGH.
InterPro; IPR006218; DAHP1/KDSA.
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                                                                                                                                                 Pfam; PF00793; DAHP_Synth_1; 1.
ProDom; PD005060; AroFGH; 1.
TIGRFAMS; TIGR00034; aroFGH; 1.
Aromatic amino acid biosynthesis; Lyase; Multigene family.
SEQUENCE 370 AA; 39749 MW; 594ED48F24175979 CRC64;
                                                                                                                                                                                                                                                                                                                                         Score 52; DB 1; Length 370; Pred. No. 2.7;
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STRAIN=cv. Columbia;
MEDLINE=21016720; PubMed=11130713;
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80 DLEAAOEYALRIKKLSDELKG 100
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HSSP; P00886; 1QR7
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RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,

RA Wurmbach E., Drzonek H., Erfle H., Jordan N., Bangert S.,

Wiedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,

RA Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simionati B.,

Ronrad A., Hornischer K., Kauer G., Loehnert T.-H., Nordsiek G.,

Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,

RA Navarro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,

RA G Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Cascuberta E.,

RA Monfort A., Argirlou A., Flores M., Liguori R., Vitale D.,

RA Manhaupt G., Raase D., Schoof H., Kudd S., Zaccaria P., Mewes H.-W.,

RA Manhaupt G., Haase D., Schoof H., Teulin L.J., Jenkins J.,

RA Rooney T., Rizzo M., Walts A., Utterback T., Fujii C.Y., Shea T.P.,

RA Rooney T., Rizzo M., Walts A., Utterback T., Fujii C.Y., Shea T.P.,

RA Rooney T., Rizzo M., Maiti R., Wu D., Peterson J., Van Aken S.,

RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,

RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,

RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,

RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,

RA Watanabe A., Yamada M., Yasuda M., Tabata S.;

RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brassica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Krizek B.A., Meyerowitz E.M.; "The Arabidopsis homeotic genes APETALA3 and PISTILLATA are sufficient to provide the B class organ identity function."; Development 122:11-22(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Riechmann J.L., Krizek B.A., Meyerowitz E.M.; "Dimerization specificity of Arabidopsis MADS domain homeotic proteins APETALA1, APETALA3, PISTILLATA, and AGAMOUS."; Proc. Natl. Acad. Sci. U.S.A. 93:4793-4798(1996).
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"Activation of the Arabidopsis B class homeotic genes by APETALA1.";
Plant Cell 13:739-753(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=cv. Columbia;
Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
"RIKEN Arabidopsis full length cDNA clones (RAFLs) sequenced by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-cv. Columbia; MEDLINE-9931127; PubMed=10382288; Brunel D., Frager N., Pelletter G.; "Development of amplified consensus genetic markers (ACGM) in napus from Arabidopsis thaliana sequences of known biological function.";
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Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSP consortium (Salk/Stanford/PGEC).";
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Full-length cDNA from Arabidopsis thaliana.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 408:820-822(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    floral organs.";
Nature 409:525-529(2001).
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PubMed=11206550;
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Feldmann K.;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Flowering; Transcription regulation; Activator; Developmental protein; Nuclear protein; DNA-binding; Coiled coil; Polymorphism.
FUNCTION: Probable transcription factor involved in the genetic control of flower development. Is required for normal development of petals and stamens in the wild-type flower. Forms an heterodimer with PISTILLATA that is required for autoregulation of both AP3 and PI genes. AP3/PI heterodimer interacts with APETALA1 or SEPALMATA3 to form a ternary complex that could be responsible for the regulation of the genes involved in the flower
                                                                                                                                                                       -:- SUBCELLULAR LOCATION: Nuclear.
-:- TISSUE SPECIFICITY: Expressed in petals and stamens.
-:- TISSUE SPECIFICITY: Expressed in petals and stamens.
-:- INDUCTION: Positively regulated by the meristem identity proteins APETALAI and LEAFY with the cooperation of UFO.
-:- MISCELLANEOUS: Mutations in AP3 cause transformation of petals into sepals and stamina into carpels.
-:- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
                                                                                                                             SUBUNIT: Forms an heterodimer with PISTILLATA, capable of binding to CArG-box sequences. AP3/PI heterodimer binds AP1 or SEP3 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Corsacalla-1).
Li-8).
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COILED COIL (POTENTIAL).
K -> R (in strain cv. Lisse).
M -> T (in strain cv. Bretagny).
N -> D (in strain cv. Corsacalla-1
T -> S (in strain cv. Li-8).
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InterPro; IPR002487; TF_Kbox.
InterPro; IPR002100; TF_MADSbox.
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AY142590; AAN13159.1;
AF056541; AAD41557.1;
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AF115801; AAD51890.1;
AF115802; AAD51891.1;
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AF115808; AAD51897.1;
AF115809; AAD51898.1;
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AAD51893.1;
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AF115806; AAD51895.1;
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VARIANT
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REDUINE EL220025; Fubmed 124,7925;

REDUINE EL220025; Fubmed 124,7925;

Richarsher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Rlausherg R.L., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

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Rhepkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

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Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Rale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Shevchenko Y., Bouffard G.G.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Reneration and initial analysis of more than 15,000 full-length

Ruman and mouse cDNA sequences.

R. Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

Proc. Instrantive Belongs to the FAM13 family.

- I - SIMILARITY: Contains 1 Rho-GAP domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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L \rightarrow V (in strain cv. Kas-1). 
 E \rightarrow K (in strains cv. Chi-1 and Gr-3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 851;
                                                                          Length 232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      between the Swiss Institute of Bioinformatics and the
                                                                                                             4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C2B26669FB6DB2CE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
13;
                                                                          DB 1;
                                                                                                                                                                                                                                                                                                           15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                             851 AA
                                                                                                           3; Mismatches
                                                                      Score 51;
Pred. No. 2
                                                                                                                                                                                  107 ORLGECLDELDIQELRRLEDEMENTEK 133
                                                                                                                                                24
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Pred. No.
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GLU-RICH.
                                                                                                                                                6 QRYG-----RELRRMSDEFEGSFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; BC031465; AAH31465.1; -.
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97054 MW;
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Pfam; PF00620; RhoGAP; 1.
SMART; SM00324; RhoGAP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34.5%;
45.5%;
                                                                                         44.48;
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                                                                          35.2%;
                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                   Protein Cforf5 homolog.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23
189
                                                                                                                                                                                                                                                                           CE05_MOUSE
Q8K2H3;
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DOMAIN
 VARIANT
                    VARIANT
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                                                                                                                                                                                                                                                            CE05_MOUSE
                                                                                                                                                                                                                                        RESULT 9
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 FF
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10;

Matches

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Chloroplast.

Yukawa T.;

MATK_LEDPA

ID MATK_LEDPA

AC 05292

DT 15-SEP

DT MATK

OC SPERMIN

OC SPERMIN

RA KUTASh

RA KUTASh

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CC 1-FU

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MATK LEDPA

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                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots;
Asteridae; Ericales; Ericaceae; Ericoideae; Rhodoreae; Rhododendron.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Investigation of sectional relationships in the genus Rhododendron (Ericaceae) based on matK sequences."; Shokubutsu Kenkyu Zasshi 73:143-154(1998).
-:- FUNCTION: Probably assists in splicing chloroplast group II introns (By similarity).
-:- SIMILARITY: BELONGS TO THE INTRON MATURASE FAMILY 2. MATK
                                                                                                      "Investigation of sectional relationships in the genus Rhododendron (Ericaceae) based on matK sequences."; Shokubutsu Kenkyu Zasshi 73:143-154(1998).
-!- FUNCTION: Probably assists in splicing chloroplast group I introns (By similarity).
-!- SIMILARITY: BELONGS TO THE INTRON MATURASE FAMILY 2. MATK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
                                              SEQUENCE FROM N.A.
Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 506;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000442; Intron_maturse2,
InterPro; IPR002866; Matk_N.
Pfam; PF01348; Intron_maturas2; 1.
Pfam; PF01824; Matk_N; 1.
MRNA processing; Chloroplast.
SEQUENCE 506 AA; 60534 MW; ADA44B25E92435E8 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :||| :| :| | | 1 | 393 VWAALSDSDIIERFGRIYRNLSHYYSGSLK 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 49.5; I
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                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch)
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36.7%;
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NCBI_TaxID=49629;
  NCBI_TaxID=49622;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBFAMILY.
                                                                                                                                                                                                                                             SUBFAMILY
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28-FEB-2003
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                                                                                          Yukawa T
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      QΫ
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                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; Ericales; Ericaceae; Ericoideae; Rhodoreae; Rhododendron.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -I.- FUNCTION: Probably assists in splicing chloroplast group II introns (By similarity).
-I.- SIMILARITY: BELONGS TO THE INTRON MATURASE FAMILY 2. MATK
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Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 49.5; DB 1; Length 506; Pred. No. 9; 7; Indels 7
  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chloroplast.
A; 60412 MW; CFEA926307DAC85E CRC64;
  7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Investigation of sectional relationships in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rhododendron (Ericaceae) based on matK sequences.
Shokubutsu Kenkyu Zasshi 73:143-154(1998).
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Last annotation update)
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Last annotation update)
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5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 LWAA-----QRYGRELRRMSDEFEGSFK 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000442; Intron maturse2.
InterPro; IPR002866; MatK_N.
                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF01348; Intron_maturas2; 1. Pfam; PF01824; Matk_N; 1.
                                          23
                                          2 LWAAQRYGRELRRMSDEFEGSF
                                                                                                                                                                                                                                                                                                                               MATK.
Ledum palustre (Wild rosemary).
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(Rel. 41, Last anno
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15-SEP-2003 (Rel. 42, Last anno
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36.78;
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Best Local Similarity 36./*
'-has 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
Conservative
                                                                                                                                                                                               STANDARD;
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28-FEB-2003 28-FEB-2003 28-FEB-2003

MATK_RHOFR

RESULT 11 MATK_RHOFR

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SEQUENCE

Chloroplast.

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Gaps

7;

Indels

DR DR DR DR SQ

g QΣ

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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.; "Complete genome sequence of enterohemorrhagic Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0157:H7 and genomic comparison with a laboratory strain K-12.";
DNA Res. 8:11-22(2001).
-:- FUNCTION: DNA N-GLYCOSYLASE WITH AN AP LYASE ACTIVITY. REQUIRED FOR THE REPAIR OF OXIDATIVE DNA DAMAGE. CLEAVES THE DNA BACKBONE BY BETA-DELTA ELIMINATION AS WELL AS 5'DEOXYRIBOSE PHOSPHATE (BY
                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7.";
                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-21074935, PubMed=11206551;
MEDLINE-21074935, PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Maybew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.
                                                                                                                                      7;
                                                                                                          DB 1; Length 506;
                                                                                                                                      Indels
                                                                  mRNA processing, Chloroplast.
SEQUENCE 506 AA, 60569 MW, AEE12FF8809C223E CRC64;
                                                                                                                                     7;
                                                                                                                                                                                                                                                                          Lorented)
Lorented)
Lorented (Rel. 41, Last sequence update)
Endonuclease VIII (EC 3.2.-.-).
Escherichia coli Arrante (Reconstruction update)
Bacterichia coli Arrante (Reconstruction)
                                                                                                                                                                                       393 VWAALSDSDIIERFGRIYRNLSHYYSGSLK 422
                                                                                                                                                                                                                                                                 262 AA
                                                                                                                                     5; Mismatches
                                                                                                                                                                2 LWAA-----QRYGRELRRMSDEFEGSFK 24
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                                                                                                        34.1%; Score 49.5; 36.7%; Pred. No. 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch)
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InterPro; IPR000214; Fapy_DNAglyco_zn.
         Interpro; IPR000442; Introm maturse2.
Interpro; IPR002866; MatK_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-0157:H7 / RIMD 0509952;
MEDLINE-21156231; PubMed=11258796;
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                                     Pfam; PF01348; Intron_maturas2; 1.
Pfam; PF01824; Matk_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE005249; AAG55037.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 409:529-533(2001).
                                                                                                                                      11; Conservative
                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; A85572; A85572.
PIR; C90721; C90721.
                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=8334;
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                                                                                                                                                                                                                                                                END8 ECO57
                                                                                                            Query Match
                                                                                                                                                                                                                                   RESULT 13
END8_ECO57
                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SECTION N.A., AND SEQUENCE OF 1-35; 188-205 AND 213-226. MEDLINE=97315255; PubMed=9171429; Jiang D., Hatahet Z., Blaisdell J.O., Melamede R.J., Wallace S.S.; "Escherichia coli endonuclasse VIII: cloning, sequencing, and overexpression of the nei structural gene and characterization of nei and nei nth mutants.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -:- FUNCTION: DNA N-GLYCOSYLASE WITH AN AP LYASE ACTIVITY. REQUIRED FOR THE REPAIR OF OXIDATIVE DNA DAMAGE. CLEAVES THE DNA BACKBONE BY BETA-DELTA ELIMINATION AS WELL AS 5'DEOXYRIBOSE PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                 DNA repair; Hydrolase; Glycosidase; Endonuclease; Zinc; Zinc-finger; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley, M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Characterization of endonuclease III (nth) and endonuclease VIII (nel) mutants of Escherichia coli K-12."; J. Bacteriol. 179:3783-3785(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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Yamamoto K.;
                                                                                                                                                                                                                                                                         33.8%; Score 49; DB 1; Length 262; 47.4%; Pred. No. 5.2;
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                                                                                                                                                                                          POTENTIAL.
37C3C5E236E07A88 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-1996 (Rel. 34, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Endonuclease VIII (EC 3.2.-.).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     262 AA
                                                                                                                                                           BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                         Mismatches
Pfam, PF01149; Fapy_DNA_glyco; 1.
ProDom; PD003680; Fapy_DNA_glyco; 1.
PROSITE, PS01242; FPG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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Bacteriol. 179:3773-3782(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                     9 GRELRRMSDEFEGSFKGLP 27
                                                                                                                                                                                 260 PG
29680 MW;
                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                               Query Match
Best Local Similarity
9; Conserve
                                                                                                                                                                                 237 2
262 AA;
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Nature 413:848-852(2001).
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SEQUENCE FROM N.A.
STRAIN=TY2 / ATCC 700931;
MEDLINE=22531367; PubMed=12644504;
MEDLINE=22531367; PubMed=12644504;
Beng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Bacteriol. 185:2330-2337(2003).
-!- FUNCTION: DNA N-GLYCOSYLASE WITH AN AP LYASE ACTIVITY. REQUIRED FOR THE REPAIR OF OXIDATIVE DNA DAMAGE. CLEAVES THE DNA BACKBONE BY BETA-DELTA ELIMINATION AS WELL AS 5'DEOXYRIBOSE PHOSPHATE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                       Probom; PD003680; Fapy DNA_glyco; 1.
PROSITE; PS01242; FPG; 1.
DNA repair; Hydrolase; Glycosidase; Endonuclease; Zinc; Zinc-finger;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 49, DB 1; Length 262;
Pred. No. 5.2;
3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       237 260 POTENTIAL.
262 AA; 29714 MW; 5010961768ADC265 CRC64;
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28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Endonuclease VIII (EC 3.2.-.-).
NEI OR STYO71 OR T2148.
Salmonella typhi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      262 AA.
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SIMILARITY: BELONGS TO THE FPG FAMILY.
                     EMBL, U38616; AAC45355.1; -.
EMBL, D89754; BAA20414.1; -.
EMBL, AE000174; AAC73808.1; -.
EMBL, D90710; BAA35378.1; -.
PIR; A64807; A64807.
PDS; IK3W; 04-027-02.
ECGGne; EG13237; nei.
InterPro; IPR000191; Fapy_DNA_glyco.
InterPro; IPR00014; Fapy_DNA_glyco.
Pfam; PF01149; Fapy_DNA_glyco.
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                                                                                                                                                                                                                                                                                                                                                                                                                   Complete proteome; 3D-structure.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33.8%;
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Best Local Similarity 47.4
Matches 9; Conservative
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EMEL: AL657268: CAD05190.1; -
DR EMBL: AL657268: CAD05190.1; -
DR EMBL: AL657268: CAD05190.1; -
DR InterPor: IPR001019; Fapy_DNA_glyco. 1.
DR PROSITE: PS01242: FPG; 1.
DR PROSITE: PS0124: TRIBUTE AND TRIBARRADE TS, 2003, 17:22:59
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Q8k016 mus musculu
Q8vjs3 mycobacteri
Q10843 mycobacteri
Q8zy71 pyrobaculum
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Q9seg0 arabidopsis
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09sq15 arabidopsis
09s7q3 arabidopsis
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Q9sq17 arabidopsis
Q9sq19 arabidopsis
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Q8lb79 arabidopsis
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                                                                     (without alignments)
237.680 Million cell updates/sec
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                                                         September 15, 2003, 17:17:31; Search time 29.3143 Seconds
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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1 NLWAAQRYGRELRRMSDEFEGSFKGLP
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Listing first 45 summaries
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Q8VJS3
Q10843
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Gapop 10.0 , Gapext 0.5
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sp_bacteria:*
sp_fungi:*
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Perfect score:
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17	10 •	35.2	232	70	Q9SQ18 09KGW3	Q9sq18 arabidopsis O9kgw3 pseudomonas
119	50.5		606	10	Q8EI34	Q8ei34 shewanella
20		*:# •	066	ο.	Q9C793	09c793 arabidopsis
21			168	<u> </u>	08K316	Q8K316 mus musculu
22			283	0.1	037,056	03/056 chimpanzee
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24			516	0	Q9SSP5	
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44	δ.	√.	206		C	<u>н</u>
45	9.	4.	206		α	062983 rhododendro

ALIGNMENTS

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[1]—SEQUENCE FROM N.A.
MEDLINE-20373792; PubMed=10917738;
Inohara N., Nunez G.;
"Genes with homology to mammalian apoptosis regulators identified in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                         Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
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cell Death Differ. 7:509-510(2000).
cell Death Differ. 7:509-510(2000).
EMBL; AF231017; AAF66962.2; -.
HSSP; Q92934; 1G5J.
ZFIN; ZDB-GENE-000616-1; bad.
SEQUENCE 146 AA; 16546 MW; 28A5650BB5107ECB CRC64;
SEQUENCE 146 AA; 16546 MW; 28A5650BB5107ECB CRC64;
                                                                                                                                                                                            Last sequence update)
Last annotation update)
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nilarity 65.2%; Pred. No. 6.7e-05;
Conservative 5; Mismatches ?.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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Best Local Simi
Matches 15;
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ID 28K016
AC 28K016;
                                                                           Q919N2
Q919N2;
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RESULT 1
                                           Q919N2
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223 AA.

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PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=H37RV
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STRAIN-CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.E., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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EMBL; AE007058; AAK46348.1; -.
                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ó
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NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36.6%; Score 53; DB 16; Length 196; 58.8%; Pred. No. 9.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41.4%; Score 60; DB 11; Length 946; 37.0%; Pred. No. 4.9;
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                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.;
Strausberg R.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC034341; AAH341.1; -.
MGD; MGI:96619; Itih2.
InterPro; IPR006587; VIT.
InterPro; IPR002035; VWF.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Inter-alpha trypsin inhibitor, heavy chain 2.
ITIH2.
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212 NVWIMEPQGMRFLHVPDTFEGHFQGVP 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 NLWAAQRYGRELRRMSDEFEGSFKGLP 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003346; Transposase_20.
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|134 NLWAADRYNRAIARGHD 150
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Best Local Similarity 37.0°
Matches 10; Conservative
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SMART; SM00327; VWA; 1.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                    TISSUE-Liver;
                            01-0CT-2002
01-MAR-2003
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Q8VJS3
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Q10843
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"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
Nature 393:537-544(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I., Miller J.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                       Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36.6%; Score 53; DB 16; Length 223; 58.8%; Pred. No. 11; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 aerophilum.";
Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).

EMBL; AE009793; AAL63125.1; -.

InterPro; IPR0006538; Elp3.

InterPro; IPR000182; GCN5acetyltransf.

Pfam; PF00583; Acetyltransf; 1.

SMART; SM00729; Elp3; 1.

Hypothetical protein; Complete proteome.

SEQUENCE 471 AA; 52952 MW; 3B1E36E8AEE2EF0A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003346; Transposase_20.
Pfam; PF02371; Transposase_20; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 223 AA; 24132 MW; 70456750017FEF37 CRC64;
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01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein Rv2014.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: TO M.PARATUBERCULOSIS IS900.
EMBL, 274025; CAA98415.1; -.
Tuberculist; Rv2014; -.
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01-MAR-2002 (TrEMBLrel. 20, Created)
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SEQUENCE FROM N.A.
STRAIN-IM2 / ATCC 51768 / DSM 7523;
PubMed-11792869;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                     Mycobacterium tuberculosis.
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Matches 10; Conservative
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Pfam; PF01486; K-box; 1.
Pfam; PF01319; SRF-TF; 1.
PRINTS; PR00404; MADSDOMAIN.
SMART; SM00432; MADS; 1.
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Best Local Similarity 44.4%;
Matches 12; Conservative
                                                                                                                                                                  Query Match 35.2%;
Best Local Similarity 44.4%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-OCT-2002 (TrEMBLrel. 22, Floral homeotic protein AP3.
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Q9SQ22;
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098020;
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae,
eurosids II; Brassicales; Brassicaceae, Arabidopsis.
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                                           Gaps
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Mol. Biol. Evol. 16:1037-1045(1999).
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=99404148; PubMed=10474900;
Lawton-Rauh A.L., Buckler E.S. IV, Purugganan M.D.;
"Patterns of molecular evolution among paralogous floral homeotic
                                                                                                                                                                                                                                                                                                                                                                             Oryciolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
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                                           0;
 DB 17; Length 471;
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                                         11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Suzuki A.;
"Rabbit inter-alpha-trypsin inhibitor heavy chain.";
Submitted (CCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB050593; EAB17301.1; -.
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SEQUENCE 946 AA; 106240 MW; B7AF05434B228CC5 CRC64;
                                                                                                                                                                                                                                                09GIY6.
01-MAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Inter-alpha-trypsin inhibitor heavy chain2.
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Last annotation update)
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                                                                                                                                                                                                                                  946 AA.
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                                         3; Mismatches
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Score 52; DB
Pred. No. 34;
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                                                                                                           3 WAAQRYGRELRRMSDEFEGSFKGL 26
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HSSP, P11746; 1MNM.
InterPro, IPR002487; FF_Kbox.
InterPro, IPR002100; TF_MADSbox.
Pfam; PF01486; K-box; 1.
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Interpro, IPR002035; VWF_A.
Pfam, PF00092; Vwa; 1.
SMART, SM00609; VIT; 1.
SMART; SM00327; VWA; 1.
35.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 33.3
Matches 9; Conservative
Query Match
Best Local Similarity 41.7
Matches 10; Conservative
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9986;
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Pfam; PF00319; SRF-TF; 1.

PRINTS; PR00404; MADSDOMAIN.
SWART; SM00432; MADS; 1.
PROSITE; PS50066; MADS_BOX_2; 1.
NON_TER 21 231 231
SEQUENCE 231 AA; 27176 MW; A67CAEIEEBDBF7AA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA-binding; Nuclear protein; Transcription, Transcription regulation.
SEQUENCE 232 AA; 27342 MW; BDFDCB59B73F4601 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
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01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Floral homeotic protein AP3.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
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22;
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3; Mismatches
                                                                                                                                                                                              3; Mismatches
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                                                                                                                                                        Score 51;
Pred. No. 2
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                                                                                                                                                                                                                                                                                                                                                                                                               Created)
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STRAIN=cv. Corscalla;
MEDLINE=99126449; PubMed=9927474;
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HSSP; P11746; 1MNM.
InterPro; IPR002487; TF_Kbox.
InterPro; IPR002100; TF_MADSbox.
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4;

24

232 AA.

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SMART; SM00432; MADS; 1.

PROSITE; PS00350; MADS_BOX_1; 1.

PROSITE; PS50066; MADS_BOX_2; 1.

DNA-binding; Nuclear protein; Transcription; Transcription regulation.

SEQUENCE 232 AA; 27284 MW; 04FCFC55B73C7729 CRC64;
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DNA-binding; Nuclear protein; Transcription; Transcription regulation.
SEQUENCE 232 AA; 27311 MW; 71AE593FB8A67EC3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TAXID=3702;
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Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                  35.2%; Score 51; DB 10; Length 232; 44.4%; Pred. No. 22;
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Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Floral homeotic protein AP3.
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                                                                                                                                                                                                                                               3; Mismatches
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01-MAY-2000 (TrEMBLrel. 13, Last sequ
01-MAR-2003 (TrEMBLrel. 23, Last anno
Floral homeotic protein AP3.
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InterPro; IPR002100; TF_MADSbox.
Pfam; PF01486; K-box; 1.
Pfam; PF00319; SRF-TF; 1.
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                                                                                                                                                                                     Query Match 35.2
Best Local Similarity 44.4
Matches 12; Conservative
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Q9SQ21
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PROSITE; P$50066; MADS_BOX_2; 1.
DNA-binding; Nuclear protein; Transcription; Transcription regulation.
SEQUENCE 232 AA; 27267 MW; 42A852D697E22A65 CRC64;
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Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae, Arabidopsis.
                                                                Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots, Rosidae, eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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MEDLINE-99126449; PubMed=9927474;
Purugganan M.D., Suddith J.I.;
Purugganan M.D., Suddith J.I.;
"Molecular population genetics of floral homeotic loci. Departures from the equilibrium-neutral model at the APETALA3 and PISTILLATA genes of Arabidopsis thaliana.";
Genetics 151:839-848(1999).
-: SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-: SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
                                                                                                                                                                                                                                                                                                    Purugganan M.D., Suddith J.I.;
"Molecular population genetics of floral homeotic loci. Departures from the equilibrium-neutral model at the APETALA3 and PISTILLATA genes of Arabidopsis thaliana.";
Genetics 151:839-848(1999)
-! SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-! SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
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Pred. No. 22;
3; Mismatches 4; Indels
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                              Arabidopsis thaliana (Mouse-ear cress).
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01-MAY-2000 (TrEMBLrel. 13, Last seq
01-OCT-2002 (TrEMBLrel. 22, Last ann
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                                                                                                                                                                                                                                       STRAIN=cv. Li-8;
MEDLINE=99126449; PubMed=9927474;
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InterPro; IPR002100; TF_MADSbox.
Pfam; PF01486; K-box; 1.
Pfam; PF00319; SRP-TF; 1.
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InterPro; IPR002487; TF_Kbox.
InterPro; IPR002100; TF_MADSbox.
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SMART; SM00432; MADS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35.2%;
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tes 12; Conservative
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Pfam; PF00319; SRF-TF; 1
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SMART; SM00432; MADS; 1.
PROSITE; PS00350; MADS_BOX_1; 1.
PROSITE; PS50066; MADS_BOX_2; 1.
DNA-binding; Nuclear protefair; Transcription; Transcription regulation.
SEQUENCE 232 AA; 27286 MW; 66976305B8BB6333 CRC64;
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Floral homeotic protein APETALA3 (AP3).
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
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Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
                                                                STRAIN=cv. Kent;
MEDLINE=99126449; PubMed=9927474;
Purugganan M.D., Suddith J.I.;
"Molecular population genetics of floral homeotic loci. Departures from the equilibrium-neutral model at the APETALA3 and PISTILLATA genes of Arabidopsis thaliana.";
                                                                                                                                         Genetics 151:839-848(1999).
-!- SUBCELLULAR LOCATION: UUCLEAR (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.
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               eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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InterPro; IPR002487; TF_Kbox.
InterPro; IPR002100; TF_MADSbox.
Pfam; PF01486; K-box; 1.
Pfam; PF00319; SRF-TF; 1.
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InterPro; IPR002487; TF_Kbox.
InterPro; IPR002100; TF_MADSbox.
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Pfam; PF00319; SRF-TF;
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                           NCBI_TaxID=3702;
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PROSITE; PS50066; MADS_BOX_2; 1.
DNA-binding; Nuclear protein; Transcription; Transcription regulation.
SEQUENCE 232 AA; 27314 MW; DB8CA1FC835557D5 CRC64;
PROSITE; PS00350; MADS_BOX_1; 1.
PROSITE; PS50066; MADS_BOX_2; 1.
DNA-binding; Nuclear protein; Transcription; Transcription regulation.
SEQUENCE 232 AA; 27339 MW; CC90703F959CFAD5 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 22, Last annotation update)
Floral homeotic protein AP3.
APETALA3.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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"Molecular population genetics of floral homeotic loci. Departures from the equilibrium-neutral model at the APETALA3 and PISTILLATA genes of Arabidopsis thaliana.";
Genetics 151:839-848(1999).
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-!- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION PACTORS.
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Arabidopsis thaliana (Mouse-ear cress).
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PRINTS; PR00404; WADSDOMAIN.
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Occ Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; Rosidae;

OX NOSI TaxID=3702;

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

September 15, 2003, 17:16:01; Search time 39.6 Seconds Run on:

(without alignments) 112.231 Million cell updates/sec

US-09-544-664-55 Perfect score: Title:

 $\frac{148}{1 \text{ KNLWAAQRYGRELRRMSDEFEGSFKGLK}/28}$ BLOSUM62 Gapop 10.0 , Gapext 0.5 Sequence:

Scoring table:

1107863 segs, 158726573 residues Searched:

1107863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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No.	-	Score	ore Match Length DB II	ength	DB	ID	Description
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ALIGNMENTS

AAB37055 standard; peptide; 28 AAB37055; RESULT 1 AAB37055

AA.

Bcl2 polypeptide BH3 domain peptide #55.

(first entry)

28-FEB-2001

Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective; cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad; apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate; colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma; melanoma; lymphocytic_leukemia; neurodegenerative disorder; AIDS; stroke; myocardial infarction

Homo sapiens

WO200059526-A1.

12-OCT-2000.

06-APR-2000; 2000WO-US09352

99US-0128202 07-APR-1999; (UYJE-) UNIV JEFFERSON THOMAS.

Lu Z; Shan S, Huang Z, Wang J, Zhang Z,

WPI; 2000-679325/66

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The invention relates to a peptide conjugate having the formula:

(R-X)n-peptide where n = 1-10; X = C=0, when the R-X group is attached to the N-terminus of the peptide, or a side chain of the peptide where the functional group of the side chain is NH2 or OH; or X = O or NH, when the R-X group is attached to the C-terminus of the peptide, or a side chain of the peptide, where the side chain functional group is COH correction of the peptide, where the side chain functional group is COH corrections of the peptide, where the side chain functional group is COH corrections of the peptide with a 1-5C straight or branched chain alkyl group, or benzyl. The peptides AAB37001-B37058 represent examples of the peptide portion of the conjugate. The peptides represent analogues of the BH3 domain of the cell death agonist Bad. The peptide conjugate is useful for modulating apoptesis in the cells of a subject, or for reversing B cell lymphoma/leukemia 2 (BCl-2)-mediated blockage of apptions in center cells. It is also useful for inhibiting BCl-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     function. In particular, the peptide conjugate is useful for treating a subject afflicted with a cancer characterized by cancer cells that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                express Bcl-2. The cancer includes prostate, colorectal, gastric, non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide conjugate is also useful for treating disorders characterized by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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             New peptide conjugates for modulating apoptosis or for inhibiting cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for treating neurodegenerative disorders, stroke, or cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   increased apoptosis, e.g. neurodegenerative disorders, acquired immunodeficiency syndrome (AIDS), stroke or myocardial infarction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 148; DB 21;
100.0%; Pred. No. 1.4e-15;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KNLWAAQRYGRELRRMSDEFEGSFKGLK 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 KNLWAAQRYGRELRRMSDEFEGSFKGLK 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bcl2 polypeptide BH3 domain peptide #56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB37056 standard; peptide; 27 AA
                                                                                                     Claim 18; Page 19; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        stroke; myocardial infarction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYJE-) UNIV JEFFERSON THOMAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-APR-2000; 2000WO-US09352.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 28; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB37056;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 2
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The invention relates to a peptide conjugate having the formula:

(R-X)n-peptide where n = 1-10; X = C=0, when the R-X group is attached
to the N-terminus of the peptide, or a side chain of the peptide where
to the N-terminus of the peptide, or a side chain of the peptide where
the functional group of the side chain is NH2 or OH; or X = O or NH,
when the R-X group is attached to the C-terminus of the peptide, or a
side chain of the peptide, where the side chain functional group is COH
corresponding and R = 2-18C alkyl or alkoxy, 2-14C alkylenyl containing one
or two double bonds, grotloburyl, cyclohearyl, cyclohearyl optionally
corresponding to benzyl The peptide or the peptide chain alkyl group,
corresponding to benzyl. The peptides AAB37001-B37058 represent examples
cof the peptide portion of the conjugate. The peptides represent analogues
cof the peptide portion of the conjugate. The peptide conjugate is
useful for modulating apoptosis in the cells of a subject, or for
reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of
cuseful for modulating apoptosis in the cells of a subject, or for
reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of
cuptosis in cancer cells. It is also useful for inhibiting Bcl-2
cuptosis in cancer cells. It is also useful for inhibiting a
cute or chronic lymphocytic and non-lymphocytic leukemia. The peptide
conjugate is also useful for thyroid cancers, neuroblastoma, melanoma, or
acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide
conjugate is also useful for treating disorders characterized by
increased apoptosis, e.g. neurodegenerative disorders, acquired
immunodeficiency syndrome (Alds), stroke or myocardial infarction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                New peptide conjugates for modulating apoptosis or for inhibiting cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for treating neurodegenerative disorders, stroke, or cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bcl2 polypeptide BH3 domain peptide #1.
တွ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB37001 standard; peptide; 26 AA.
                                                                                                                                                                       Claim 18; Page 19; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            stroke; myocardial infarction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-APR-2000; 2000WO-US09352.
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Zhang Z,
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Best Local Similarity 100.
Matches 27; Conservative
                                        WPI; 2000-679325/66.
Wang J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27 AA;
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  Huang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δŽ
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WO200059526-A1
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δŏ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a peptide conjugate having the formula:

(R-X)n-peptide where n = 1-10; X = C=0, when the R-X group is attached to the N-terminus of the peptide, or a side chain of the peptide where the functional group of the side chain is NH2 or X = O or NH, when the R-X group is attached to the C-terminus of the peptide, or a side chain of the peptide, where the side chain functional group is COOH or CONH2; and R = 2-18C alkyl or alkoxy, 2-14C alkylenyl containing one or two double bonds, cyclobutyl, cyclopentyl, cyclobexyl optionally containing one or two double bonds, cyclobutyl, cyclopentyl, cyclobexyl optionally containing one or two double bonds, cyclobutyl, cyclopentyl, cyclobexyl optionally containing one or two double bonds, cyclobutyl, cyclopentyl, cyclobexyl optionally alkyl group, or benzyl. The peptides AhB37001-B37058 represent examples alkyl group, or benzyl. The peptide conjugate. The peptides chain analogues of the peptide portion of the conjugate. The peptides represent analogues of the BH3 domain of the cell death agonist Bad. The peptides conjugate is useful for modulating apoptosis in the cells of a subject, or for reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of apoptosis in cancer cells. It is also useful for inhibiting Bcl-2 function. In particular, the peptide conjugate is useful for treating a subject afflicted with a cancer characterized by cancer cells that express Bcl-2. The cancer includes prostate, colorectal, gastric, contains anall lung, renal or thyroid cancers, neuroblastoms, melanoma, or contains and c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide conjugate is also useful for treating disorders characterized by increased apoptosis, e.g. neurodegenerative disorders, acquired immunodeficiency syndrome (AIDS), stroke or myocardial infarction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                New peptide conjugates for modulating apoptosis or for inhibiting B cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for treating neurodegenerative disorders, stroke, or cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective; cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad; apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate; colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       melanoma; lymphocytic leukemia; neŭrodegeneratîve disorder; AIDS; stroke; myocardial infarction.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.6e-14;
hes 0;
                                                                             Lu Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 100.0%; Pred. No. 4.6 tes 26; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93.2%; Score 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bcl2 polypeptide BH3 domain peptide #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 NEWAAQRYGRELRRASDEFEGSFKGL 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 NLWAAQRYGRELRRMSDEFEGSFKGL 27
                                                                             Wang J, Zhang Z, Shan S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB37002 standard; peptide; 26 AA.
                                                                                                                                                                                                                                                                                      Claim 18; Page 17; 74pp; English.
                     (UYJE-) UNIV JEFFERSON THOMAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26 AA;
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                                                                           Huang Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 4
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The invention relates to a peptide conjugate having the formula:

(R-X)1-peptide where n = 1-10; X = C=0, when the R-X group is attached

to the N-terminus of the peptide, or a side chain of the peptide where

the functional group of the side chain is NH2 or X = O or NH,

when the R-X group is attached to the C-terminus of the peptide, or a

side chain of the peptide, where the side chain functional group is COCH

CC or CONH2; and R = 2-18C alkyl or alkoxy, 2-14C alkylenyl containing one

CC or two double bonds, cycloburyl, cycloberyl, cycloheryl oritionally

monosubstituted with a 1-5C straight or branched chain

CC or two double bonds, cycloburyl, cycloheryl oritionally

monosubstituted with a 1-5C straight or branched chain

CC or two double bonds, cycloburyl, cycloheryl oritionally

cc or two double bonds, cycloburyl, cycloheryl oritionally

monosubstituted with a 1-5C straight or branched chain

CC or two douple bonds, cycloburyl, cycloheryl oritionally

cc or two double bonds, cycloburyl, cycloheryl, cycloheryl oritionally

cc or two double bonds, cycloburyl, cycloheryl, cycloheryl oritionally

cc or two double bonds, cycloburyl, cycloheryl, cycloheryl oritionally

cc or two double bonds, cycloburyl, cycloheryl, cycloheryl oritionally

cc or two double bonds, cycloburyl, cycloheryl, cycloheryl oritionally

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cc or two double bonds, cycloburyl, cycloheryl, cycloheryl

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New peptide conjugates for modulating apoptosis or for inhibiting B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ncreased apoptosis, e.g. neurodegenerative disorders, acquired mmunodeficiency syndrome (AIDS), stroke or myocardial infarction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for treating neurodegenerative disorders, stroke, or cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 NLWAAQRYGRELRRMSDEFEGSFKGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 18; Page 17; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     stroke; myocardial infarction.
                                                                                                                                                                                                  (UYJE-) UNIV JEFFERSON THOMAS
                                                                                                                                                                                                                                                                                                  Zhang Z,
06-APR-2000; 2000WO-US09352
                                                                                                   99US-0128202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-679325/66.
                                                                                                                                                                                                                                                                                                      Huang Z, Wang J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                   07-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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Mus musculus.
Synthetic.
                                                                                                                                                                                                                                                                                                                                          Zhou X;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR95168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a peptide conjugate having the formula:

(R-X)n-peptide where n = 1-10; X = C=0, when the R-X group is attached to the N-terminus of the peptide, or a side chain of the peptide where the lunctional group of the side chain is NH2 or X = O ON NE, when the R-X group is attached to the C-terminus of the peptide, or a side chain of the peptide, where the side chain functional group is COOH or CONH2; and R = 2-18C alkyl or alkoxy, 2-14C alkylenyl containing one or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally monosubstituted with a 1-5C straight or branched chain phenyl optionally monosubstituted with a 1-5C straight or branched chain alkyl group, or benzyl. The peptides AAB37001-B37058 represent analogues of the peptide portion of the conjugate. The peptides represent analogues of the BH3 domain of the coll death agonist Bad. The peptide conjugate is useful for modulating apoptosis in the cells of a subject, or for reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of reversing B cells upphoma/leukemia 2 (Bcl-2)-mediated blockage of function. In particular, the peptide conjugate is useful for treating a construction of the conjugate is useful for treating a construction of the peptide conjugate is useful for treating a construction of the conjugate is useful for treating a construction of the peptide conjugate is useful for treating a construction of the peptide conjugate is useful for treating a construction of the peptide conjugate is useful for treating a cancer cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             express Bol-2. The cancer includes prostate, colorectal, gastric, non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide conjugate is also useful for treating disorders characterized by increased apoptosis, e.g. neurodegenerative disorders, acquired immunodeficiency syndrome (AIDS), stroke or myocardial infarction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis; immunostimulant; neuroprotective; nootropic; antiischaemic; vulnerary; cytostatic; antiviral; antiarthritic; antiinflammatory; wound healing; immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer; immunodeficiency disease; neurodegenerative disease; viral infection; ischaemic cell death; reperfusion cell death; arthritis; infertility; lymphoproliferative condition; inflammation; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                 New peptide conjugates for modulating apoptosis or for inhibiting cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for treating neurodegenerative disorders, stroke, or cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shorter murine BAD mutant amino acid sequence SEQ ID NO:3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93.2%; Score 138; DE 100.0%; Pred. No. 4.8 tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 NIWAAQRYGRELRRMSDEFEGSFKGL 26
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                                                                                                                                                                                                                 Huang Z, Wang J, Zhang Z, Shan S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB70370 standard; protein; 162 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 18; Page 17; 74pp; English.
                                                                                                                                                                    (UYJE-) UNIV JEFFERSON THOMAS.
                                                                      06-APR-2000; 2000WO-US09352.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-MAY-2001 (first entry)
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Matches 26; Conservative
                                                                                                                                                                                                                                                                   WPI; 2000-679325/66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27 AA;
                      12-0CT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB70370;
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Epitope; murine; bcl-x(L)/bcl-2 associated death promoter; Bad; stroke; polypeptide; bcl-x; cell death; regulate; BH1; BH2; apoptotic cell death; cytokine deprivation; LL-3 dependent cell line; immunodeficiency; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for activity that promote cell survival or apoptosis. Other uses include inducing or inhibiting apoptosis in a cell. Candidate compounds identified and (mutant) BAD polypeptides are useful in treating immunodeficiency diseases, neurodegenerative diseases, ischaeming cell death, reperfusion cell death, wound healing, cancer, viral infections, lymphoproliferative conditions, arthritis, infertility, inflammation autoimmune diseases. The present sequence represents a specifically claimed shorter murine BAD mutant amino acid sequence from the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes an isolated or synthetic polypeptide (I) comprising a less than full length amino acid sequence of a mutant Bcl-XL/Bcl-2 associated cell death regulator polypeptide (BAD) or its fragment, which contains amino acid substitutions at Seril8 of a human BAD, Seri55 of a murine BAD (longer murine BAD) or Seri13 of a murine BAD (shorter murine BAD). (I) has immunostimulant, neuroprotective, nootropic, antistinflammatory and immunosuppressive activities, and antiarthritic, antiinflammatory and immunosuppressive activities, and polymoclectides can be used as an apoptosis inducer or inhibitor. BAD polypeptides and polymuclectides can be used for screening candidate compounds and drugs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New mutant Bci-XL/Bcl-2 Associated Cell Death Regulator polypeptide, useful for screening for candidate compounds which induce or inhibit apoptosis, comprises amino acid substitutions at Ser118, Ser155 or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
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Pred. No. 3.5e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neurodegenerative disease; senescence; ischaemia; neoplasia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93.2%; Scor.
100.0%; Pred. No. J.
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 7; Page 148-149; 157pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 NLWAAQRYGRELRRMSDEFEGSFKGL
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                                                                                                                                                                                                                                                                                            (APOP-) APOPTOSIS TECHNOLOGY INC.
                                                                                                                                                                                                                       99US-0136783.
                                                                                                                                        30-MAY-2000; 2000WO-US11864
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                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-138734/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      162 AA;
WO200110888-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-JAN-1997
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                                                                                                                                                                                                                       28-MAY-1999;
                                                                       15-FEB-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR95168;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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Best Local 8
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204 AA;
                                                                                                                                                                                                       N-PSDB; AAV27833
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                                                                                                                                                          Korsmeyer SJ;
WO9817682-A1.
                                                              17-0CT-1997;
                                                                                           18-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus sp.
Synthetic.
                                30-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW61316;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents the murine bcl-x(L)/bcl-2 associated death promoter (Bad) gene. Bad is a 22.1 kD protein which interacts with bcl-2 and bcl-x proteins and regulates cell death. It has homology to the bcl-2-related family clustered in the BH1 and BH2 domain. Bad has been found to hybridise to bcl-x(L) and bcl-2 in yeast two-hybrid assays and in vivo in mammalian cells. Overexpressed bad counters the countering the death inhibitory activity of bcl-x(L), but is much less effective at accelerate apoptotic cell death induced by cytckine deprivation in an it.3 dependent cell line expressing bcl-x(L). Bad expression can death repressor activity of bcl-x(L). Bad competes with Bax for binding to bcl-x(L). Bad may be used to identify agents which inhibit its binding to bcl-x(L) to form heterodimers. Such agents may be used to treat neurodegenerative diseases, immunodeficiency diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein; serine substituted mutant; apoptosis; cancer; viral infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                           Polynucleotide encoding bcl-x(L)/bcl-2 associated death promoter useful to treat neoplasia and apoptosis and to identify agents inhibiting its binding to bcl-2 or bcl-x(L) to form heteromultimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93.2%; Score 138; DB 17; Length 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Murine BCL-XL/BCL-2 associated cell death regulator.
                              /note= "BH1 conserved amino acids"
191..192
                                                           /note= "BH2 conserved amino acids"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.5e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 93.2%; Score 138; DB Best Local Similarity 100.0%; Pred. No. 4.5 Matches 26; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      140 NLWAAQRYGRELRRMSDEFEGSFKGL 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 NLWAAQRYGRELRRMSDEFEGSFKGL 27
                                                                                                                           /note= "PEST sequence"
                                                                                           /note= "PEST sequence"
111..130
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             e.g. AIDS, senescence or ischaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW61315 standard; Protein; 204 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 3; Fig 1; 130pp; English
                                                                                                                                                                                                                     95WO-US14246.
                                                                                                                                                                                                                                                    94US-0333565.
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                                                                              38..61
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N-PSDB; AAT29479.
                                                                                                                                                                                                                                                                                                                   Korsmeyer SJ;
                                                                                                                                                                                                                       31-OCT-1995;
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AAW61315
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The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell death regulator) proteins, having an amino acid other than Ser at position 112 and/or 136, relative to the murine BAD 204 aa sequence. The position 112 and/or 136, relative to the murine BAD 204 aa sequence. The fragments of mutant BAD protein. Also described are: (1) fragments of mutant BAD protein. Also decrease cell viability; (2) (usion proteins of mutant BAD proteins are used to treat or prevent diseases associated with reduced apoptosis, e.g. cancer, viral infection, lymphoproliferation, arthritis, infertility.

CC or prevent diseases associated with reduced apoptosis, e.g. cancer, viral infection, lymphoproliferation, arthritis, infertility.

CC or prevent diseases associated with reduced apoptosis, e.g. cancer, viral infection, lymphoproliferation, arthritis, infertility.

CC or prevent diseases associated with reduced apoptosis, e.g. cancer, inflammation and autoimmune disease. Polynucleotide sequences encoding mutant BAD proteins can be used similarly by gene therapy or to produce transgenic animals for use as disease models or in drug screening. BAD proteins and inhibitors of serine-phosphatase. Inhibitors are potentially useful in treatment of excessive apoptosis such as AIDS, neurodegeneration, aging or ischaemic cell death. The apoptotic status of cells is determined by measuring relative amounts of phosphorylated and non-phosphorylated by usual immunoassays. Mutant BAD proteins have greater death-promoting activity than wild-type BAD which can become phosphorylated on the specified Ser, forming a product that does not heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family but an substituted cannot bind 14-3-3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New mutant BAD polypeptide with phosphorylatable serine replaced - useful for, e.g. treating reduced apoptosis such as in cancer or viral infection
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97WO-US19175
                                                                                       96US-0733505
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Best Local Similarity 100.
Matches 26, Conservative
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30-APR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               death regulator) proteins, having an amino acid other than Ser at position 112 and/or 136, relative to the murine BAD 204 as sequence. The present sequence represents a mutant BAD protein. Also described are: (1) fragments of mutant BAD protein able to decrease cell viability; (2) fragments of mutant BAD protein able to decrease cell viability; (2) fragments of mutant BAD protein able to decrease cell viability; (2) increases intracellular delivery. Mutant BAD proteins are used to treat or prevent diseases associated with reduced apoptosis, e.g. cancer, infal infection, lymphoproliferation, arthritis, infertility.

CC or prevent diseases associated with reduced apoptosis, e.g. cancer, infalmmation and autoimmune disease. Polymucleotide sequences encoding mutant BAD proteins can be used similarly by gene therapy or to produce transgenic animals for use as disease mydels or in drug screening. BAD croteins phosphorylated at specified Ser are used to screen for enhancers and inhibitors of serine-phosphatase. Inhibitors are potentially useful to reatment of excessive apoptosis such as AIDS, neurodegeneration, aging or ischaemic cell death. The apoptotic status of cells is sequenced determined by measuring relative amounts of phosphorylated and non-phosphorylated mutants of phosphorylated on the specified Ser, forming a product that does not heterodimerise with BCL-2 or BCL-XI but instead binds to 14-3-3 family conteins in the cytosol, thus promoting cell survival. The mutants with
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                                                                                                                                                                                                                                                                                                                                             Claim 7; Page 59; 95pp; English.
                                                                                            96US-0733505.
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Best Local Similarity 100.0
Matches 26, Conservative
                                                                                                                               (UNIW ) UNIV WASHINGTON
                                                                                                                                                                                                           WPI; 1998-261422/23.
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The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell death regulator) proteins, having an amino acid other than Ser at position 112 and/or 136, relative to the murine BAD 204 as sequence. The present sequence represents a mutant BAD protein. Also described are: (1) fragments of mutant BAD protein able to decrease cell viability; (2) fusion proteins of mutant BAD with a heterologous polypeptide that increases intracellular delivery. Mutant BAD proteins are used to treat or prevent diseases associated with reduced appropsis, e.g. cancer, viral infection, lymphoproliferation, arthritis, infertility.

CC or prevent diseases associated with reduced approtesis, e.g. cancer, viral infection, lymphoproliferation, arthritis, infertility.

CC inflammation and autoimmune disease. Polynucleotide sequences encoding mutant BAD proteins can be used similarly by gene therapy or to produce transgenic animals for use as disease models or in drug screening. BAD proteins phosphorylated at specified Ser are used to screen for enhancers and inhibitors of serine-phosphatase. Inhibitors are potentially useful in treatment of excessive apoptosis such as AIDS, neurodegeneration, aging or ischaemic cell death. The apoptotic status of cells is sequenced and non-phosphorylated on the specified Ser, forming a product that does not phosphorylated on the specified Ser, forming a product that does not beterodimerise with BCL-2 or BCL-XI but instead binds to 14-3-3 family concent in the cytosol, thus promoting cell survival. The mutants with the substituted cannot bind 14-3-3.
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97WO-US19175.
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Best Local Similarity
Matches 26; Conserve
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28-MAY-1999;
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            12-MAR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BAD protein, Bcl-XL/Bcl-2 associated cell death regulator; 14-3-3; serine phosphorylation; post-translational modification; apoptosis; signal transduction regulator; phosphoserine phosphatase; senescence; immunodeficiency disease; neurodegenerative disease; infertility; cancer, viral infection; lymphoproliferative condition; arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                 New mutant BAD polypeptide with phosphorylatable serine replaced useful for, e.g. treating reduced apoptosis such as in cancer or
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                                         96US-0733505.
            97WO-US19175
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Matches 26; Conserv
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              17-OCT-1997;
                                                                                                Korsmeyer SJ;
                                         18-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW58832;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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This sequence represents a novel serine-phosphorylated protein, BAD

(Bc1-X1/Bc1-2 associated cell death regulator). The serine residue is
phosporylated in a post-translational modification and allows binding

to the 14-3-3 protein which is a signal transduction regulator.

Modulators of phosphorylated BAD, which act through inhibition/activation

of a phosphoserine phosphatase, are useful for preventing/treating
increased/decreased apoptosis in a cell. The increased apoptosis may

result from immunodeficiency diseases, senescence, neurodegenerative

disease, ischaemic cell death, reperfusion cell death, infertility and

wound-healing. Decreased apoptosis may result from cancer viral

infection, lymphoproliferative conditions, arthritis, infertility,
infection, lymphoproliferative conditions, arthritis, infertility,
inflammation and autoimmune diseases. Measuring the amount of
phosphorylated compared to unphosphorylated BAD polypeptide and/or total
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunostimulant; neuroprotective; nootropic; antischaemic; rulneary; cytostatic; antiviral; antiarthritic; antiinflammatory; wound healing; immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer; immunodeficiency disease; neurodegenerative disease; viral infection; ischaemic cell death; reperfusion cell death; arthritis; infertility; lymphoproliferative condition; inflammation; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                Serine-phosphorylated Bcl-X-1/Bcl-2 Associated cell Death regulator polypeptide - useful for modulation of apoptosis associated with, e.g. cancer and immunodeficiency diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 204;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 3; Fig 8; 61pp; English.
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                                                                        96US-0707868.
97WO-US15871
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                                                                                                                                                 (UNIW ) UNIV WASHINGTON.
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Matches 26; Conserva-
                                                                                                                                                                                                                                                                                               WPI; 1998-207049/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                204 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200110888-A1.
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Query Match
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                                                                                                                                                                                                                                                                                                                                                   for activity that promote cell survival or apoptosis. Other uses include inducing or inhibiting apoptosis in a cell. Candidate compounds identified and (mutant) BAD polypeptides are useful in treating immunodeficiency diseases, neurodegenerative diseases, ischaemic cell death, reperfusion cell death, wound healing, cancer, viral infections, lymphoproliferative conditions, arthritis, infertility, inflammation and autoimmune diseases. The present sequence represents a specifically claimed longer murine BAD mutant amino acid sequence from the present
                                                                                                                                                                                                    The present invention describes an isolated or synthetic polypeptide (I) comprising a less than full length amino acid sequence of a mutant Bal-XL/Bal-2 associated cell death regulator polypeptide (BAD) or its fragment, which contains amino acid substitutions at Seril3 of a human BAD, Seril55 of a mutine BAD (onger mutine BAD) or Seril3 of a mutine BAD (shorter mutine BAD). (I) has immunostimulant, neuroprotective, nootropic, antischaemic, vulnerary, cytostatic, antiviral, antischaemic, vulnerary, cytostatic, antiviral, antischaemic, antiducer or inhibitor. BAD polypeptides and polynucleotides can be used as an apoptosis inducer or inhibitor. BAD polypeptides and polynucleotides can be used for screening candidate compounds and drugs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Murine; BAD; herpes simplex virus; HSV; US3; herpes virus; apoptosis;
                                                                                                New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide, useful for screening for candidate compounds which induce or inhibit apoptosis, comprises amino acid substitutions at Serl18, Serl55 or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 204;
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hes 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93.2%; Score 138; DB 22; 100.0%; Pred. No. 4.5e-13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             140 NLWAAQRYGRELRRMSDEFEGSFKGL 165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABR39082 standard; Protein; 204 AA
                                                                                                                                                                        Claim 4; Page 148; 157pp; English.
            (APOP-) APOPTOSIS TECHNOLOGY INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Murine BAD protein SEQ ID NO:4.
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Best Local Similarity 100.0
Matches 26; Conservative
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                                                                     WPI; 2001-138734/14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        204 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                         Zhou X;
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ABR39082
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                                                                                                                                                                                                                               The present invention describes a method (MI) for inducing apoptosis in a cell infected with herpes simplex virus (HSV), which comprises administering to the cell, a composition having an agent that inhibits phosphorylation of pro-apoptotic polypeptide BAD by HSV US3. Also described is a method (M2) for treating a patient infected with HSV, by administering to the patient, a composition comprising a peptide comprising a sequence of 4-100 continuous amino acids of a 168 residue amino acid sequence (see ABR39081), where the peptide comprises seril2, seril5, or their combinations. BAD has virucide activity. MI is useful for inducing apoptosis in a cell infected with HSV, where the cell is in a human. M2 is useful for treating a patient infected with HSV. The present sequence represents murine BAD, which is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse; Bad-DTTR; apoptosis; cancer; spinal muscular atrophy; diphtheria toxin receptor binding domain; DTR; neoplasm; tumour; hyper-proliferation; Alzheimer's disease; neurodegenerative disorder; transient ischaemic neuronal injury; stroke; spinal cord injury;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                     Inducing apoptosis in a cell infected with herpes simplex virus, HSV, by administering to the cell, a composition comprising an agent that inhibits phosphorylation of pro-apoptotic polypeptide BAD by HSV US3
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Pred. No. 4.5e-13;
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100.0%; Pred. No. ..
0; Mismatches
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/note= "10x histidine tag'
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(USSH ) US DEPT HEALTH & HUMAN SERVICES.
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Corynebacterium diptheriae.
Synthetic.
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                                                                                                                                                                                  Claim 15; Page 168; 192pp; English.
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les 26; Conservative
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N-PSDB; ABZ81201.
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Chimeric - C
Chimeric - S
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Novel fusion protein for modifying apoptosis in target cell and reducing apoptosis after transient ischaemic neuronal injury, has two domains which targets protein to a cell and modifies apoptotic response of cell

Claim 4; Page 59-61; 65pp; English

The sequence represents the amino acid sequence of Bad-DITR apoptosismodifying fusion protein comprising Bad gene sequence fused via a short
linker to diphtheria toxin translocation domain (DTTR). The
linker to diphtheria toxin translocation domain (DTTR). The
current call and integrating into or crossing a capable of binding a
cc target cell. The apoptosis-modifying fusion protein comprises at least
cut domains: the DTR domain, which targets the fusion protein to the
target cell. The Bcl-XL domain, which modifies an apoptotic response
cc target cell. The fusion protein is useful for modifying
clinhibiting or enhancing) apoptosis in a target cell, such as neuron,
controliferative cell or an adipocyte. It is also useful for reducing
apoptosis in a subject after transient ischaemic neuronal injury,
cspecially spinal cord injury. The fusion protein may be used to treat
controliferases and injury. The fusion protein may be used to treat
controliferative cellular response, including neurodegenerative disorders
controphy, stroke episodes and unregulated cell growth as in tumours and
controliferative the body and targeted to selective tissue and
controliferative. THE TEXT SOURCE SOURCE

567 AA; Sednence

Gaps 0; ch 93.2%; Score 138; DB 22; Length 567; Similarity 100.0%; Pred. No. 1.4e-12; 26; Conservative 0; Mismatches 0; Indels C Query Match Best Local Similarity Matches 26; Conserv

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2 NLWAAQRYGRELRRMSDEFEGSFKGL 27

QΣ

g Search completed: September 15, 2003, 17:22:14 Job time : 39.6 secs

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93.2%; Score 138; DB 1; Length 204; 100.0%; Pred. No. 1.5e-13; ive 0; Mismatches 0; Indels
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Best Local Similarity 100.
Matches 26; Conservative
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OTHER INFORMATION:
OTHER INFORMATION:
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STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: Protein
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                                                 45
45,5
                                                                                                                                                                                                                                                                                                                                                                     RESULT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                            September 15, 2003, 17:22:21; Search time 14.6 Seconds (without alignments) 81.144 Million cell updates/sec
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Sequence 2
Sequence 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                              148
1 KNLWAAQRYGRELRRMSDEFEGSFKGLK 28
                                                                                                                                                                                                                                                                                   328717 seqs, 42310858 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                 using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                 US-09-544-664-55
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                                                               protein search,
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Match
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Sequence 3145%. A Sequence 23807, A Sequence 2144, Appli Sequence 4, Appli Sequence 17508, A Sequence 28775, A Sequence 27, Appli Sequence 27, Appli Sequence 27, Appli Sequence 20, Appli 4656, Ap 19594, A 3, Appli 3, Appli 1, Appli 31458, A 23807, A Sequence Sequence GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: BC1-x/BC1-2 ASSOCIATED CELL DEATH
TITLE OF INVENTION: REGULATOR
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION WINBER: US/08/33,565
FILING DATE: 31-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726A-000700
TELEPHONE: (415) 326-2420
INFORMATION FOR SEQ ID NO: 2: US-09-328-352-4656
US-09-074-579-3
US-09-09-388-774-3
US-09-388-774-3
US-09-346-153-1
US-09-252-991A-31458
US-09-252-991A-31458
US-09-252-991A-23807
US-09-235-103-4
US-09-235-103-4
US-09-252-991A-17508
US-09-252-991A-17508
US-09-252-991A-17508
US-09-252-991A-17508
US-09-252-991A-28775
US-09-252-991A-28775
US-09-252-991A-28775
US-09-252-991A-28775
US-09-252-991A-28775
US-09-252-991A-28775
US-09-252-991A-28581 US-09-252-991A-18729 Sequence 2, Application US/08333565 Patent No. 5622852 ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible SEQUENCE CHARACTERISTICS: LENGTH: 204 amino acids TYPE: amino acid

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Gaps

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us-09-544-664-55.rai

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STRANDEDNESS:
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                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 4
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APPLICANT: KORSMEYER, STANLEY J.

APPLICANT: KORSMEYER, STANLEY J.

TITLE OF INVENTION: BCL.XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
NUMBER OF SEQUENCES: 60

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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Pred. No. 1.5e-13;
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of mouse BAD."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                              APPLICANT: KOREMEYER, Stanley J.
TIYLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
TITLE OF INVENTION: REGULATOR
TITLE OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DAPR:
APPLICATION NUMBER: US/08/661,479
FILING DATE: 11-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93.2%; Scor.
100.0%; Pred. No. ..
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION: 435
PRIOR APPLICATION 1 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/333,565
FILING DATE: 31-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,23
REFERENCE/DOCKET NUMBER: 15726A-000700
TELEPHONE: (415) 326-2400
TELEPHONE: (415) 326-2422
INFORMATION FOR SEQ ID NO: 2;
SEQUENCE CHARACTERICTICS:
LENGTH: 204 amino acids
TYPE: amino acids
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2 NLWAAQRYGRELRRMSDEFEGSFKGL 27
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                                                                                                             US-08-661-479-2; Sequence 2, Application US/08661479; Patent No. 5834209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COCATION: 1.204
CHER INFORMATION:
CTHER INFORMATION:
US-08-661-479-2
                                                                                                                                                                                                                                                                                                    STREET: 379 Lyttor
CITY: Palo Alto
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: KORSME
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US-08-733-505A-1
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Gaps
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
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100.0%; Pred. No. 1.5e-13;
iive 0; Mismatches 0;
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.0 NLWAAQRYGRELRRMSDEFEGSFKGL 165
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38, 197
388: 965458
                                                                                                                                                                                                                                                                   CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 9654
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 204 amino acids IYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 93.2
Best Local Similarity 100.
Matches 26; Conservative
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MOLECULE TYPE: protein
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us-09-544-664-55.rai

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Sequence 3, Application US/08717123 Patent No. 5965703 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISFRATION NUMBER: 35,197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Campbell, Cathryn A. REGISTRATION NUMBER: 31,815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION: NAME: Campbell, Cathryn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 204 amino acids TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: California
COUNTRY: United States
ZIP: 92122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
TITLE OF INVENTION: SE
TITLE OF INVENTION: BC
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
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                                                                                                                               MISSOURI
                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                     63105
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US-08-717-123-3
                                                                                                                                                      COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: CREMETER, STANLEY J.
APPLICANT: CREMETER, STANLEY J.
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
NUMBER OF SEQUENCES: 60
COPRESSED: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
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Pred. No. 1.5e-13;
                                                                                                                                                  Length 204;
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                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                    Score 138; DB 2; I Pred. No. 1.5e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93.2%; SCCL.
100.0%; Pred. No. L.
... 0; Mismatches
                                                                                                                                                  Query Match 93.2%; Score 138; DE Best Local Similarity 100.0%; Pred. No. 1.5 Matches 26; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                 140 NLWAAQRYGRELRRMSDEFEGSFKGL 165
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                                                                                                                                                                                                                              2 NLWAAQRYGRELRRMSDEFEGSFKGL 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 530
ATORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 965458
TELEPHONE: (314) 727-6092
TELEFAX: (314) 727-6092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 14, Application US/08733505A Patent No. 5856445 GENERAL INFORMATION: APPLICANT: KORSMEYER, STANLEY J.
                                                                                                                                                                                                                                                                                                                                                       Sequence 13, Application US/08733505A Patent No. 5856445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 204 amino acids amino acid
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 93.2
Best Local Similarity 100.
Matches 26, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-733-505A-13
                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-733-505A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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US-08-733-505A-14
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US-08-733-505A-13
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Gaps
SERINE SUBSTITUTED MUTANTS OF BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Horne, William A.
APPLICANT: Oltersdorf, Tilman
TITLE OF INVENTION: Human BAD Polypeptides, Encoding Nucleic
TITLE OF INVENTION: Acids and Methods of Use
NUMBER OF SEQUENCES:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93.2%; Score 138; DB 2; Length 204; 100.0%; Pred. No. 1.5e-13; Live 0; Mismatches 0; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/717,123
FILING DATE: 20-SEP-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                           ADDRESSE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 140 NLWAAQRYGRELRRMSDEFEGSFKGL 165
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APPLICATION NUMBER: US/08/733,505A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 965458
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
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Gaps
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; Patent No. 5965703
; GENERAL INFORMATION:
APPLICANT: Horne, William A.
APPLICANT: Oltersdorf, Tilman
TITLE OF INVENTION: Human BAD Polypeptides, Encoding Nucleic
TITLE OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77.0%; Score 114; DB 2; Length 168; 91.7%; Pred. No. 5.5e-10; iive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                   Query Match 77.0%; Score 114; DB 1; Length 166; Best Local Similarity 91.7%; Pred. No. 5.4e-10; Matches 22; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPBEARING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-ID 1929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        103 NLWAAQRYGRELRRMSDEFVDSFK 126
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20-SEP-1996
               NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: CL-8
TELEPHONE: (352) 375-8100
TELEPHONE: (352) 372-8800
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
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TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1: 168 amino acids amino acids
   ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                       LENGTH: 166 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 91.7
Matches 22; Conservative
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APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , MOLECULE TYPE: protein US-08-717-123-2
                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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                                                                                                                                                                                                                                                                                               US-08-665-617-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/09375257

Sequence 3, Application US/09375257

GENERAL INFORMATION:
APPLICANT: Horne, William A.
APPLICANT: Oltersdorf, Tilman
TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC
TITLE OF INVENTION: ACIDS AND METHODS OF USE
FILE REFERENCE: 480140.428D1
CURRENT APPLICATION NUMBER: US/09/375,257
CURRENT FILING DATE: 1999-08-16
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 3
SEQ ID NO 3
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Pred. No. 4.2e-13;
1; Mismatches 0; Indels
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. 4.2e-13;
... 0; Indels
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ZIP: 32606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM C COMPATIble

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN RELEASE #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/665,617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NE: Saliwanchik & Saliwanchik
2421 N.W. 41st Street, Suite A-1
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REFERENCE/DOCKET NUMBER; P-ID 1929
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Patent No. 5663316
                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR ESQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91.2%;
96.2%;
                                                                                                                                                                                                                             91.2%;
96.2%;
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Best Local Similarity 96.23
Matches 25; Conservative
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Matches 25; Conservative
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 2421 N.W. CITY: Gainesville STATE: Florida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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TOPOLOGY:
US-08-717-123-3
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US-08-665-617-2
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77.0%; Score 114; DB 3; Length 168; 91.7%; Pred. No. 5.5e-10; tive 0; Mismatches 2; Indels
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APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
APPLICANT: Lal, Preet,
APPLICANT: Shah, Purvi
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
TITLE OF INVENTION: PROLIFERATION
                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPOTER: IBM Compatible
OPPERAING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,335
FILING DATE: Filed Herewith
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 3174 Porter Dr. CITY: Palo Alto STATE: CA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/410,372
                 ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Dr. CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0421 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       103 NLWAAQRYGRELRRMSDEFVDSFK 126
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; Patent No. 6281334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 91.73
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GenBank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDILLI
LIBRARY: General 1683637
                                                                                                   COUNTRY: US
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                                                                                     CA
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                                                                                                                                                        APPLICANT: Yue, Henry
APPLICANT: Lal, Preeti
APPLICANT: Shah, Purvi
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil
TITLE OF INVENTION: PROLIFERATION
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Hilman, Jennifer L.
APPLICANT: Yue, Henry
APPLICANT: Lal, Preeti
APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
FITLE OF INVENTION: PROLIFERATION
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,335
FILING DATE: Filed Herewith
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 97,749
RETERENCE/DOCKET NUMBER: 9F-0421 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEPA: 650-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      103 NIWAAQRYGRELRRMSDEFVDSFK 126
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                                                                                  ; Sequence 1, Application US/08985335 ; Patent No. 6080847
                                                                                                                                               Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 77.0%;
Best Local Similarity 91.7%;
Matches 22; Conservative
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; CLONE: 358673
US-08-985-335-1
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                                                                                                                          GENERAL INFORMATION:
APPLICANT: Hillman
APPLICANT: Yue, E
                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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US-08-985-335-7
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                                           RESULT 11
US-08-985-335-1
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RESULT 15
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Sequence 7, Application US/09410372

Patent No. 6281334

GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.

APPLICANT: Lal, Preeti

APPLICANT: Shah, Purvi

APPLICANT: Shah, Purvi

TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL

TITLE OF INVENTION: PROLIFERATION

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Dr.

CIPY: Palo Alto
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ZIP: 94304
SIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FactESQ for Windows Version 2.0
SOFTWARE: FactESQ for Windows Version 2.0
SOFTWARE: FOR WINDOWS VERSION 2.0
SOFTWARE: FACTESQ for Windows Version 2.0
SOFTWARE: FOR WINDOWS VERSION 2.0
FILING DATE:
APPLICATION NUMBER: US/09/410,372
FILING DATE:
APPLICATION NUMBER: 08/985,335
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0421 US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHONE: 650-855-0555
TELECPA: 650-865-0555
TELECPA: 650-865-0555
TELECPA: SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                  ATTORNEY AGENT:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0421 US
REFERENCE/DOCKET NUMBER: PF-0421 US
TELEPHONE: 650-855-0555
TELEPHONE: 650-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            103 NIWAAQRYGRELRRMSDEFVDSFK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 NLWAAQRYGRELRRMSDEFEGSFK 25
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/985,335
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 168 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                     LIBRARY: SYNORAB01
CLONE: 358673
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                                                                                                                                                                                                                                                                                                                                                                                                                                                ; CLONE: 3
US-09-410-372-1
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US-09-410-372-7
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                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Horne, William A. APPLICANT: Oltersdorf, Tilman TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC FILLE OF INVENTION: ACIDS AND METHODS OF USE FILE REFERENCE: 480140, 428D1 CURRENT APPLICATION NUMBER: US/09/375, 257 CURRENT FILING DATE: 1999-08-16 NUMBER OF SEQ ID NOS: 15 SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                          77.0%; Score 114; DB 3; Length 168; 91.7%; Pred. No. 5.5e-10; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77.0%; Score 114; DB 4; Length 168; 91.7%; Pred. No. 5.5e-10; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: September 15, 2003, 17:45:06 Job time : 14.6 secs
                                                                                                                                                                                                                                    103 NLWAAQRYGRELRRMSDEFVDSFK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 NLWAAQRYGRELRRMSDEFEGSFK 25
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                                                                                                                                                                                                                                                                                                                                US-09-375-257-2; Sequence 2, Application US/09375257; Patent No. 6504022; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 77.0°
Best Local Similarity 91.7
Matches 22; Conservative
                                                                                                                                               Best_Local Similarity 91.7
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Homo sapiens US-09-375-257-2
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
US-09-410-372-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE.
SEQ ID NO 2
                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
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Sequence 3, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 145, Appli
Sequence 1077, Appli
Sequence 1077, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 241, Appli
Sequence 3, Appli
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Sequence 3, Appli
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Sequence 11541,
                                                                                                                                                                                                                     (without alignments)
184.034 Million cell updates/sec
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                                                                                                                                                                                      September 15, 2003, 17:25:56; Search time 22.2 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

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10: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

15: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 US-10-066-179-3
US-10-059-261-258
US-09-922-378-2
US-09-984-657-1
US-09-894-657-1
US-09-894-657-5
US-10-066-179-2
US-10-156-761-9145
S US-10-128-075-1077
S US-10-092-750-1
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US-09-934-455-162
US-10-156-761-11541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                     148
1 KNLWAAQRYGRELRRMSDEFEGSFKGLK 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-922-378-3
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                          sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                       using
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                              US-09-544-664-55
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                                                                                                                                                                                                                                                                                                              Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                        Scoring table:
                                                                                                                                protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Database :
                                                                                                                                                                                                                                                                                                                                                                       Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Searched:
                                                                                                                                                                                         Run on:
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        29.7
        426
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        US-09-815-242-5704
        Sequence 5704, Appliance 17

        17
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        712
        US-10-008-355-2
        Sequence 2. Appliance 124
        Sequence 2. Appliance 124
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        712
        US-10-369-294-20
        Sequence 2. Appliance 124
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        19.5
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        380
        US-09-881-752A-238
        Sequence 23, Appliance 29, Appliance 29, Appliance 39, A
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ALIGNMENTS

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Gaps
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Sequence 3, Application US/10066179
Sequence 3, Application US/10066179
Sequence 3, Application No. US20020115631A1
SEMERAL INFORMATION:
APPLICANT: HOTHOR, WILLIAM A.
APPLICANT: Oltersdorf, Tilman
TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC
TITLE OF INVENTION: ACIDS AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 204;
                                                                                                                                           ENCODING NUCLEIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                              91.2%; Score 135; DB 9; 96.2%; Pred. No. 8.2e-12;
                                                       GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Oltersdorf, Tilman
TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENC
TITLE OF INVENTION: ACIDS AND METHODS OF USE
FILE REPRENCE: 480140.428D3
CURRENT APPLICATION NUMBER: US/09/922,378
CURRENT FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    140 NIWAAQRYGRELRRMTDEFEGSFKGL 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 NIWAAQRYGRELRRMSDEFEGSFKGL 27
US-09-922-378-3
; Sequence 3, Application US/09922378
; Patent No. US20020037869A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25; Conservative
                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                               204
                                                                                                                                                                                                                                                                                                                                                                                                   US-09-922-378-3
                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
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us-09-544-664-55.rapb

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LIBRARY: SYNORAB01
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Lal, Preeti
Shah, Purvi
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22; Conservative
                                                                                                                     22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMMEDIATE SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                  Query Match
Best Local Similarity
Matches 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: CA
                                us-09-922-378-2
                                                                                                                                                                                                                                                                           RESULT 5
US-09-894-657-1
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US-09-894-657-7
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Sequence 258, Application US/20030077826A1

GENERAL INFORMATION:
APPLICANT: EDELMAN, LENA

APPLICANT: EDELMAN, JEAN-PAUL

TITLE OF INVENTION: CHIMERC MOLECULES CONTAINING A MODULE ABLE TO TARGET

TITLE OF INVENTION: SPECIFIC CELLS AND A MODULE REGULATING THE APOPTOGENIC

TITLE OF INVENTION: (PTPC)

TITLE OF INVENTION: (PTPC)

TITLE OF INVENTION: (PTPC)

FILE REFERENCE: 03495.0216

CURRENT APPLICATION NUMBER: 05/2055,261

CURRENT FILING DATE: 2001-02-02

PRIOR FILING DATE: 2001-02-02

NUMBER OF SEQ ID NOS: 325

SOFTWARE: PATENTIN Ver. 2.1

SEQ ID NO 258

LENGTH: 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 2, Application US/09922378
; Patent No. US20020037869A1.
; GENERAL INFORMATION:
; APPLICANT: Horne, William A.
; APPLICANT: Oltersdorf, Tilman; TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC; TILE OF INVENTION: ACIDS AND METHODS OF USE; FILE REPRENCE: 480140.428D3
; CURRENT APPLICATION NUMBER: US/09/922.378
; CURRENT FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                  Query Match
91.2%; Score 135; DB 14; Length 204;
Best Local Similarity 96.2%; Pred. No. 8.2e-12;
Matches 25; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 25;
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; FILE REFERENCE: 480140.428C1
; CURRENT APPLICATION NUMBER: US/10/066,179
; CURRENT FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 204
; TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                  140 NLWAAQRYGRELRRMTDEFEGSFKGL 165
                                                                                                                                                                                                                                                                                                                                       2 NLWAAQRYGRELRRMSDEFEGSFKGL 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Unknown Organism
                                                                                                                                                                                  ; ORGANISM: Mus musculus
US-10-066-179-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-059-261-258
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LENGTH: 168
TYPE: PRT
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US-09-922-378-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
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Length 168;
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                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOSTWARE: FastSEG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/894,657
FILING DATE: 28-Jun-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/410,372
FILING DATE: <URKNOWN>
                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL PROLIFERATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77.0%; Score 114; DB 9; L. 91.7%; Pred. No. 7.2e-09; Live 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Incyte Pharmaceuticals, Inc
STREET: 3174 Porter Dr.
77.0%; Score 114; DB 9; 91.7%; Pred. No. 7.2e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PF-0421 US
                                        0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION UNDRER: 36,749
REFERENCE/DOCKET NUMBER: PF-04
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             103 NLWAAQRYGRELRRMSDEFVDSFK 126
                                                                                                         103 NLWAAQRYGRELRRMSDEFVDSFK 126
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                                                                                2 NIWAAQRYGRELRRMSDEFEGSFK 25
                                                                                                                                                                                                                                                                                          APPLICANT: Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGIH: 168 amino acids
                                                                                                                                                                                                                             Sequence 1, Application US/09894657; Patent No. US20020098569A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 650-845-4166 INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
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FULLICALION NO. USZUUJUOBBOSZAI

GENERAL INFORMATION:
APPLICANT: Cell Signaling Technology, Inc.
APPLICANT: COMB, Michael J.
APPLICANT: TAN, Yi
TITLE OF INVENTION:
FILE REFERENCE: CST-138 CIP3
CURRENT APPLICATION NUMBER: US/10/174,105A
CURRENT APPLICATION NUMBER: US/10/174,105A
CURRENT APPLICATION NUMBER: US 09/148,712
PRIOR APPLICATION NUMBER: US 09/148,712
PRIOR PRILING DATE: 1998-09-04
PRIOR FILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 193
SOFTWARE: Patentin version 3.1
FEMALE SEQ ID NO 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTHER INFORMATION: PHOSPHORYLATION; serine at position 8 is phosphorylated US-10-174-105a-147
                                                                                     Ouery Match 77.0%; Score 114; DB 14; Length 168; Best Local Similarity 91.7%; Pred. No. 7.2e-09; Matches 22; Conservative 0; Mismatches 2; Indels
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100.0%; Pred. No. v..
0; Mismatches
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CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
                                                                                                                                                                                                                103 NLWAAQRYGRELRRMSDEFVDSFK 126
                                                                                                                                                                                     2 NLWAAQRYGRELRRMSDEFEGSFK 25
                                                                                                                                                                                                                                                                                                                         US-10-174-105A-147; Sequence 147, Application US/10174105A; Publication No. US20030068652A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 9145, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Synthetic Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: IGHTKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Artificial Sequence
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Best Local Similarity lou...
                     ORGANISM: Homo sapiens
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                                            US-10-066-179-2
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APPLICANT: ADTECANT: Olteradorf, Tilman; APPLICANT: Olteradorf, Tilman; TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC; TITLE OF INVENTION: ACIDS AND METHODS OF USE; FILE REFERENCE: 480140.428C1; CURRENT APPLICATION NUMBER: US/10/066,179; CURRENT PILING DATE: 2002-02-01; NUMBER OF SEQ ID NOS: 15; SOFTWARE: FastSEQ for Windows Version 4.0; SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77.0%; Score 114; DB 9; Length 168; 91.7%; Pred. No. 7.2e-09; tive 0; Mismatches 2; Indels
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FILING DATE: 28-Jun-2001

PRIOR APPLICATION NUMBER: 09/410,372

FILING DATE: CUNROWN>
ATTORNEY/AGENT INFORMATION:
NAME: BILLINGS, LUCY J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                  COLLEY, Neil C.
TITLE OF INVENTION: PROLIFERATION
                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: PF-0421 US TELECOMMUNICATION INFORMATION: TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE DESCRIPTION: SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             103 NLWAAQRYGRELRRMSDEFVDSFK 126
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                                                                        APPLICANT: Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 168 amino acids
Sequence 7, Application US/09894657
Patent No. US20020098569A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
                                                                                                                       Lal, Preeti
Shah, Purvi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIBRARY: GenBank
CLONE: 1683637
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                                                                                               Yue, Henry
                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMMEDIATE SOURCE
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Best Local Similarity
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US-10-066-179-2
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Length 15; Indels us-09-544-664-55.rapb

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                                                                                                                                          Sequence 241, Application US/10092750
; Publication No. US20030032157A1
; GENERAL INFORMATION:
; APPLICANT: Hammond, Philip W.
APPLICANT: Wright, Julia
; APPLICANT: Wright, Martin C.
; TITLE OF INVENTION: Polypeptides Interactive with BCL-X1
; FILE REFERENCE: 50036/050002
; CURRENT APPLICATION NUMBER: US/10/092,750
; CURRENT APPLICATION NUMBER: US 60/274,526
; PRIOR APPLICATION NUMBER: US 60/274,526
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patterson, Chandra
TITLE OF INVENTION: GROWTH-ASSOCIATED TRYPSIN-TYPE
INHIBITOR HEAVY CHAIN PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Word Perfect 6.1/MS-DOS 6.2
CURRINT APPLICATION DATA:
APPLICATION NUMBER: US/09/828,423
FILING DATE: 05-Apr-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0505 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 09/388,774
FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/09828423
; Patent No. US20020099178A1
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; Guegler, Karl J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :| || || ||||: ||| :
86 IWIAQ----ELRRIGDEFNAYY 103
                            3 LWAAORYGRELRRMSDEFEGSF 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 LWAAQRYGRELRRMSDEFEGSF 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Cerrone, Michael C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                         RESULT 12
US-10-092-750-241
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                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 241
LENGTH: 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 13
US-09-828-423-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
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Publication No. US20030148324A1
GRNERAL INFORMATION:
APPLICANT: I.N.S.B.R.M.
TITLE OF INVENTION: Polynuclectides which are of nature B2/D+ A- and which are isolat FILE OF INVENTION: E.coli, and biological uses of these polynuclectides and of their FILE REFERENCE: BLANDINE
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Pred. No. 37;
                                                                                                                                                                   DB 15; Length 215;
8.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 1, Application US/10092750; Sequence 1, Application No. US2030032157A1; Sequence 1, Application No. US2030032157A1; GENERAL INFORMATION:
APPLICANT: Hammond, Philip W.
APPLICANT: Hammond, Philip W.
APPLICANT: Wright, Martin C.
TITLE OF INVENTION: Polypeptides Interactive with BCL-Xl
FILE REFERBNCE: 50036/050002; CURRENT FILING DATE: 2002-03-07; PRIOR APPLICATION NUMBER: US 60/274,526; PRIOR FILING DATE: 2001-03-08; NUMBER OF SEQ ID NOS: 253; SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 35;
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45.5%; Pred. No. 6.7;
tive 3; Mismatches 5.
                                                                                                                                                                                                           5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 52;
Pred. No. 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/238,075 CURRENT FILING DATE: 2002-09-10 PRIOR APPLICATION NUMBER: 0003145 PRIOR FILING DATE: 2000-03-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 KNLWAAQRYGRELRRMSDEFEGSFKGL 27
                                                                                                                                                                                                                                                                           7 ORYGRELRRMSDEFEGSFKGLK 28
                                                                                    ; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-9145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34.5%;
40.7%;
                                                                                                                                                                   35.1%;
45.5%;
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SOFTWARE: Patentin version 3.1
SEQ ID NO 1077
LENGTH: 682
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 9145
                                                                                                                                                                     Query Match
Best Local Similarity 45.55
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 40.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10; Conservative
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US-10-092-750-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
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US-10-238-075-1077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-238-075-1077
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US-10-092-750-1
                                                                 LENGTH: 215
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us-09-544-664-55.rapb

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TYPE: PRT
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Pred. No. 1.5e+02;
4; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 946;
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APPLICANT: Dubell, Arnold
APPLICANT: Heard, Jacqueline
APPLICANT: Jiang, Cai-Zhong
APPLICANT: Jiang, Cai-Zhong
APPLICANT: Seddie, James
APPLICANT: Ratcliffe, Oliver
APPLICANT: Ratcliffe, Oliver
APPLICANT: Reuber, Lynne
APPLICANT: Pineda, Omaira
APPLICANT: P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 31.1%; Score 46; DB 9; Length 946 Best Local Similarity 30.8%; Pred. No. 2.7e+02; Matches 8; Conservative 5; Mismatches 13; Indels
                                                                                                                                                                                                                                        ; IMMEDIATE SOURCE:
LIBRARY: GENEBANK
CLONE: 9133985
; SEQUENCE DESCRIPTION: SEQ ID NO: 3 :
US-09-828-423-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78 NMFQPQIYGRDFKRSS----SSMVGLK 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 NLWAAQRYGRELRRMSDEFEGSFKGLK 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              212 DVWVIEPQGLRFLHVPDTFEGHFDGV 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 NLWAAQRYGRELRRMSDEPEGSFKGL 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
US-10-156-761-11541
; Sequence 11541, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OWURA, SATOSHI
; APPLICANT: IKEDA, HARUO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 162, Application US/09934455 publication No. US20030121070A1 GENERAL INFORMATION:
                              INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 946 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT CRGANISM: Arabidopsis thaliana US-09-934-455-162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29.7%;
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APPLICANT: Creelman, Robert
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Best Local Similarity 40.7
Matches 11; Conservative
TELEX; <Unknown>
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US-09-934-455-162
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Gaps
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                                         APPLICANT: SHIEA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLECTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR RILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-06-30
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 11541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: September 15, 2003, 17:47:53 Job time: 22.2 secs
                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Streptomyces avermitilis US-10-156-761-11541
                                                                                                                                                                                                                                                                                                                                                                                                                                                     29.7%;
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29 WIAAAHGAELRRAAD 43
                        HORIKAWA, HIROSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 53.33
Matches 8; Conservative
ISHIKAWA, JUN
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

sw model using - protein search, protein Ö

September 15, 2003, 17:18:16 ; Search time 12.6 Seconds
 (without alignments)
213.708 Million cell updates/sec Run on:

US-09-544-664-55 Title: Perfect score:

1 KNLWAAQRYGRELRRMSDEFEGSFKGLK 28

Sequence:

Scoring table:

283308 segs, 96168682 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

283308 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	bad protein - mous	inter-alpha-trypsi	hypothetical prote	inter-alpha-inhibi	2-dehydro-3-deoxy-	floral homeotic pr		probable threonine	DNA-directed RNA p	glycerol-3-phospha	conserved hypothet	Ig kappa chain - h	annexin P35 - maiz	transforming prote	oxidoreductase, so	threonine synthase	hypothetical prote	Antho-RFamide neur				oxoglutarate dehyd	1	- 1		chlorocruorin chai	probable polyamine	inter-alpha-trypsi	conserved hypothet
QI QI	A55671	P~	D70760	S54354	538185	A42095	C84338	A96753	A81393	A11210	E83517	S40376	T02975	C36365	F72289	T08545	T24806	A39172	T09486	S43852	230	266	S	296	4430	859899	T35440	IYHU2	G69510
DB	1 0	N	C)	~	N	~	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	~	N	Н	7
Length 1	204	946	223	946	370	232	374	516	1378	127	453	134	314	206	220	526	1164	334	1140	287	597	296	5138	314	435	165	399	946	261
% Query Match	.2.	36.5	35.8	35.8	35.1	34.5	33.8	33.8	33.8	33.4	33.1	32.8	32.8	32.4	32.4	32.4	32.4	32.1	32.1	31.8	31.8	31.8	31.8	31.4	31.4	31.1	31.1	31.1	30.7
Score	138	54	53	53	52	51	20	50	20	49.5	49	48.5	•	48	48	48	48	47.5		47	47	47	47	ė.	46.5	46	46	7	45.5
Result No.		7	~ R	4	Ŋ	Ø	7	œ	6	10	II	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

conserved hypothet	probable secreted	hypothetical prote	NADH dehydrogenase	excinuclease ABC c	photosystem II oxy	manganese-stabilzi	conserved hypothet	conserved hypothet	hypothetical prote	sodium ion pumb ox	oxaloacetate decar	oxaloacetate decar	oxaloacetate decar	probable membrane	env polyprotein -
AF2859	D97636	C71473	G83314	T36031	806736	AG2287	F83201	H95406	T31294	B44465	AB0509	AE0909	A28088	S52675	VCLJG4
7	7	2	7	7	7	7	7	7	7	N	N	C)	(7)	C)	П
327	327	562	905	1014	273	273	295	346	486	591	591	591	296	715	864
30.7	30.7	30.7	30.7	30.7	30.4	30.4	30.4	30.4	30.4	30.4	30.4	30.4	30.4	30.4	30.4
			2	Ŋ	Ŋ	5	5	5	45	45	45	45	45	45	S.
45.5	45.5	45.5	45.	45.	4	7	7								7

ALIGNMENTS

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Abd protein - mouse
C; Species: Mus musculus (house mouse)
C; Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 05-Nov-1999
C; Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 05-Nov-1999
C; Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 05-Nov-1999
C; Date: 03-Mar-1995 #sequence_revision for Bol-x-L and Bol-2, Gisplaces Far and promot A; Reference number: A55671; MUID:95136361; PMID:7834748
A; Accession: A55671
A; Accession: A55671
A; Molecule type: mRNA
A; Residues: 1-204 < MAN>
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100.0%; Pred. No. 1.2e-12;
ive 0; Mismatches 0;
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Matches 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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2 NLWAAQRYGRELRRMSDEFEGSFKGL 27 qq δλ

inter-alpha-trypsin inhibitor heavy chain 2 - golden hamster C;Species: Mesocricetus auratus (golden hamster) C;Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 20-Jun-2000 C;Accession: JC5575; PC4485 R;Nakatani, T.; Suzuki, Y.; Yamamoto, T.; Sinohara, H.
J. Biochem: 122, 71-82, 1997 A;Title: Molecular cloning and sequencing of CDNAs encoding three heavy-chain precurs sin inhibitor heavy chain family. A;Reference number: JC5574; MUID:97420688; PMID:9276673

A;Molecule type: mRNA A;Residues: 1-946 <NAX> A;Cross-references: DDBJ:D89286; NID:g1694689; PIDN:BAA13939.1; PID:g1694690 A;Experimental source: liver

A;Accession: P04485 A;Accession: P04485 A;Molecule type: protein A;Residues: 55-64;140-146;151-156;424-447;500-528;577-605 <NA2> C;Comment: In the plasma three inter-alpha-trypsin inhibitor heavy chains 1, 2 and 3 that the complexes play important role for panceatic cancer.

C, Superfamily: inter-alpha-trypsin inhibitor complex component II F; 261-264,717-916/Disulfide bonds: #status predicted

36.5%; Score 54; DB 2; Length 946; 34.6%; Pred. No. 11; Query Match Best Local Similarity

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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C;Accession: A42095; S52633; T47593
R;Jack, T.; Brockman, L.L.; Meyerowitz, E.M.
Cell 68, 683-697, 1992
A;Title: The homeotic gene APETALA3 of Arabidopsis thaliana encodes a MADS box and is A;Reference number: A42095; MUID:92154682; PMID:1346756
A;Accession: A42095
A;Title: The complete sequence of a 6794 bp segment located on the right arm of chron A;Reference number: S38185; MUID:94078675; PMID:8256522 A;Accession: S38185 A;Status: translation not shown A;Nolecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-370 cAIG>
A;Residues: 1-370 cAIG>
A;Residues: 1-370 cAIG>
A;Cross references: EMEL:236118; NID:9536664; PIDN:CAA85212.1; PID:9536665; MIPS:YBRZ
B;Kuenzler, M.; Paravicini, G.; Egli, C.M.; Irniger, S.; Braus, G.H.
Gene 113, 67-74, 1992
A;Title: Cloning, primary structure and regulation of the ARO4 gene, encoding the tyr
A;Reference number: JN0322; MUID:92225349; PMID:1348717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A)Residues: 1-370 <ALJ>
A)Cross-references: EMBL:Z36118; NID:g536664; PIDN:CAA85212.1; PID:g536665; MIPS:YBR; R;Aigle, M.; Baclet, M.C.; Barthe, C.; Bitcau, N.; Crouzet, M.; Dolgnon, F. submitted to the Protein Sequence Database, August 1994
A;Reference number: $45940
A;Accession: $46130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Title: Cloning, primary structure, and regulation of the HIS7 gene encoding a bifur A, Reference number: A48551; MUID:93374850; PMID:8366040
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A)Description: aldehyde-lyase; carbon-carbon lyase
A)Pathway: aromatic amino acid biosynthesis; shikimate pathway
A)Note: first step in shikimate pathway
C)Superfamily: phospho-2-dehydro-3-deoxyheptonate aldolase
C;Keywords: aldehyde-lyase; aromatic amino acid biosynthesis; carbon-carbon lyase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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N.Alternate names: homeotic protein APETALA3; MADS-box regulatory protein AP3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                     A.Residues: 1-370 <box/>
A.Residues: 1-370 <box/>
A.Cross-references: GB:L20296; NID:g311101; PIDN:AAA65607.1; PID:g311102 R;Aljinovic, G.; Pohl, F.M.; Pohl, T.M. submitted to the Protein Sequence Database, August 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-204,208-370 <KUE>
A; Cross-references: EMBL:X61107
R; Kuenzler, M.; Balmelli, T.; Egli, C.M.; Paravicini, G.; Braus, G.H.
J. Bacteriol. 175, 5548-5558, 1993
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A;Cross-references: SGD:S0000453; MIPS:YBR249c
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DLEAAQEYALRIKKLSDELKG 100
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A,Residues: 352-370 <KU2>
A,Cross-references: GB:X61107
                                                                                                                                                                                                                                                                                                                                                                                 A; Reference number: S45906
A; Accession: S46126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA A; Residues: 1-370 <ALJ>
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A; Status: preliminary
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C; Species: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 03-Jun-2002
C; Accession: S38185; S46126; S46130; JN0322; B48651
R; Doignon, F.; Biteau, N.; Aigle, M.; Crouzet, M.
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C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 20-Aug-1999
C.Accession: S54354
R.Chan, P.; Risler, J.L.; Raguenez, G.; Salier, J.P.
Blochem J. 306, 505-512, 1995
A.Title: The three heavy-chain precursors for the inter-alpha-inhibitor family in mouse: A.Reference number: S54353; MUID:95194326; PMID:7534067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Aluthors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: D70760
A;Actus: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1.223 <COL>
A;COL>
A;
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                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein Rv2014 - Mycobacterium tuberculosis (strain H37RV)
C; Species: Mycobacterium tuberculosis
C; Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C; Accession: D70760
R; Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
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Pred. No. 16;
5; Mismatches 12; Indels
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       Indels
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12;
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Mismatches
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Pred. No. 3
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                                                                                                                         2 NLWAAQRYGRELRRMSDEFEGSFKGL 27
                                                                                   27
                                                                                   2 NLWAAQRYGRELRRMSDEFEGSFKGL
   5.
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58.8%;
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Best Local Similarity 34.6%;
Matches 9; Conservative
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Best Local Similarity 58.88
Matches 10; Conservative
   Conservative
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9:
   Matches
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C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C; Accession: A96753
R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alor Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Hulzar, L.
Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzik Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallc ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MulD:21016719; PMID:11130712
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C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 01-Mar-2002
C;Accession: A11210
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloe
D; Dominguez-Bernal, G; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi
D; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Maduenc, E.; Maitournam, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA-directed RNA polymerase (EC 2.7.7.6) beta chain Cj0478 [imported] - Campylobacte. C;Species: Campylobacter jejuni
C;Species: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: A81393
R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chi. C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Ba. Nature 403, 665-668, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals A; Reference number: A81250; MVID:20150912; PMID:10688204
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-1378 < PARN>
A; Residues: 1-1378 < PARN>
A; Residues: 1-1378 < PARN>
A; Residues: GB: AL1111168; NID: g6967817; PIDN: CAB75116.1; PID: g69
A; Experimental source: serotype O2, strain NCTC 11168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   glycerol-3-phosphate cytidylyltransferase (gct), CDP-glycerol pyrophosphorylase (tei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:AE005173; NID:95903070; PIDN:AAD55628.1; GSPDB:GN00141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33.8%; Score 50; DB 2; Length 516; 35.3%; Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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A;Gene: rpoB; Cj0478
C;Superfamily: DNA-directed RNA polymerase beta chain C;Keywords: nucleotidyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :|| : || | || || || || || 1306 WALEAYGAAHTLREMLTIKSDDVEGRFSAYK 1337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 LWAAQRYG--RELRRM----SDEFEGSFKGLK 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---EFEGSFKGL
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Best Local Similarity 40.65
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-516 <STO>
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                                                 A; Cross_references: GB:M86357; NID:g166607; PIDN:AAA32740.1; PID:g166608
A; Experimental source: petals, stamens
A; Note: sequence extracted from NCBI backbone (NCBIN:82520, NCBIP:82521)
B; Note: sequence extracted from NCBI backbone (NCBIN:82520, NCBIP:82521)
B; Okamoto, H.; Yano, A.; Shiraishi, H.; Okada, K.; Shimura, Y.
Plant Mol. Biol. 26, 465-472, 1994
A; Nitle: Genetic complementation of a floral homeotic mutation, apetala3, with an Arabid A; Recession: S52633, MUID:95036018; PMID:7948893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Accession: C84338
R; Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.: Maddocks, D.G.; Jablo Jung, K.H.; Alam, M.; Freitas, T.
Froc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A; Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li A; Reference number: A84160; MUID:20504483; PMID:11016950
A; Accession: C84338
                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:D21125
R;Bloecker, H.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Quetier, F.; Salanoubat M.Mewes, submitted to the Protein Sequence Database, March 2000
A;Reference number: 224469
A;Accession: T47593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Superfamily: transcription factor squa; serum response factor DNA-binding domain homol
C;Keywords: DNA binding; nucleus; transcription regulation
F;2-57/Domain: serum response factor DNA-binding domain homology <SRF>
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C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
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Pred. No. 7.3;
3; Mismatches 4; Indels
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A, Experimental source: cultivar Columbia, BAC clone T12E18
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Pred. No. 17;
1; Mismatches
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A,Introns: 63/2; 85/3; 106/2; 139/3; 153/3; 168/3
A,Note: T12E18.30
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76.9%;
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ilarity 44.4%;
Conservative
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ELRRISDAVEGSF 209
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Best Local Similarity
Matches 10; Conserv
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ses 12; Conserv
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A; Residues: 1-374 <STO>
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                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-63 <OKA>
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fungus Mucor racemosus which ex
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:X98245; NID:g1370602; PIDN:CAA66901.1; PID:g1370603
A;Experimental source: cultivar clipper; root tip
C;Superfamily: annexin I; annexin repeat homology
F;14-85/Domain: annexin repeat homology <AXR>
                                                                                                                                                                                                                                                                                                                                                     oxidoreductase, sol/devB family - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: F72289
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C;Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 19-Jan-2001
C;Accession: C36365
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         11;
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A;Title: Expression of a gene family in the dimorphic fungus Mucor A;Reference number: A36365; MUID:91061774; PMID:1701021
A;Accession: C36365
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         Mismatches
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Pred. No. 23;
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47.6%;
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Best Local Similarity 47.6
Matches 10; Conservative
      13; Conservative
                                                                              4 WAAQRYGRELRRM---
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A; Molecule type: DNA
A; Residues: 1-206 <CAS>
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      Matches
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Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathor, Reference number: A82950; MUID:20437337; PMID:10984043
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Reference number: A82950; Muid: 20437337; PMID:10984043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GB:AE004091; NID:99946936; PIDN:AAG04420.1; GSPDB:GN001
C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.: Voss, H.; Wehland,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   conserved hypothetical protein PA1031 [imported] - Pseudomonas aeruginosa (strain PA01) C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
                                                                                                                                                                                                                                               A;Cross-references: GB:NC_003210; PIDN:CAC99167.1; PID:g16410491; GSPDB:GN00177 A;Experimental source: strain EGD-e C;Genetics:
                                                                                                                                                                                                                                                                                                                                                     A,Gene: tagD
C;Superfamily: Bacillus subtilis glycerol-3-phosphate cytidylyltransferase tagD
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C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: 840376
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Bur, J. Immunol. 23, 3248-3271, 1993
A;Fitie: Expressed human immunoglebulin chi genes and their hypermutation.
A;Reference number: 840312; MUID:94080891; PMID:8258341
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A. COSS-references: EMBL:X72486; NID:g441440; PIDN:CAA51154.1; PID:g441441
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 34-113/Domain: immunoglobulin homology <IMM>
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                             A,Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MOTD:21537279; PMID:11679669
A;Scession: AI1210
A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-127 <GLA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 49.5; DB 2;
Pred. No. 6.5;
6; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 KNLWAAQR----YGRELRRMSDEFEGSFKGLK 28
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Pred. No. 9.7;
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28;
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Pred. No. 2
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Best Local Similarity 36.4%; Pre
Matches 12; Conservative 6;
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A) Cross-references: GB:AE004535; GB
A) Experimental source: strain PAO1
C) Genetics:
A) Gene: PA1031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32.8%;
38.2%;
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Best Local Similarity
Matches 10; Conserv
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R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; C.M.

C.M.

Nature 399, 323-329, 1999

Nature 299, 323-329, 1999

A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq. A; Reference number: A72200: MUID: 99287316; PMID: 10360571

A;Accession: F72289

A; Molecule type: DNA

A;Residues: 1-220 <ARN>
A; Molecule type: DNA

A; Residues: 1-220 <ARN>
A; Molecule type: DNA

A; Experimental source: strain MSB8
C;Genetics:
A;Gene: TM1154
C;Superfamily: yeast SOL3 protein

Query Match

Best Local Similarity 34.8; Pred. No. 19;
Matches 8; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

Matches 8; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

A AQNYSKERERRSANDQFDLALIGM 133
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Search completed: September 15, 2003, 17:27:03 Job time : 12.6 secs

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September 15, 2003, 17:16:55; Search time 6.6 Seconds (without alignments) 199:507 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                     OM protein - protein search, using sw model
                                                                                                                                                        Run on:
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US-09-544-664-55 148 1 KNLWAAQRYGRELRRMSDEFEGSFKGLK 28 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

127863 seqs, 47026705 residues Searched:

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	mus 1	035147 rattus norv		P97279 mesocricetu						P35632 arabidopsis		Q46124 campylobact				Q9mt28 solanum tub	Q9s7b5 arabidopsis	Q01133 calliactis	O47169 loiseleuria	043521 homo sapien	P21259 polyorchis	Q16994 anthopleura	P10419 anthopleura	P19823 homo sapien	stre				klebsi		simiar	homo sap	caenoi
SUMMARIES		ID	BAD_MOUSE	BAD_RAT	BAD_HUMAN	ITH2_MESAU	ITH2_MOUSE	MATK_LEDPA	MATK_RHOFR	MATK_RHOTS	AROG_YEAST	AP3_ARATH	CE05_MOUSE	RPOB_CAMJE	RMUC_PSEAE	RAS3_RHIRA	6PGL_THEMA	THRC_SOLTU	THRC_ARATH	FMRA_CALPA	MATK_LOIPR	BIM_HUMAN	PRFA_POLPE	FMR2_ANTEL	FMR1_ANTEL	ITH2_HUMAN	UVRA_STRCO	PSBO_ANASP	SNF4_KLULA	DCOA_SALTY	DCOA_KLEPN	HT2A_HUMAN	ENV_SIVAT	- 1	LML1_CABEL
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MDN1_HUMAN	MATK_GAUPR	MATK_LILTS	NUOG_ECOLI	NUOG_SALTY	BIM_MOUSE	BIM_RAT	END8_ECO57	END8_ECOLI	END8_SALTI	END8_SALTY	SYM_THEMA
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34	in m	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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us-09-544-664-55.rsp

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InterPro; IPR000712; Bcl2_BH
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Ser-136 is the major site of AKT/PKB phosphorylation, Ser-155 the major site of protein kinase A (CAPK) phosphorylation. SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain. SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S->A: NO PHOSPHORYLATION.
S->A: NO PHOSPHORYLATION.
S->A: NO PHOSPHORYLATION, INTERACTS WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hsu S.Y., Kaipia A., Zhu L., Hsueh A.J.W.; "Interference of BAD (Bcl-xL/Bcl-2-associated death promoter)-induced apoptosis in mammalian cells by 14-3-3 isoforms and Pll."; Mol. Endocrinol. 11:1858-1867(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           D'Agata V., Magro G., Travali S., Musco S., Cavallaro S.; "Cloning and expression of the programmed cell death regulator BAD in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                PKB).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PKB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BAD_RAT STANDARD; PRT; 205 AA. 035147; 070256; 09JHX1; 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Bcl2-antagonist of cell death (BAD) (Bcl-2 binding component 6) (Bcl-xL/Bcl-2 associated death promoter).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93.2%; Score 138; DB 1; Length 204; 100.0%; Pred. No. 2.5e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [1]
SEQUENCE FROM N.A., AND MUTAGENESIS OF SER-113 AND SER-137
                                                                                                                                                                                                                                                                                                                                                                                                                    PHOSPHORYLATION (BY PKA AND PHOSPHORYLATION (BY PKA AND PHOSPHORYLATION (BY PKA AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6C2BA910205053F7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       140 NLWAAQRYGRELRRMSDEFEGSFKGL 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 NLWAAQRYGRELRRMSDEFEGSFKGL 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21109372; PubMed=11161472;
                                                                                                                                                                                                                                                                                                                MGD; MGI:1096330; Bad.
InterPro; IPR000712; Bcl2_BH.
PROSITE; PS01259; BH3; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=98194755; PubMed=9535132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=98034386; PubMed=9369453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neurosci. Lett. 243:137-140(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22080 MW;
                                                                                                                                                                                                                                                           EMBL; 137296; AAA64465.1; -.
                                                                                                                                                                                                                                                                                                                                                                               Apoptosis; Phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BAD.
Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                        112
1136
1136
1136
1136
                                                                                                                                                                                                                                                                                 PIR; A55671; A55671.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                204 AA;
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                                                                                                                                                                                                                                                                                                       1657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the rat brain.
                                                                                                                                                                                                                                                                                                 HSSP; Q92934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                      MOD_RES
MOD_RES
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
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   STEETE TEETER SARANA STEETER SARANA 
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S->A: NO HETERODIMERIZATION WITH 14-3-3 PROTEINS. NO EFFECT ON HETERODIMERIZATION WITH BCL2 NOR WITH PROTEIN P11. SDAGGR -> ERRGKK (IN REF. 1). 7AFA71DAE9CF4A81 CRC64;

34 SI 22228 MW;

29 205 AA;

S->A: NO EFFECT ON HETERODIMERIZATION WITH 14-3-3 PROTEINS. EVAMFPLRYWTALRRIC (in isoform Beta). /FIId=VSP_000534.

> 113 137

> 113 137

-> EELTYSVEFLPVRAIAMEGWPLLWSFQSFPHTLPPTPP

PHOSPHORYLATION (BY PKA AND PKB)
(BY SIMILARIIY).
LPRPKSAGTATOMRQSASWTRIIQSWWDRNLGKGGSTPSQ

(BY SIMILARITY).
PHOSPHORYLATION (BY PKA AND PKB)
(BY SIMILARITY). PHOSPHORYLATION (BY PKA AND PKB)

501259; BH3; FALSE_NEG. Phosphorylation; Alternative splicing.

162 113 137 156 205

> 113 137 156 166

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Hamner S., Arumae U., Yu L.-Y., Sun Y.-F., Saarma M., Lindholm D.;

"Functional characterization of two splice variants of rat BAD and
their interaction with Bcl-w in sympathetic neurons.";

Mol. Cell. Neurosci. 17:97-106(2001).

C. -!- FUNCTION: Promotes cell death. Successfully competes for the
binding to Bcl-x(L), Bcl-2 and Bcl-w, thereby affecting the level
C heterodimerization of these proteins with BAX. Can reverse the
death repressor activity of Bcl-x(L), but not that of Bcl-2 (By
similarity). Appears to act as a link between growth factor
receptor signaling and the apoptotic pathways.

C SUBUNIT: Forms heterodimers with the anti-apoptotic proteins, Bcl-
x(L), Bcl-2 and Bcl-w. Also binds protein Sloodlo. The Ser-
113/Ser-137 phosphorylated form binds 14-3-3 proteins.

C SUBCELLULAR LOCATION: Outer mitochondrial membrane. Upon
preparation locates to the cytoplasm (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bcl-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN: Intact BH3 domain is required by BIK, BID, BAK, BAD AND BAX for their pro-apoptotic activity and for their interaction with anti-apoptotic members of the Bcl-2 family.

PTM: Phosphorylated on Ser-113 in response to Survival Stimuli. Subsequent phosphorylation on Ser-137 promotes heterodimerization with 14-3-3 proteins. This interaction then facilitates the phosphorylation at Ser-156, a site within the BH3 domain, leading to the release of Bcl-x(L) and the promotion of cell survival. Ser-137 is the major site of AKT/PKB phosphorylation, Ser-156 the major site of protein kinase A (CAPK) phosphorylation (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE SPECIFICITY: Expressed in all tissues tested, including brain, liver, spleen and heart. In the brain, restricted to epithelial cells of the choroid plexus. Isoform alpha is the more abundant form.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain. SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=035147-2; Sequence=VSP_000534;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId=035147-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, AF003523; AAC53374.1; -.
EMBL, AF031227; AAC15100.1; -.
EMBL, AF279910; AAF91427.1; -.
EMBL, AF279911; AAF91428.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q92934; 1G5J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=Alpha;
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Atlausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Jordan H., Moore T. Wang J., Hasieh F.,
Baltschul S.F., Jordan H., Moore T. Wang J., Hasieh F.,
Baltchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Wagna P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Brichards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Nillalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pialey J., Helton E., Ketteman M., Madan A., Rodriques S., Sanchez A.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnenz A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnenztion and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yin D.X., Li Z., Huang B., Chen S., Zhou H.;
"A human protein that interacts with Bcl-2 and have homology to mouse
                                                                                                                                                                                                                                                    092934; 014803; 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
BC12-antagonist of cell death (BAD) (BC1-2 binding component 6) (BC1-XL/BC1-2 associated death promoter) (BC12-1ike 8 protein).
BAD OR BBC6 OR BC1218.
                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
                                                .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ottilie S., Diaz J.-L., Horne W., Chang J., Wang Y., Wilson G. Chang S., Weeks S., Fritz L.C., Oltersdorf T.; "Dimerization properties of human BAD."; J. Biol. Chem. 272:30866-30872(1997).
93.2%; Score 138; DB 1; Length 205; 100.0%; Pred. No. 2.5e-13; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND PHOSPHORYLATION BY RAF-1.
MEDLINE=97083574; PubMed=8929532;
Wang H.-G., Rapp U.R., Reed J.C.;
"Bcl-2 targets the protein kinase Raf-1 to mitochondria.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Takayama S., Reed J.C.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                      168 AA.
                                                                                                           141 NIWAAQRYGRELRRMSDEFEGSFKGL 166
                                                                                      2 NLWAAQRYGRELRRMSDEFEGSFKGL 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND DIMERIZATION.
                                                                                                                                                                                                                                      PRT;
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MEDLINE=98049554; PubMed=9388232;
                                            26; Conservative
                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87:629-638(1996)
                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                      HUMAN
   Query Match
                         Best Local
                                            Matches
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                                                                                                                FIGURE 1. Promotes cell death. Successfully competes for the binding to Bcl-x(L), Bcl-2 and Bcl.w, thereby affecting the level of heterodimerization of these proteins with BAX. Can reverse the death repressor activity of Bcl-x(L), but not that of Bcl-2 (By similarity). Appears to act as a link between growth factor receptor signaling and the apoptotic pathways.

-!- SUBUNIT: Forms heterodimers with the anti-apoptotic proteins, Bcl-x(L), Bcl-2 and Bcl-w. Also binds protein S100Al0 (By similarity). The Ser-75/Ser-99 phosphorylated form binds 14-3-3 proteins (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CAUTION: Ref.1 sequence differs from that shown due to frameshifts in position 64 and 91.
                                                                                                                                                                                                                                                                                    Meadows R.P.
                                                         Fesik S.W.;
"Rationale for Bcl-xL/Bad peptide complex formation from structure, mutagenesis, and biophysical studies.";
Protein Sci. 9:2528-2534(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PHOSPHORYLATION (BY PKA AND PKB)
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                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Outer mitochondrial membrane. Upon
            MEDLINE=21073561; Pubmed=11206074;
Petros A.M., Nettesheim D.G., Wang Y., Olejniczak E.T.,
Mack J., Swift K., Matayoshi E.D., Zhang H., Thompson C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polymorphism; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY),
A -> S (in dbSNP:3729933),
/FTId=VAR_015380,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69FD8D27DDEE3241 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60; GO:0005737; C:cytoplasm; NAS.
GO; GO:0005741; C:mitochondrial outer membrane; NAS.
GO; GO:0005515; F:protein binding activity; NAS.
GO; GO:0008632; P:apoptotic program; TAS.
GO; GO:0006917; P:induction of apoptosis; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U66879; AAB36516.1; ALT_FRAME.
EMBL; AF021792; AAB72092.1; -.
EMBL; AF031523; AAB88124.1; -.
EMBL; BC001901; AAH01901.1; -.
PDB; 1G5J; 07-FEB-01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000712; Bcl2_BH.
PROSITE; PS01259; BH3; FALSE_NEG
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18392 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Apoptosis; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   106
168 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
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                                                                                                                                                                                                                                                             similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HELIX
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MIM;
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Score 114; DB 1; Length 168;

77.0%;

Query Match

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NAME TO THE PET TO THE
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                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nakatani T., Suzuki Y., Yamamoto T., Sinohara H.;
"MoFecular cloning and sequencing of cDNAs encoding three heavy-chain precursors of the inter-alpha-trypsin inhibitor in Syrian hamster: implications for the evolution of the inter-alpha-trypsin inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: I-ALPHA-I PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN, BIKUNIN. INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2 AND BIKUNIN, INTER-ALPHA-LIRE INHIBITOR (I-ALPHA-LI) OF H2 AND BIKUNIN, AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND PIM: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN 4-SULFARE BRIDGE TO THE THEIR C-TERMINAL ASPARTATE (BY
                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hamster urine and plasma.";
J. Biochem. 120:145-152(1996).
-!-FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN, INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY
                                                                                                                                                                                                                                                                                                                                                          15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
28-FBE-2003 (Rel. 41, Last annotation update)
Inter-alpha-trypsin inhibitor heavy chain H2 precursor (ITI heavy chain H2) (Inter-alpha-inhibitor heavy chain 2) (HC2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 55-64; 140-146; 151-156; 424-447; 500-528 AND 577-605,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yamamoto T., Yamamoto K., Sinohara H.;
"Inter-alpha-trypsin inhibitor and its related proteins in Syrian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                      ..
O
                                   Indels
  . 7.6e-10;
cches 2;
                                                                                                                                                                                                                                                                                                      946 AA.
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                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
        No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mesocricetus auratus (Golden hamster).
                                                                                                                             103 NLWAAQRYGRELRRMSDEFVDSFK 126
                                                                                          25
                                                                                                                                                                                                                                                                                                      PRT;
     Pred.
                                                                                          2 NLWAAQRYGRELRRMSDEFEGSFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=97420688; PubMed=9276673;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=97018241; PubMed=8864857;
                                ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biochem. 122:71-82(1997).
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InterPro; IPR002035; VWF_A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; D89286; BAA13939.1;
                              Conservative
                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00092; vwa; 1.
SMARI; SM00609; VII; 1.
Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            heavy chain family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10036;
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Best Local
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                                Matches
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                                                                                            BY SIMILARITY.
INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-C57BL/6W; TISSUE-Liver;

MEDLINE=95194326; PubMed=7534067;

Chan P., Risler J.-L., Raquenez G., Salier J.-P.;

"The three heavy-chain precursors for the inter-alpha-inhibitor family in mouse: new members of the multicopper oxidase protein group with differential transcription in liver and brain.";

Blochem. J. 306:505-512(1995).

-! FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN, INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SUBUNIT: I ALPHA-I PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN, BIKUNIN, INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2 AND BIKUNIN, INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND BIKUNIN, AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN.
-!- TISSUE SPECIFICITY: EXPRESSED IN BOTH LIVER AND BRAIN.
-!- TISSUE SPECIFICITY: EXPRESSED IN BOTH LIVER AND BRAIN.
-!- PTM: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN 4-SULFATE BRIDGE TO THE THEIR C-TERMINAL ASPARTATE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                         N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
CHONDROITIN 4-SULFATE, CROSS-LINK SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OGI703;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Inter-alpha-trypsin inhibitor heavy chain H2 precursor (III heavy
chain H2) (Inter-alpha-inhibitor heavy chain 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                           (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                      ô
                                      Repeat; Signal; Multigene family;
                                                                                                                                                                                                                                                                                                                                                                            36.5%; Score 54; DB 1; Length 946; 34.6%; Pred. No. 4.3;
                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                          CA8BF565458E7B2E CRC64;
                                                                                                                                                                                       N-LINKED (GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                                                                                                                    12;
                                                                                                                                                                                                                                                                                                V -> Y (IN REF. 2).
E -> I (IN REF. 2).
                                                                                                                                                                                                                                                                                    (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          946 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: BELONGS TO THE ITIH FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                    5; Mismatches
                                                                                                                                                    SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 NIWAAQRYGRELRRMSDEFEGSFKGL 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                          106580 MW;
                 PROSITE; PS50234; VWFA; 1.
Serine protease inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                      9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
 VWA: 1.
                                                                       18
54
702
                                                                                                                                                 946
468
1118
263
445
702
                                                                                                                                                                                                                                                                                                    510
                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 9; Conserva
                                                                                                                                                                                                                                                                                                                       595
946 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                      510
SM00327;
                                                         Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ITH2_MOUSE
                                                                                                                                                                                                         CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                    CONFLICT
                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                         CONFLICT
                                                                                                                                                                                                                                                                 BINDING
                                                                                              PROPEP
                                                                                                                                                    PROPEP
                                                                                                                                                                    DOMAIN
                                                                           SIGNAL
                                                                                                              CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                        BY SIMILARITY.
INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; Ericales; Ericaceae; Ericoideae; Rhodoreae; Rhododendron. NCBI_TaxID=75583;
                                                                                                                                                                                                                                                                                                                                                                         CHONDROITIN 4-SULFATE, CROSS-LINK SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- FUNCTION: Probably assists in splicing chloroplast group II
                                                                                                                                                                                                                                                                                                                             N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 introns (By similarity).
                                                                                                                                                                                                           Repeat; Signal; Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [1]
SEQUENCE FROM N.A.
Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi
                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 946;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12; Indels
                                                                                                                                                                                                                                                                                                                                                                                        BY SIMILARITY), 40DB6716433ED9DC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Investigation of sectional relationships in the genus Rhododendron (Ericaceae) based on matK sequences."; Shokubutsu Kenkyu Zasshi 73:143-154(1998).
                                                                                                                                                                                                                                                                                                                                                             N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    506 AA.
                                                                                                                                                                                                                                                                                                 BY SIMILARITY. VWFA.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 53;
Pred. No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  212 NVWIIEPQGMRFLHVPDTFEGHFQGV 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 NLWAAQRYGRELRRMSDEFEGSFKGL 27
                                                                                                                                                                                                                                        POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ledum palustre (Wild rosemary).
                                                                                                                                                                                                                                                                                                                                                                                                         MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-5FF-2003 (Rel. 42, Created)
15-5FP-2003 (Rel. 42, Last seq.
15-5FP-2003 (Rel. 42, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Maturase K (Intron maturase).
                                                                                     PIR, S54354; S54354.
MGD; MGI:96619; Itih2.
InterPro; IPR006587; VWI-.
Interpro; IPR02035; VWF_A.
Pfam; PF00092; Vwa; I.
SMART; SM00609; VIT; I.
SMART; SM00377; VWA; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                   35.8%;
34.6%;
                                                                         EMBL; X70392; CAA49842.1; -.
                                                                                                                                                                                           PROSITE: PS50234; WWFA; 1.
Serine protease inhibitor;
Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                      946 AA; 105927
                                                                                                                                                                                                                                                                                                                                                                                                                                                               9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                 946
468
1118
263
445
702
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                               DOMAIN
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                       SIĞNAL
                                                                                                                                                                                                                                                                     CHAIN
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                                                                                                                                                                          ä
                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta, eudicotyledons; core eudicots; Asteridae; Ericaceae; Ericoideae; Rhodoreae; Rhododendron.NCBI_TaxID=49622;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -1- FUNCTION: Probably assists in splicing chloroplast group II introns (By similarity).
-1- SIMILARITY: BELONGS TO THE INTRON MATURASE FAMILY 2. MATK
                                                                                                                                                                          7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35.5%; Score 52.5; DB 1; Length 506; 37.5%; Pred. No. 3.6;
                                                                                                                                       DB 1; Length 506;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |IJ|
SEQUENCE FROM N.A.
Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi
Yukawa T.;
                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Investigation of sectional relationships in the genus Rhododendron (Ericaceae) based on matK sequences."; Shokubutsu Kenkyu Zasshi 73:143-154(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mRNA processing; Chloroplast.
SEQUENCE 506 AA; 60534 MW; ADA44B25E92436E8 CRC64;
                                                                                                    CFEA926307DAC85E CRC64;
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&
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(Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                           391 KPVWAALSDSDIIERFGRIYRNLSHYYSGSLK 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 KNLWAA-----QRYGRELRRMSDEFEGSFK 25
                                                                                                                                     Score 52.5; DB red. No. 3.6; 5; Mismatches
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                                                                                                                                                                                                                                                                                                                                 506 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 3.6;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AB012741; BAA25862.1; -.
InterPro; IPR000442; Intron_maturse2.
InterPro; IPR002866; MatK_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rhododendron ferrugineum (Alpenrose).
EMBL, AB012751; BAA25872.1; -.
Interpro; IPR000442; Intron_maturse2.
Interpro; IPR002866; MatK_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF01348; Intron_maturas2; 1. Pfam; PF01824; Matk_N; 1.
                                                 Pfam; PF01348; Intron_maturas2; 1.
Pfam; PF01824; MatK_N; 1.
                                                                                                                                                                                                                                                                                                                                                              28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last seq
28-FEB-2003 (Rel. 41, Last anno
                                                                                       Chloroplast.
                                                                                                                                       35.5%;
37.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                  Maturase K (Intron maturase)
                                                                                                                                                     Local Similarity 37.5
nes 12, Conservative
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                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                     mRNA processing; Ch
SEQUENCE 506 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MATK_RHOTS
O62991;
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062984;
                                                                                                                                       Query Match
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ID MATK_RI
AC 062991
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first step.
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   Kuenzler
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIIND=92225349; PubMed=1248717; Kuenzler M., Paravicini G., Egli C., Irniger S., Braus G.H.; "Cloning, primary structure and regulation of the ARO4 gene, encoding the tyrosine-inhibited 3-deoxy-D-arabino-heptulosonate-7-phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-021.7

01-021.93 (Rel. 28, Last sequence update)

01-FEB-1994 (Rel. 28, Last sequence update)

28-FEB-2003 (Rel. 41, Last annotation update)

Phospho-2-dehydro-3-deoxyheptonate aldolase, tyrosine-inhibited

(EC 4-1.2.15) (Phospho-2-keto-3-deoxyheptonate aldolase) (DAHP

synthetase) (3-deoxy-D-axabino-heptulosonate 7-phosphate synthase).
                                                                         Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; Ericales; Ericaceae; Ericoideae; Rhodoreae; Rhododendron. NCBI_TaxID=49629;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                "Investigation of sectional relationships in the genus Rhododendron (Ericaceae) based on matK sequences."; Shokubutsu Kenkyu Zasshi 73:143-154(1998).
-!- FUNCTION: Probably assists in splicing chloroplast group II introns (By similarity).
-!- SIMILARITY: BELONGS TO THE INTRON MATURASE FAMILY 2. MATK
                                                                                                                                                           SEQUENCE FROM N.A.
Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35.5%; Score 52.5; DB 1; Length 506; 37.5%; Pred. No. 3.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam: PF01348; Intron_maturas2; 1.
Pfam: PF01824; MatK_N; 1.
mRNA processing; Chloroplast.
SEQUENCE 506 AA; 60569 MW; AEE12FF8809C223E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8;
              Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  370 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   synthase from Saccharomyces cerevisiae.";
Gene 113:67-74(1992).
                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AB012750; BAA25871.1; -.
InterPro; IPR000442; Intron_maturse2.
InterPro; IPR002866; MatK_N.
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  Created)
                                         Maturase K (Intron maturase).
                                                                  Rhododendron tsusiophyllum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
28-FEB-2003 (Rel. 41,
28-FEB-2003 (Rel. 41,
28-FEB-2003 (Rel. 41,
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REVISIONS TO 205-207.
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                 SUBFAMILY.
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                                                                                                                                                                                        Yukawa T.;
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GC; GO:0003849; F:2-dehydro-3-deoxyphosphoheptonate aldolase . . .; IDA.
InterPro; IPR006219; AroFGH.
InterPro; IPR006218; DAHP1/KDSA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.

Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: STEREOSPECIFIC CONDENSATION OF PHOSPHOENOLPYRUVATE (PEP)
AND D-ERTHHOSE-4-PHOSPHATE (E4P) GIVING RISE TO 3-DEOXY-D-
ARABINO-HEPTULOSONATE-7-PHOSPHATE (DAHP).

-!- CAPALYTIC ACTIVITY: 2-dehydro-3-deoxy-D-arabino-heptonate 7-
phosphate + phosphate = phosphoenolpyruvate + D-erythrose 4-
phosphate + H(2)0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AP3_ARATH STANDARD, PRT; 232 AA.
P35632; Q39003; Q8LB79; Q98703; Q98014; Q98015; Q98016; Q98017;
P35632; Q39003; Q8R202; Q98021; Q98021; Q98015; Q98017;
O1-JUN-1994 (Rel. 29, Created)
O1-JUN-1994 (Rel. 29, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
AP3 OR AT3654340 OR T12818_30.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                           MEDLINE-94078675; PubMed=8256522; Doignon F., Biteau N., Aigle M., Crouzet M.; Withe complete sequence of a 6794 bp segment located on the right arm of chromosome II of Saccharomyces cerevisiae. Finding of a putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- ENZYME REGULATION: INHIBITED BY TYROSINE.
-!- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
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-!- SIMILARITY: BELONGS TO CLASS-I DAHP SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Aromatic amino acid biosynthesis; Lyase, Multigene family.
SEQUENCE 370 AA; 39749 MW; 594ED48F24175979 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Indels
Submitted (NOV-1993) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DLEAAQEYALRIKKLSDELKG 100
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ProDom; PD005060; AroFGH; 1.
TIGRFAMS; TIGR00034; aroFGH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 NLWAAQRYGRELRRMSDEFEG
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                                                                                                                                                                                                                                                                                                                         duTPase in a yeast.";
Yeast 9:1131-1137(1993).
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es 10; Conserv
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RA Salanoubat M., Lemcke K., Rieger M., Ansorge W., Unseld M.,

Balanoubat M., Lemcke K., Rieger M., Ansorge W., Unseld M.,

Bathmann B., Valle G., Blocker H., Perez-Alonso M., Obermaier B.,

Belseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,

Be Simone V., Choisne N., Artiguenave F., Robert C., Brotter P.,

RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Ouetier F.,

RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Ouetier F.,

RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Ouetier F.,

RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Ouetier F.,

RA Winckelmann R., Kranz H., Voss H., Holland R., Brangert S., Nyakatura G.,

RA Wurmbach E., Drzonek H., Erfle H., Jordan N., Bangert S.,

RA Gonrad A., Hornischer K., Kauer G., Loehnert T.-H., Nordsiek G.,

RA Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,

Racichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,

Ravarro P., Collado C., Perez-Perez A., Ottetwaelder B., Macuy D.,

Ger Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,

Mondrott A., Argiriou A., Flores M., Liguori R., Vitale D.,

RA Monhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,

RA Monhaupt G., Malts A., Utterback T., Fujii C.Y., Shea T.P.,

RA Roney T., Rizzo M., Walts A., Utterback T., Fujii C.Y., Shea T.P.,

RA Fraser C.M., Kaneko T., Nekamura Y., Salberg S.L., White O., Venter J.C.,

RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kauta T., Rabanto S., Klmura T., Indeswa C., Kautshina K., Kishida Y.,

RA Nakayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T.,

RA Watanabe A., Yamada M., Tabata S.;

RH Fraser C.M., Kamada M., Tabata S.;

RH Frain "September B. Takeuchi C., Wada T.,

RH Fraina "September B. Takeuchi C., Wada T.,

RH Hallen "Septemb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Purugganan M.D., Suddith J.I.;
"Molecular population genetics of floral homeotic loci: departures from the equilibrium-neutral model at the APETALA3 and PISTILLATA genes of Arabidopsis thaliana.";
Genetics 151:839-848(1999).
                                                                                                                                                  Jack T., Brockman L.L., Meyerowitz E.M.; "The homeotic gene APETALAS of Arabidopsis thaliana encodes a MADS box and is expressed in petals and stamens."; Cell 68:683-597(1992).
                                                                                                                                                                                                                                                                                             STRAIN-cv. Landsberg erecta;
MEDLINE=95036018; PubMed=7948893;
Okamoto H., Yano A., Shiraishi H., Okada K., Shimura Y.;
"Genetic complementation of a floral homeotic mutation, apetala3,
with an Arabidopsis thaliana gene homologous to DEFICIENS of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND VARIANTS.
STRAIN=cv. Bla-1, cv. Bretagny, cv. Bs-1, cv. Bu-0, cv. Bu-2, cv. Chi-1, cv. Co-1, cv. Columbia, cv. Corsacalla-1, cv. Cvi-0, cv. Gr-3, cv. Id-1, cv. Kas-1, cv. Kent, cv. Landsberg erecta, cv. Li-8, and cv. Lisse;
MEDLINE-99126449; PubMed-9927474;
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Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Full-length cDNA from Arabidopsis thaliana.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
  Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=cv. Columbia;
MEDLINE=21016720; PubMed=11130713;
                                                                                                                                                                                                                                                                                                                                                                                                                           Antirrhinum majus.";
Plant Mol. Biol. 26:465-472(1994).
                                                                                                                           MEDLINE=92154682; PubMed=1346756;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 408:820-822(2000).
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                       NCBI_TaxID=3702;
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Feldmann K.;
                                                                                                      TISSUE-Petal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      thaliana
    eurosids
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Nature 409:525-529(2001).
-!- FUNCTION: Probable transcription factor involved in the genetic control of flower development. Is required for normal development of petals and stamens in the wild-type flower. Forms an heterodimer with PISTILLATA, that is required for autorequiation of both Ap3 and PI genes. Ap3/PI heterodimer interacts with APBTALAI or SEPALLATA3 to form a ternary complex that could be responsible for the regulation of the genes involved in the flower
                                                                                                                                                                                                                                                                   STRAIN=cv. Columbia;
MEDLIND=99311297; PubMed=10382288;
Brunel D., Froger N., Pelletier G.;
"Development of amplified consensus genetic markers (ACGM) in Brassica
napus from Arabidopsis thaliana sequences of known biological
function.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Riechmann J.L., Krizek B.A., Meyerowitz E.M.; "Dimerization specificity of Arabidopsis MADS domain homeotic proteins APETALA1, APETALA3, PISTILLATA, and AGAMOUS."; Proc. Natl. Acad. Sci. U.S.A. 93:4793-4798(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Krizek B.A., Meyerowitz B.M.; "The Arabidopsis homeotic genes APETALA3 and PISTILLATA are sufficient to provide the B class organ identity function."; Development 122:11-22(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -:- SUBCELLUIAR LOCATION: Nuclear.
-:- TISSUE SPECIFICITY: Expressed in petals and stamens.
-:- TISSUE SPECIFICITY: Expressed in petals and stamens.
-:- INDUCTION: Positively regulated by the meristem identity proteins APETALAI and LEAFY with the cooperation of UFO.
-:- MISCELLANEOUS: Mutations in the care transformation of petals into sepals and stamina into arrapels.
-:- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Honma T., Goto K.; "Complexes of MADS-box proteins are sufficient to convert leaves into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: Forms an heterodimer with PISTILLATA, capable of binding to CArG-box sequences. AP3/PI heterodimer binds AP1 or SEP3 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NG M., Yanofsky W.F.;
"Activation of the Arabidopsis B class homeotic genes by APETALAL.";
Plant Cell 13:739-753(2001).
Shinozaki K., Davis R.W., Ecker J.R., Theologis A.; "RIKEN Arabidopsis full length cDNA clones (RAFLs) sequenced by the SSP consortium (Salk/Stanford/PGEC)."; Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: Contains 1 K-box dimerization domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M86357; AAA32740.1; -.
EMBL; D21125; BAA04665.1; -.
EMBL; AF115798; AAD51887.1; -.
EMBL; AF115799; AAD51888.1; -.
                                                                                                                                                                                                                              SEQUENCE OF 36-128 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome 42:387-402(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENETIC REGULATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          form complexes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=11206550;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=8565821;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=8643482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION
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RPOB CAMJE
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 12
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                                                                                                                                                                                                                                                                                                 PROSITE; PS00350; MADS_BOX_1; 1.
PROSITE; PS50066; MADS_BOX_2; 1.
Flowering; Transcription regulation; Activator; Developmental protein; Nuclear protein; DNA-binding; Coiled coil; Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                    K-BOX.
COILED COIL (POTENTIAL).
K -> R (in strain cv. Lisse).
N -> D (in strain cv. Corsacalla-1).
T -> S (in strain cv. Li-8).
L -> V (in strain cv. Kas-1).
E -> K (in strain cv. Kas-1).
Gr-3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=FVB/N;
MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 51; DB 1; Length 232;
Pred. No. 2.6;
3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-5EP-2003 (Rel. 42, Created)
15-5EP-2003 (Rel. 42, Last sequence update)
15-5EP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            851 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                107 ORLGECLDELDIQELRRLEDEMENTFK 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 ORYG-----RELRRMSDEFEGSFK 25
                                                                                                                                                                                                                                                                                                                                           MADS.
                                                                                                                                                                                                                          TRANSFAC; T01776; -.
InterPro; IPR002487; TF_Kbox.
InterPro; IPR002100; TF_MADSbox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           34.5%;
                                                                                                             AAD51900.1;
AAD51901.1;
AAD51902.1;
                                                                                                                                                                                                                                                                                PRINTS; PR00404; MADSDOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ilarity 44.4%;
Conservative
                                                                                                                                                                          AY070397; AAL49893.1;
AY142590; AAN13159.1;
AF056541; AAD41557.1;
                                                AAD51894.1;
AAD51895.1;
                                                                              AAD51897.1;
AAD51898.1;
                                                                                                                                              AAD51903.1;
                                                                                                                                                     CAB81799.1;
AAM64919.1;
                   AAD51891.1;
                             AAD51892.1;
                                       AAD51893.1;
                                                                      AAD51896.1;
                                                                                                    AAD51899.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                         Pfam; PF01486; K-box; 1
Pfam; PF00319; SRF-TF;
                                                                                                                                                                                                                                                                                                                                           165
164
131
47
61
109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein C5orf5 homolog
                                                                                                                                                                                                                                                                                         SMART; SM00432; MADS;
                                                                                                                                                                                                        PIR; A42095; A42095.
HSSP; P11746; 1MNM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 12; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                AF115805;
AF115806;
                                                                              AF115808;
AF115809;
                                                                                                                                              AF115814;
                                                                                                                                                                  AY087369;
                                                                                                                                                                                                                                                                                                                                               3
93
31
47
61
73
109
                                       AF115804;
                                                                                                               AF115811;
AF115812;
                             AF115803;
                                                                      AF115807;
                                                                                                    AF115810;
                                                                                                                                 AF115813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CE05_MOUSE
Q8K2H3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                DOMAIN
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                      VARIANT
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                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                      EMBL;
EMBL;
                                                                                                                        EMBL;
EMBL;
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EMBL;
EMBL;
                                                EMBL;
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                             EMBL;
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                                        EMBL;
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RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Ba biatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RR Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Rodriguez A.C., Grimwood J.S., Schmutz J., Marra M.A.;

ROHNERT Schein J.E., Jones S.J.M., Marra M.A.;

RGeneration and initial analysis of more than 15,000 full-length

RI Proc. Natl. Acad. Sci. U.S. A. 99:16899-16903(2002).

-! SIMIARITY: Contains 1 Rho-GAP domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-NCTC 11168;

STRAIN-NCTC 11168;

STRAIN-NCTC 11168;

PARTAINI J., WHEN B.W., Mungall K., Ketley J.M., Churcher C.,

Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S.,

Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,

Justin M.A., Rajandréam W.A., Rutherford K.M., van Vliet A.H.M.,

Whitehead S., Barrell B.G.;

"The genome sequence of the food-borne pathogen Campylobacter jejuni

reveals hypervariable sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Campylobacter jejuni.
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Campylobacteraceae; Campylobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 046124; Q9PI31;
01-NOV-1997 (Rel. 35, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
DNA-directed RNA polymerase beta chain (EC 2.7.7.6) (Transcriptase beta chain) RNA polymerase beta subunit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 851;
11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       256 GLU-RICH.
97054 MW; C2B26669FB6DB2CE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 51;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RHO-GAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 KNLWAAQRYGRELRRMSDEFEGSF 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; BC031465; AAH31465.1; -. InterPro; IPR000198; RhoGAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam, PF00620, RhoGAP, 1.
SMART, SM00324, RhoGAP, 1.
PROSITE, PS50238, RHOGAP, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             851 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
es 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTPase activation.
DOMAIN 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=197;
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RAS3_RHIRA
P22280;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mucor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5
                                                                                                                                                                                                                                       FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=ATCC 15692 / PAO1;
MEDLINE=20437337; PubMed=10984043;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2).
                                                                                                                  Calva E.;
"Identification of Campylobacter jejuni and C.coli using the rpoB gene and a cryptic DNA fragment from C.jejuni.";
Gene 165:1-8(1995).
                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND
                                                                                                                                                                                                                                                                                                                                 CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: Belongs to the RNA polymerase beta chain family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NDLANGVDAA -> MTWLMALMQP (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
9
                                                                                         Bustamante V.H., Puente J.L., Sanchez-Lopez F., Bobadilla M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 50; DB 1; Length 1378; pred. No. 25; 3; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | DiterPro; | PRO1572; RNA_pol_B. |
| Pfam; PF04563; RNA_pol_Rpb2_1; 1. |
| Pfam; PF04561; RNA_pol_Rpb2_2; 1. |
| Pfam; PF00565; RNA_pol_Rpb2_3; 1. |
| Pfam; PF00562; RNA_pol_Rpb2_6; 1. |
| Pfam; PF04560; RNA_pol_Rpb2_6; 1. |
| PROSITE; PS01166; RNA_POL_BETA; 1. |
| PROSITE; PS01166; RNA_POL_BETA; 1. |
| Transferase; Transcription; DNA-directed RNA polymerase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58 A -> R (IN REF. 2).
71 C -> S (IN REF. 2).
91 A -> R (IN REF. 2).
155915 MW; AB7467C305028EB5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 LWAAQRYG--RELRRM----SDEFEGSFKGLK 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        453 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                           SEQUENCE OF 338-1031 FROM N.A. MEDLINE=96084944; PubMed=7489896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AL139075; CAB75116.1; -. EMBL; X77304; CAA54509.1; -. PIR, A81393; A81393. PIR; S41868; S41868. HSSP; Q9KWU7; 1HQM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pseudomonadaceae; Pseudomonas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                558
671
691
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1378 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                     SUBSTRATES
                                                                                                                                                                                                                                                                                                                                                                  [RNA](N).
                                                                                                                                                                                                                                             ! - FUNCTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RMUC_PSEAE
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RMUC_PSEAE
LD RMUC_PSEAE
LD RMUC_S014U_S
DT 28-FEB
DT 28
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NAMES OF THE PROPERTY OF THE P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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         Kowalik D.J., Lagrou M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-ATCC 1216B;
MEDLINE=91061774; PubMed=1701021;
Casale W.L., McConnell D.G., Wang S.-Y., Lee Y.-J., Linz J.E.;
"Expression of a gene family in the dimorphic fungus Mucor racemosus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M. Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.B.W., Lory S., Olson M.V., "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: BELONGS TO THE SMALL GTPASE SUPERFAMILY. RAS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            which exhibits striking similarity to human ras genes.";
Mol. Cell. Biol. 10:6654-6663(1990).
-!- ENZYME REGULATION: ALTERNATE BETWEEN AN INACTIVE FORM BOUND TO AND AN ACTIVE FORM BOUND TO GTP. ACTIVATED BY A GUANINE NUCLEOTIDE-EXCHANGE FACTOR (GEF) AND INACTIVATED BY A GTPASE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Plasma membrane.
DEVELOPMENTAL STAGE: IN SPORULATING MYCELIUM AND MUCH LESS IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rhizomucor racemosus (Mucor circinelloides f. lusitanicus).
Eukaryota, Fungi, Zygomycota, Zygomycetes, Mucorales, Mucoraceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .,
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                                                                                                                                                                                                        DB 1; Length 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1E7EA97E82EC5E4B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA recombination; Coiled coil; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               205 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 WAAQRYGR--ELRRMSDE 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ||::| || ||||::|
65 WASERQGREEELRRLASE 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE004535; AAG04420.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51539 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; E83517; E83517.
InterPro; IPR003798; DUF195.
Pfam; PF02646; RmuC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACTIVATING PROTEIN (GAP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best_Local Similarity 55.6
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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453 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ras-like protein 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN-MSB8 / DSM 3109;

MEDLINE-99287316; PubMed-10360571;

MEDLINE-99287316; PubMed-10360571;

Melson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,

Melson K.E., Utterback T.R., Malek J.R., Linher K.D., Garrett M.M.,

Mechanid L., Utterback T.R., Malek J.R., Linher K.D., Garrett M.M.,

Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,

Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,

Ralzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;

"Byidence for lateral gene transfer between Archaea and Bacteria from genome sequence of Thermotoga maritima.";

Nature 399:323-329(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PATHWAY: Pentose phosphate pathway; second step. SIMILARITY: BELONGS TO THE GLUCOSAMINE/GALACTOSAMINE-6-PHOSPHATE ISOMERASE FAMILY. 6-PHOSPHOGLUCONOLACTONASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- CATALYTIC ACTIVITY: 6-phospho-D-glucono-1,5-lactone + H(2)0 = 6-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
NCBI_TaxID=2336;
                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                   GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
EFFECTOR REGION (PROBABLE).
FARNESYL (BY SIMILARITY).
W; DBF086466F090F50 CRC64;
                                                                                                                                                                                                                                                                                                                        DB 1; Length 205; 6.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- FUNCTION: HYDROLYSIS OF 6-PHOSPHOGLUCONOLACTONE TO 6-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
6-phosphogluconolactonase (EC 3.1.1.31) (6PGL)
PGL OR DEVB OR TM1154.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 220 AA.
                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                         Score 48;
Pred. No. 6
                                                                                                                                  PRINTS; PR00449; RASTRNSFRANG.
SMART; SM00173; RAS; 1.
TIGRFAMS; TIGR00231; small_GTP; 1.
GTP-binding; Prenylation; Lipoprotein.
                                                              InterPro; IPR003577; GIPase_Ras.
InterPro; IPR001806; Ras_trnsfrmng.
InterPro; IPR005225; Small_GTP.
Pfam; PF00071; ras; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR006148; Gluc_gal_isom
                                                                                                                                                                                                                                                                                                                                                         5;
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                                                                                                                                                                                                                                                                                        205 AA; 23408 MW;
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168 REIRRMNKEQEGRSKG 183
                                                                                                                                                                                                                                                                                                                         32.4%;
62.5%;
               EMBL; M55177; AAA83379.1; -. PIR; C36365; C36365.
                                                                                                                                                                                                                                                                                                                                                                                           11 RELRRASDEFEGSFKG 26
                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 62.5
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             phospho-D-gluconate.
                                                                                                                                                                                                       23
67
125
46
202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thermotoga maritima.
                                                    HSSP; P01112; 1PLL
                                                                                                                                                                                                                       63
122
38
202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6PGL_THEMA
                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                        NP_BIND
NP_BIND
                                                                                                                                                                                                     NP_BIND
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                                                                                                                                                                                                                                                          DOMAIN
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6PGL_THEMA
                                                                                                                                                                                                                                                                         LIPID
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DR InterPro; IPR005900; Phosphogluconlac.

DR Pfam; PF01182; Glucosamine_iso; 1.

DR TIGRPAMS; TIGR01198; pg1; 1.

KW Hydrolase; Complete proteome.

SQ SEQUENCE 220 AA; 25325 WW; 9B0FD07EE01E60C3 CRC64;

Query Match

Best Local Similarity 34.8%; Pred. No. 6.8;

Matches 8; Conservative 8; Mismatches 7; Indels 0; Gaps

QY 5 AAQRYGRELRRWSDEFGSFKGL 27

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Db 111 ACEKYEREIRSATDQFDLAILGM 133
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Search completed: September 15, 2003, 17:23:01 Job time : 6.6 secs

protein

on:

Run MO

Sequence:

Title:

Searched:

Database

menziesia m

062981 062971 047168 062988 062973 062992

Q8hspl r Q8hsp0 r Q8hsn9 r Q8hsn8 r Q8hsn8 r

rhododendro rhododendro rhododendro rhododendro rhododendro rhododendro rhododendro menziesia p rhododendro rhododendro ledum palus rhododendro rhododendro

047173

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062993
                                062983
062980
062981
                                               062977
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047175
                                                                               Q8HSP1
Q8HSP0
Q8HSN9
Q8HSN8
Q8HSN8
                                                                                                         Q8HSN6
Q8HSN5
                                                                                                                    Q8HSN4
062985
                                                                                                                               062986
062979
047153
047160
Q8HSP4
                                                          062988
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 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                 Similarity
16;
Query Match
Best Local 3
                                                                                                                                                                                                   0919N2;
                                                                                                                                                                                              Q919N2
                                                                                                                                                                                                                                                                                                                                  Best Loc
Matches
                                                                                                                                                                                    RESULT 1
 0919N2
                                                                                                                                                                                               QY
                                                                                                                                                                                                                                                                                                           Q919D2 brachydanio
Q8zy71 pyrobaculum
Q8vjs3 mycobacteri
Q10843 mycobacteri
Q8k016 mus musculu
                                                                                                                                                                                                                                                                                                                                      047148 menziesia c
047149 rhododendro
047171 rhododendro
063960 rhododendro
062975 rhododendro
062972 rhododendro
062978 rhododendro
062978 rhododendro
062978 rhododendro
067978 rhododendro
047155 rhododendro
                                         (without alignments)
237.680 Million cell updates/sec
                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                    ; Search time 30.4 Seconds
                                                                                                                                                                                                                                                                                                  Description
                                                                                                         830525
    GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                        Total number of hits satisfying chosen parameters:
                                                                    28
                                                                                              830525 segs, 258052604 residues
                                                                   1 KNLWAAQRYGRELRRMSDEFEGSFKGLK
                                                                                                                                                                                                                                                                                 SUMMARIES
                                    September 15, 2003, 17:17:31
                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                         protein search, using sw model
                                                                                                                                                                                                                                                                                                           Q919N2
Q8ZY71
Q8VJS3
Q10843
Q10843
Q8K016
O47148
O47171
O62996
O62975
O62975
                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                  sp_unclassified:*
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sp_mammal:*
sp_mhc:*
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sp_bacteria:*
sp_fungi:*
sp_human:*
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                                                                                                                   Minimum DB seq length: 0 Maximum DB seq length: 2000000000
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sp_rodent:*
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Match 1
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rhododendro rhododendro

28hsp4

ALIGNMENTS

08hsn6 Q8hsn5

0 [1]
SEQUENCE FROM N.A.
MEDLINE-20373792; PubMed=10917738;
Inohara N., Nunez G.;
"Genes with homology to mammalian apoptosis regulators identified in Brachydanio rerio (Zebrafish) (Danio rerio). Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio. Gaps ò Length 146; Indels zebrafish."; Cell Death Differ. 7:509-510(2000). EMBL; AR231017; AAF66962.2; -. HSSP; 092934; 165J. ZEIN; ZDB-GENE-000616-1; bad. SEQUENCE 146 AA; 16546 MW; 28A5650BB5107ECB CRC64; Last sequence update)
Last annotation update) Score 91; DB 13; Pred. No. 2.1e-05; 5; Mismatches 4; 471 AA. 146 AA |||||::||::|||||||||: LWAAKKYGQQLRRMSDEFDKGMKRVK 114 3 LWAAQRYGRELRRMSDEFEGSFKGLK 28 Created) PRT; PRT; . 9 61.5%; ilarity 61.5%; Conservative (PRELIMINARY; 89 Q8ZY71 Q8ZY71; RESULT 2 Q8ZY7. ID AC Op

062989 062978 047155 047152

Result No.

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Query Match
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Q8K016;
                                    Q10843
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Matches
             RESULT 4
Q10843
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Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Feterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
Bishai W.;
"Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                         Miller J.H.; "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum aerophilum.";
                                                                                                                                                      Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
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Corynebacterineae, Mycobacteriaceae, Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35.8%; Score 53; DB 16; Length 196; 58.8%; Pred. No. 10; cive 1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                        38.5%; Score 57; DB 17; Length 471; 44.0%; Pred. No. 7; tive 3; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AE007058; AAK46348.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF02371; Transposase_20; 1.
SEQUENCE 196 AA; 21349 MW; C145A8D836FD9C2D CRC64;
                                                                                                                                                                                                                                                                      Hypothetical protein; Complete proteome.
SEQUENCE 471 AA; 52952 MW; 3B1E36E8AEEZEFOA CRC64;
                                                         Pyrobaculum aerophilum.
Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
Thermoproteaceae; Pyrobaculum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
01-MAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein PAE0922.
                                                                                                                                                                                               ENCC. Natl. Acad. Sci. U.S.A. 99:984-989 (2002).

EMBL, AE009793; AAL63125.1; -.

InterPro; IPR000638; Elp3.

InterPro; IPR000182; GCNSacetyltransf.

Pfam; PF00583; Acetyltransf; 1.

SMART; SM00729; Elp3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                        196 AA.
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                                                                                                                  SEQUENCE FROM N.A.
STRAIN=IM2 / ATCC 51768 / DSM 7523;
PubMed=11792869;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                 11; Conservative
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Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                      Best Local Similarity
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                                                                                              NCBI_TaxID=13773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=1773;
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MEDLINE—98295987; PubMed=9634230; MEDLINE—98295987; PubMed=9634230; Garnier T., Churcher C., Harris D., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devies R., Hollingworth T., Connor R., Hornsby T., Jagels K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; Pociphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                               Mycobacterium tuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC034341; AAH34341.1; -.
MGD; MGI:96619; Itih2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPRO06587; VIT.
InterPro; IPRO02035; VWF_A.
SMART; SM00307; VWF; 1.
PROSITE; PS50277; VWF; 1.
PROSITE; PS50234; VWFs; 1.
SEQUENCE 946 AA; 105945 WW; 8B17DBA71B85BC5C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF02371; Transposase 20; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 223 AA; 24132 MW; 70456750017FEF37 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Inter-alpha trypsin inhibitor, heavy chain 2.
                                                      01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complete genome sequence.";
Nature 393:537-544(1998).
-!- SIMILARITY: TO M.PARATUBERCULOSIS IS900.
EMBL; Z74025; CAA98415.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          946 AA
223 AA
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Mismatches
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Interpro; IPR003346; Transposase_20.
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PRT;
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                                                                                                                                                Hypothetical protein Rv2014. RV2014 or MTCX39.03C.
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PRELIMINARY;
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hes 10; Conserv
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SEQUENCE FROM N.A.
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MATK OR YCF14. Rhododendron tashiroi, and
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chloroplast,
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-!- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,
AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY
MITOCHONDRIAL INTRONS.
EMBL, U61331, AAC15245.2, .
Interpro, IPR000442; Intron_maturse2.
Interpro, IPR002866; Matk.N.
Pfam; PF01348; Intron_maturas2; 1.
                             Gaps
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                                                                                                                                                                                                                                                                                Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; Ericales; Ericaceae; Ericoideae; Rhodoreae; Menziesia.
NCBI_TaxID=49154;
                                                                                                                                                                                                                                                                                                                                                                                     "Phylogenetics of Rhododendroideae (Ericaceae).";
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Phylogenetics of Rhododendroideae (Ericaceae).";
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
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                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Ribosomal maturase (Intron maturase) (Maturase K) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 8; Length 505;
Length 946;
                             12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EE5F927AD2E57DE5 CRC64;
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Ribosomal maturase (Intron maturase) (Maturase K).
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                                                                                                                                                         505 AA.
 DB
58;
                             5; Mismatches
Score 53;
Pred. No. 5
                                                                                   212 NVWIMEPOGMRFLHVPDTFEGHFOGV 237
                                                        2 NLWAAQRYGRELRRMSDEFEGSFKGL 27
                                                                                                                                                                                   01-JUN-1998 (TrEMBLrel. 06, Created)
01-MAY-2000 (TrEMBLrel. 13, Last seq
01-OCT-2002 (TrEMBLrel. 22, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          505 AA; 60233 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mRNA processing; Chloroplast.
NON_TER 1 1
SEQUENCE 505 AA; 60233 MW;
35.8%;
34.6%;
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Best Local Similarity 37.55
Matches 12; Conservative
                             9; Conservative
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                                                                                                                                                                                                                                                            Menziesia ciliicalyx.
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                         Chloroplast
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047148
ID 04714
                             Matches
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SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS, AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY MITOCHONDRIAL INTRONS.
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-!- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,

AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED

MITOCHONDRIAL INTRONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Phylogenetics of Rhododendroideae (Ericaceae).";
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7;
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Pfam; PF01824; Matk_N; 1.
mRNA processing; Chloroplast.
SEQUENCE 506 AA; 60485 MW; 8A6353BFC5F4DC85 CRC64;
                                                                                                                                                                                                                                0009EA88CD28549F CRC64;
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Ribosomal maturase (Intron maturase) (Maturase K).
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Ribosomal maturase (Intron maturase) (Maturase K).
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Pred. No. 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Mismatches
                                                                                                                                                                                                                                                                                 Score 52.5; 1
Pred. No. 34;
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InterPro; IPR000442; Intron_maturse2.
InterPro; IPR002866; MatK_N.
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InterPro; IPR000442; Intron_maturse2.
InterPro; IPR002866; MatK_N.
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                                                                                                                                                                                                                                                                                                           Pred.
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37.5%;
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Chloroplast.
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062975
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                                                                                                                                    ALLEALLY I., WILLE W., NODEYASDI N., HANDE T., TEKAYANGJI K.,
YUKAWA T.,
YUDAWA T.,
J. JPD. BOT. 0:0-0(1998).
-!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
INTRONS (BY SIMILARITY).
-!- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,
AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCOPED BY
MITOCHONDRIAL INTRONS.
EMBL, AB012749; BAA25806.1; -
INTERPRO; IPR001442; INTRON_MATURASE.
INTERPRO; IPR001442; INTRON_MATURASE.
INTERPRO; IPR001442; INTRON_MATURASE.
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-!- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,
AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED
MITOCHONDRIAL INTRONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; Eticales; Ericadeae; Ericadeae; Rhodoreae; Rhododendron.NCBI_TaxID=75577;
                            Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Asteridae, Ericales, Ericaceae, Ericoideae, Rhodoreae, Rhododendron.NCBI_TaxID=75582, 75580;
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J. Jpn. Bot. 0:0-0(1998).
-!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
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                                                                                                             SEQUENCE FROM N.A.
Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 8; Length 506;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi
Yukawa T.,
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Last annotation update)
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37.5%; Pred. No. 34;
live 5; Mismatches
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InterPro; IPR000442; Intron_maturse2.
InterPro; IPR002866; MatK.N.
Pfam; PF01348; Intron_maturas2; 1.
Pfam; PF01824; MatK.N. 1.
mRNA processing; Chloroplast.
SEQUENCE 506 AA; 60419 MW; IF95132CA
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Best Local Similarity 37.5
Matches 12; Conservative
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Rhododendron farrerae.
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Best Local Similarity
Matches 12; Conserv
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Gaps
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-!- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,
AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED
MITOCHONDRIAL INTRONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudlcotyledons; core eudicots; Asteridae; Ericales; Ericaceae; Ericoldeae; Rhodoreae; Rhododendron. NCBI_TaxID=49628;
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J. Jpn. Bot. 0:0-0(1998).
-!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
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J. Jpn. Bot. 0:0-0(1998).
-!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
INTRONS (BY SIMILARITY).
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SEQUENCE FROM N.A.
Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi
Vnkawa T.,
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Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi
Yukawa T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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Last annotation update)
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Ribosomal maturase (Intron maturase) (Maturase K).
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                                     391 KPVWAALSDSDIIERFGRIYRNLSHYYSGSLK 422
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37.5%; Pred. No. 34;
ive 5; Mismatches
1 KNLWAA------QRYGRELRRMSDEFEGSFK
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InterPro; IPR000442; Intron_maturse2.
InterPro; IPR002866; MatK.N.
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01-AUG-1998 (TrEMBLrel. 07, Last seq
01-OCT-2002 (TrEMBLrel. 22, Last anno
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01-AUG-1998 (TrEMBLrel. 07, Last seq
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Matches 12; Conservative
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INTRONS (BY SIMILARITY).
-!- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,
AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY
MITOCHONDRIAL INTRONS.
                                                                       Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; - Asteridae; Ericales; Ericaceae; Ericoideae; Rhodoreae; Rhododendron.
                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                            Rhododendron(Ericaceae) based on matK Sequences.";
J. Jpn. Bot. 0:0-0(1998).
-!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
                                                                                                                         SEQUENCE FROM N.A.
Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
Yukawa T.,
Yukawa T.,
                                                                                                                                                                                                                                                                                                                                                                                                                        mRNA processing, Chloroplast.
SEQUENCE 506 AA; 60350 MW; 5E832589ED64EA25 CRC64;
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37.5%; Pred. No. 5.,
'.. 5; Mismatches
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InterPro; IPR000442; Intron_maturse2.
InterPro; IPR002866; MatK_N.
                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF01348; Intron_maturas2; 1. Pfam; PF01824; MatK_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INTRONS (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rhododendron hongkongense.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                     Rhododendron canadense.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
les 12; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                         NCBI_TaxID=49465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kron K.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                     QΫ
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H
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-!- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,
AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY
MITOCHONDRIAL INTRONS.
                                   BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                   Gaps
SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS, AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED MITOCHONDRIAL INTRONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; Ericales; Ericaceae; Ericoideae; Rhodoreae; Rhododendron.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Jpn. Bot. 0:0-0(1998).
-!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
                                                                                                                                                                                                                                                7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35.5%; Score 52.5; DB 8; Length 506; 37.5%; Pred. No. 34; Live 5; Mismatches 8; Indels
                                                                                                                                                                                                          Length 506;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.
Yukawa T.;
                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Investigation of Sectional Relationships in the Genus Rhododendron(Ericaceae) based on matX Sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sing; Chloroplast.
506 AA; 60489 MW; 6D38AlD4D6FEC9BF CRC64;
                                                                                                                                                                          506 AA; 60493 MW; D230E54B8C20FEF0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Ribosomal maturase (Intron maturase) (Maturase K).
MATK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-1998 (TrEMBLrel. 07, Last sequence update) 01-OCT-2002 (TrEMBLrel. 22, Last annotation update) Ribosomal maturase (Intron maturase) (Maturase K).
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                                                                                                                                                                                                              DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | :||| :||| | 391 KPVWAALSDSDIIERFGRIYRNISHYYSGSLK 422
                                                                                                                                                                                                                                                                                                                  391 KPVWAALSDSDIIERFGRIYRNLSHYYSGSLK 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 KNLWAA-----QRYGRELRRMSDEFEGSFK 25
                                                                                                                                                                                                                                                                                  1 KNLWAA-----QRYGRELRRMSDEFEGSFK 25
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                                                                                                                                                                                                          35.5%; Score 52.5; D
37.5%; Pred. No. 34;
tive 5; Mismatches
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Interpro; IPR000442; Intron_maturse2.
Interpro; IPR000866; MatK_N.
Pfam; PF01348; Intron_maturas2; 1.
Pfam; PF01824; MatK_N, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                         07, Created)
07, Last sequ
22, Last anno
                                                                  EMBL; AB012729; BAA25850.1; -.
InterPro; IPR000442; Intron_maturse2.
InterPro; IPR002866; MatK_N.
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                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                   Pfam: PF01348; Intron_maturas2; 1. Pfam; PF01824; Matk_N; 1. mRNA processing; Chloroplast.
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Best Local Similarity 37.59
Matches 12; Conservative
                                                                                                                                                                                                                                              12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1998 (TrEMBLrel. 01-OCT-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rhododendron indicum
                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=75581;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA processing;
SEQUENCE 506 A2
                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chloroplast.
                                                                                                                                                                             SEQUENCE
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062989
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Gaps

7;

. 8

8; Length 506; Indels

DB

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-!- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS, AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY MITOCHONDRIAL INTRONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; Ericales; Ericaceae; Ericoideae; Rhodoreae; Rhododendron. NCBI_TaxID=49165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Phylogenetics of Rhododendroideae (Ericaceae).";
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8; Length 506;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, 061338, ABB93751.1; -
InterPro; IPR000442; Intron_maturse2.
InterPro; IPR002866; Matk_N.
Pfam; PF01348; Intron_maturas2; 1.
Pfam; PF01824; Matk_N: 1.
mRNA processing; Chloroplast.
SEQUENCE 506 AA; 60406 MW; 4B5C675CE32218D8 CRC64;
                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                  Ribosomal maturase (Intron maturase) (Maturase K)
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506 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35.5%; Score 52.5; 37.5%; Pred. No. 34;
                                                    01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequ
01-OCT-2002 (TrEMBLrel. 22, Last anno
PRT;
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g

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GERFFE

Dp

Search completed: September 15, 2003, 17:25:50 Job time : 31.4 secs

OM protein - protein search, using sw model

September 15, 2003, 17:16:01 ; Search time 38.1857 Seconds
(without alignments)
112.231 Million cell updates/sec Run on:

US-09-544-664-56

143 1 KNLWAAQRYGRELRRMSDEFEGSFKGL (77) Perfect score: Sequence: Title:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1107863 segs, 158726573 residues Searched:

1107863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_19Jun03:*

| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
| SIDSI/gcgdata/geneseqy/geneseqp-embl/AA1981.DAT:*
| SIDSI/gcgdata/geneseqy/geneseqp-embl/AA1982.DAT:*
| SIDSI/gcgdata/geneseqy/geneseqp-embl/AA1984.DAT:*
| SIDSI/gcgdata/geneseqy/geneseqp-embl/AA1986.DAT:*
| SIDSI/gcgdata/geneseqy/geneseqp-embl/AA1986.DAT:*
| SIDSI/gcgdata/geneseqy/geneseqp-embl/AA1989.DAT:*
| SIDSI/gcgdata/geneseqy/geneseqp-embl/AA1989.DAT:*
| SIDSI/gcgdata/geneseqy/geneseqp-embl/AA1989.DAT:*
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| SIDSI/gcgdata/geneseqy/geneseqp-embl/AA1991.DAT:*
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| SIDSI/gcgdata/geneseqy/geneseqp-embl/AA1995.DAT:*
| SIDSI/gcgdata/geneseqy/geneseqp-embl/AA1997.DAT:*
| SIDSI/gcgdata/geneseqy/geneseqqp-embl/AA1997.DAT:*
| SIDSI/gcgdata/geneseqy/geneseqqp-embl/AA1997.DAT:*
| SIDSI/gcgdata/geneseqy/geneseqqp-embl/AA1997.DA

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. /SIDS1/gogdata/geneseg/genesegr-emb1/AA2001.DAT:*/SIDS1/gogdata/geneseg/genesegp-emb1/AA2002.DAT:*/SIDS1/gogdata/geneseg/genesegp-emb1/AA2003.DAT:*

SUMMARIES

Description	BC12 polypeptide B	Bcl2 polypeptide B	Bcl2 polypeptide B	Bcl2 polypeptide B	Bcl2 polypeptide B	Shorter murine BAD	bcl-x(L)/bcl-2 ass	Murine BCL-XL/BCL-	Mutant BCL-XL/BCL-
ID	AAB37056	AAB37055	AAB37001	AAB37002	AAB37003	AAB70370	AAR95168	AAW61315	AAW61316
DB	21	21	21	21	21	22	17	19	19
% Query Match Length DB	3		26					204	. ,
% Query Match	100.0	100.0	96.5	96.5	96.5	96.5	96.5	96.5	96.5
Score	143		138	138	138	138	138	138	138
Result No.	1	7	ന	4	n	Ø	7	00	Q
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204 19 AAW61317 204 19 AAW61318 204 22 AAW58832 204 24 ABK39082 204 24 ABK39082 24 23 AAU78620 25 23 ABG78493 25 23 ABG78493 25 23 ABG78493 25 23 ABG78493 26 23 AAU78610 27 24 AAB73779 168 22 AAB73779 168 22 AAB7620 29 23 AAG78490 20 23 AAG78490 25 23 AAG78490 25 23 AAG78490 25 23 AAG78490 25 23 AAG78615 25 23 AAG78615 25 23 AAG78616 25 23 AAG78612	Mutant BCL-XL/BCL-	- 1	Murine BAD protein	Longer murine BAD	Murine BAD protein	Bad-DTTR apoptosis	n Bad pe	PTPC-interacting T	Mutant Bc12 compet	t Bcl2	Human Bad peptide	Bad	n for		Human cell prolife	Human BAD mutant a		Amino acid sequenc	prot	Human ovarian anti	r) /p	Mutant Bc12 compet	Human Bad peptide	Mutant Bc12 compet	Mutant Bc12 compet	24		Bad 1		t Bcl2	212	d pe	ฑ	พ	`~i	d pep
44444444444444444444444444444444444444	51	5131	5883	7036	908)22	362	516	348	349	361	362	247	577	351	336	28	89	908	163	516	849	861	848	848	861	861	862	48	49	349	361	361	362	348	7861
	04 1	04 1	04 1	04 2	04 2	67 2	C1	a	CI	N	N	7	66 1	68 1	68 2	68 2	68 2	68 2	68 2	01 2	1	CA	CA	CA.	Ø	(A	C/I	(A	(A	(4	(4	(1	14	14	(4	
	3	$^{\circ}$	3	ന	$^{\circ}$	$^{\circ}$	\vdash	\leftarrow	П	-	\vdash	$\overline{}$	М		Н	\vdash	Н	114	114	114	113	111	111	110	110	110	110	109	109	109	109	109	109	109	108	108
	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

AAB37056 standard; peptide; 27 AA RESULT 1 AAB37056

AAB37056;

(first entry) 28-FEB-2001

Bcl2 polypeptide BH3 domain peptide #56.

Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective; cardiant; Bc1-2 superfamily; BH3 domain; cell death agonist; Bad; apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate; colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma; melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS; stroke; myocardial infarction.

Homo sapiens

WO200059526-Al.

12-OCT-2000

06-APR-2000; 2000WO-US09352.

99US-0128202. 07-APR-1999;

Lu 2; Huang Z, Wang J, Zhang Z, Shan S, (UYJE-) UNIV JEFFERSON THOMAS

WPI; 2000-679325/66.

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The invention relates to a peptide conjugate having the formula:

(R-Xin-peptide where n = 1-10; X = C=0, when the R-X group is attached

to the N-terminus of the peptide, or a side chain of the peptide where

the functional group of the side chain is NH2 or OH; or X = O or NH,

when the R-X group is attached to the C-terminus of the peptide, or a

side chain of the peptide, where the side chain functional group is COOH

COONH2; and R = 2-18C alkyl or alkoxy, 2-14C alkylenyl containing one

or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally

monosubstituted with a 1-5C straight or branched chain alkyl group,

phenyl optionally monosubstituted with a 1-5C straight or branched chain

alkyl group, or benzyl. The peptides ABB37001-B37058 represent analogues

of the peptide portion of the conjugate. The peptides represent analogues

of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of

the DH3 domain of the cell death agonist Bad. The peptide conjugate is

cuseful for modulating apoptosis in the cells of a subject, or for

reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of

subject affilicted with a cancer characterized by cancer cells that

cushiect affilicted with a cancer characterized by cancer cells that

custue or chronic lymphocytic and non-lymphocytic leukemia. The peptide

conjugate is also useful for treating disorders, acquired

increased apoptosis, e.g. neurodegenerative disorders, acquired

immunodeficiency syndrome (AIDS), stroke or myocardial infarction.
                  New peptide conjugates for modulating apoptosis or for inhibiting cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for treating neurodegenerative disorders, stroke, or cancer
                                                                                                                      Claim 18; Page 19; 74pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  stroke; myocardial infarction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB37055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 2
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0;
                            Gaps
                                                                                                                                                                                                                                                    Cytostatic, neuroprotective; anti-HIV; virucide; cerebroprotective; cardiant, Bcl-2 superfamily; BH3 domain; cell death agonist; Bad; apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate; colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma; melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;
                            .;
0
  Length 27;
                            Indels
Score 143; DB 21;
Pred. No. 7.3e-15;
0; Mismatches 0;
                                                                                                                                                                                                                             Bcl2 polypeptide BH3 domain peptide #55.
                                                      1 KNLWAAQRYGRELRRMSDEFEGSFKGL 27
                                                                              KNLWAAORYGRELRRMSDEFEGSFKGL 27
                                                                                                                                               AAB37055 standard; peptide; 28 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYJE-) UNIV JEFFERSON THOMAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0128202.
                                                                                                                                                                                                                                                                                                                                                                                                                                 06-APR-2000; 2000WO-US09352.
                                                                                                                                                                                                                                                                                                                                                                           WO200059526-A1
                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                       12-OCT-2000.
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The invention relates to a peptide conjugate having the formula:

(R-X)n-peptide where n = 1-10; X = C=O, when the R-X group is attached to the V-terminus of the peptide, or a side chain of the peptide where the lunctional group is tatached to the C-terminus of the peptide where the side chain of the peptide, or a side chain of the peptide, or a side chain functional group is attached to the C-terminus of the peptide, or a side chain functional group is attached to the C-terminus of the peptide, or a side chain functional group is COH CONHE; and R = 2-18C alkyl or alkoxy, 2-14C alkylenyl containing one or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally companies and the alikyl group, or benzyl. The peptides ABB37001-B37058 represent examples of the peptide portion of the conjugate. The peptides confuse confuse confuse confuse is a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of the BH3 domain of the cell death agonist Bad. The peptide conjugate is useful for modulating apoptosis in the cells of a subject, or for reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of unction. In particular, the peptide conjugate is useful for treating a cubject afflicted with a cancer characterized by cancer cells that concerning an orest characterized by cancer cells that concerning allows, remalor thymphocytic and non-lymphocytic leukemia. The peptide conjugate is also useful for treating disorders characterized by increased apoptosis, e.g. neurodegenerative disorders, acquired immunodeficiency syndrome (AIDS), stroke or myocardial infarction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                            or for inhibiting
                                                                                             cell lymphoma/leukemia 2 (BC1-2) function, especially useful for treating neurodegenerative disorders, stroke, or cancer
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100.0%; Pred. No. 7.6e-15;
ive 0; Mismatches 0;
                                                                                apoptosis
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                                                                            New peptide conjugates for modulating
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     တွဲ
   Shan
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                                                                                                                                                        Claim 18; Page 19; 74pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       stroke; myocardial infarction
Ζ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-APR-2000; 2000WO-US09352.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 100.
   Zhang
                                     WPI; 2000-679325/66.
     Wang J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28 AA;
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     Ζ,
       Huang
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Matches
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06-APR-2000; 2000WO-US09352.
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                                                                                                                       Huang Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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Matches
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(R-X)n-peptide where n = 1-10; X = C=0, when the R-X group is attached

to the N-terminus of the peptide, or a side chain of the peptide where

the functional group of the side chain is NH2 or X = O or NH,

when the R-X group is attached to the C-terminus of the peptide, or a

side chain of the peptide, where the side chain functional group is

con CONH2; and R = 2-18C alkyl or alkoxy, 2-14C alkylenyl containing one

or two double bonds, cycloburyl, cyclopentyl, cyclohexyl optionally

monosubstituted with a 1-5C straight or branched chain alkyl group,

phenyl optionally monosubstituted with a 1-5C straight or branched chain

alkyl group, or benzyl. The peptides AbB37001-B3708 represent examples

of the peptide portion of the conjugate. The peptides represent analogues

of the BB1-2 superfamily polypeptide corresponding to amino acids 72-97 of

the BH3 domain of the cell death agonist Bad. The peptide conjugate is

cuseful for modulating apoptosis in the cells of a subject, or for

reversing B cell lymphoma/leukemia 2 (Bc1-2)-mediated blockage of

apoptosis in cancer cells. It is also useful for inhibiting Bc1-2

cuboct afflicted with a cancer characterized by cancer cells that

express Bc1-2. The cancer includes prostate, colorectal, gastric,

consider a simple or thyroid cancers, neuroblastoma, melanoma, or
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                                                                                                                                  New peptide conjugates for modulating apoptosis or for inhibiting
                                                                                                                                                      cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for treating neurodegenerative disorders, stroke, or cancer
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Pred. No..4.1e-14;
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                                                          Shan S,
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                                                                                                                                                                                                               Claim 18; Page 17; 74pp; English.
                  (UYJE-) UNIV JEFFERSON THOMAS.
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                                                          Wang J, Zhang Z,
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Best Local Similarity 100.0
Watches 26; Conservative
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                                                                                             WPI; 2000-679325/66
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                                                       Huang Z,
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The invention relates to a peptide conjugate having the formula:

(R-X)1-peptide where n = 1-10; X = C=0, when the R-X group is attached to the N-terminus of the peptide, or a side chain of the peptide where the side chain of the peptide where the side chain of the peptide, or a side chain of the peptide, where the side chain functional group is conside chain of the peptide, where the side chain functional group is COOH or CONH3; and R = 2-18C alkyl or alkoxy, 2-14C alkylenyl containing one or CONH3; and R = 2-18C alkyl or alkoxy, 2-14C alkylenyl containing one or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally monosubstituted with a 1-5C straight or branched chain alkyl group, or benzyl. The peptides ARB3701-B37058 represent examples of the peptide portion of the conjugate. The peptides represent analogues of the BH3 domain of the conjugate. The peptides represent analogues of the BH3 domain of the conjugate. The peptides conjugate is useful for modulating apoptosis in the cells of a subject, or for eversing B cell lymphoma/leukemia 2 (BCI-2)-mediated blockage of apoptosis in cancer cells. It is also useful for inhibiting BcI-2 function. In particular, the peptide conjugate is useful for treating a conjugate is that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         express Bcl-2. The cancer includes prostate, colorectal, gastric, non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide conjugate is also useful for treating disorders characterized by
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                                                                                                                                                                                                                                                                                                                                             New peptide conjugates for modulating apoptosis or for inhibiting cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for treating neurodegenerative disorders, stroke, or cancer
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                                                                                                                                                                              Lu Z;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 18; Page 17; 74pp; English.
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                                                                                 (UYJE-) UNIV JEFFERSON THOMAS.
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99US-0128202.
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07-APR-1999;
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(R-X)n-peptide where n = 1-10; X = C=0, when the R-X group is attached to the N-terminus of the peptide, or a side chain of the peptide where the functional group of the side chain is MH2 or OH; or X = O or NH, when the R-X group is attached to the C-terminus of the peptide, or a side chain of the peptide, where the side chain functional group is COOH or two double bonds, cyclobutyl, cyclopentyl, cyclopentyl optionally one or two double bonds, cyclobutyl, cyclopentyl, cyclohearyl optionally consubstituted with a 1-5C straight or branched chain alkyl group, or benzyl. The peptides AAB37001-B37058 represent examples of the peptide portion of the conjugate. The peptide conjugate is alkyl group, or benzyl. The peptides AAB37001-B37058 represent analoques of the BH3 domain of the cell death agonist Bad. The peptide conjugate is useful for modulating apoptosis in the cells of a subject, or for reversing B cell lymphoma/leukemia 2 (Bcl-2) andiated blockage of apoptosis in cancer cells. It is also useful for inhibiting Bol-2 function. In particular, the peptide conjugate is useful for treating a subject afflicted with a cancer characterized by cancer cells that
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         express Bc1-2. The cancer includes prostate, colorectal, gastric, non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide conjugate is also useful for treating disorders characterized by
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es 26; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                              Claim 18; Page 17; 74pp; English.
                                                                                                                                                   (UYJE-) UNIV JEFFERSON THOMAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96.5%;
                                                            06-APR-2000; 2000WO-US09352.
                                                                                                          99US-0128202.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                        WPI; 2000-679325/66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-MAX-2001
                                                                                                          07-APR-1999;
                12-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB70370;
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Matches
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The present invention describes an isolated or synthetic polypeptide

(1) comprising a less than full length amino acid sequence of a mutant

Bcl-XL/Bcl-2 associated cell death regulator polypeptide (BAD) or its

fragment, which contains amino acid substitutions at Serl18 of a human

fragment, which contains amino acid substitutions at Serl18 of a human

EAD, Ser155 of a mutine BAD). (1) has immunostimulant, neuroprotective,

nootropic, antischaemic, vulnerary, cytostatic, antiviral,

antiarthritic, antiniflammatory and immunosuppressive activities, and

can be used as an apoptosis indover or inhibitor. BAD polypeptides and

polynucleotides can be used for screening candidate compounds and drugs

for activity that promote cell survival or apoptosis. Other uses include

inducing or inhibiting apoptosis in a cell. Candidate compounds

identified and (mutant) BAD polypeptides are useful in treating

immunodeficiency diseases, neurodegenerative diseases, ischeemic cell

death, reperfusion cell death, wound healing, cancer, viral infections,

autoimmune diseases. The present sequence represents a specifically

claimed shorter murine BAD mutant amino acid sequence from the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Epitope; murine; bcl-x(L)/bcl-2 associated death promoter; Bad; stroke; polypeptide; bcl-x; cell death; regulate; BH1; BH2; apoptotic cell death; cytokine deprivation; IL-3 dependent cell line; immunodeficiency; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide, useful for screening for candidate compounds which induce or inhibit apoptosis, comprises amino acid substitutions at Serl18, Serl55 or Serl13 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neurodegenerative disease; senescence; ischaemia; neoplasia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bcl-x(L)/bcl-2 associated death promoter protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 7; Page 148-149; 157pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                 (APOP-) APOPTOSIS TECHNOLOGY INC.
                                                                                                                                                                                                                                                                                                                    99US-0136783.
                                                                                                                                                                                                                                   30-MAY-2000; 2000WO-US11864
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Matches 26; Conservative
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                                                                         WO200110888-A1
                                                                                                                                                                                                                                                                                                                    28-MAY-1999;
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Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zhou X;
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N-PSDB; AAV27833
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                                                              17-0CT-1997;
 WO9817682-A1
                                                                                            18-OCT-1996;
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                                30-APR-1998
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Synthetic.
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  This sequence represents the murine bcl-x(L)/bcl-2 associated death promoter (Bad) gene. Bad is a 22.1 kD protein which interacts with bcl-2 and bcl-x proteins and requiates cell death. It has homology to the bcl-2-related family clustered in the BHI and BH2 domain. Bad has been found to hybridise to bcl-x(L) and bcl-2 in yeast two-hybrid assays and in vivo in mammalian cells. Overexpressed Bad counters the death inhibitory activity of bcl-x(L), but is much less effective at countering the death inhibitory activity of bcl-2. Bad expression can accelerate apoptotic cell death induced by cytokine deprivation in an IL-3 dependent cell line expressing bcl-x(L), and its also counters the death repressor activity of bcl-x(L). Bad competes with Bax for binding to bcl-x(L). Bad may be used to identify agents which inhibit its binding to bcl-x(L) to form heterodimers. Such agents may be used to identify agents which inhibit its used to treat neurodegenerative diseases, immunodeficiency diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Murine, mouse, BCL-XL/BCL-2 associated cell death regulator, BAD protein, serine substituted mutant, apoptosis, cancer, viral infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                            Polynucleotide encoding bcl-x(L)/bcl-2 associated death promoter useful to treat neoplasia and apoptosis and to identify agents inhibiting its binding to bcl-2 or bcl-x(L) to form beteromultimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96.5%; Score 138; DB 17; Length 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Murine BCL-XL/BCL-2 associated cell death regulator.
                          /note= "BH1 conserved amino acids"
                                           191..192
/note= "BH2 conserved amino acids"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Pred. No. 4e-
tive 0; Mismatches
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                                                                                          /note= "PEST sequence"
111..130
                                                                                                                         /note= "PEST sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             e.g. AIDS, senescence or ischaemia.
cocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 3; Fig 1; 130pp; English
                                                                                                                                                                                                                     95WO-US14246.
                                                                                                                                                                                                                                                    94US-0333565
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                                                                                                                                                                                                                                                                                   (UNIW ) UNIV WASHINGTON.
                                                                               38..61
                                                                                                                                                                                                                                                                                                                                                WPI; 1996-251465/25.
N-PSDB; AAT29479.
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Matches 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             204 AA;
                                                                                                                                                                                                                                                                                                                   Korsmeyer SJ;
                                                                                                                                                                                                                     31-0CT-1995;
                                                                                                                                                                                                                                                    31-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-0CT-1998
                                                                                                                                                         WO9613614-A1
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                                                Region
                                                                               Domain
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              Region
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AAW61315
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The present invention describes mutant BAD (BCL-XI/BCL-2 associated cell death regulator) proteins, having an amino acid other than Ser at position 112 and/or 136, relative to the murine BAD 204 aa sequence. The position 112 and/or 136, relative to the murine BAD 204 aa sequence. The present sequence is the murine BAD protein. Also described are: (1) fragments of mutant BAD protein able to decrease cell viability; (2) fusion proteins of mutant BAD with a heterologous polypeptide that increases intracellular delivery. Mutant BAD proteins are used to treat or prevent diseases associated with reduced apoptosis, e.g. cancer, viral infection, lymphoproliferation, arthritis, infertility, interangenic animals for use as disease models or in drug screen for enhancers and inhibitors of serine-phosphatase. Inhibitors are potentially useful in treatment of excessive apoptosis such as AIDS, neurodegeneration, determined by measuring relative amounts of phosphorylated and non-phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have greater death-promoting activity than wild-type BAD which can become phosphorylated cannot in the specified Ser, forming a product that does not beterodimerise with BCL-2 or BCL-XL but inscead binds to 14-3-3 family contents in the cytosol, thus promoting cell survival. The mutants with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Murine, mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein; serine substituted mutant; apoptosis; cancer; viral infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New mutant BAD polypeptide with phosphorylatable serine replaced useful for, e.g. treating reduced apoptosis such as in cancer or viral infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Pred. ...
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97WO-US19175
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Korsmeyer SJ;
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                                   17-0CT-1997;
                                                                        18-OCT-1996;
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30-APR-1998.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                         The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell death regulator) proteins, having an amino acid other than Ser at position 112 and/or 136, relative to the mutine BAD 204 as sequence. The presents aguence represents a mutant BAD protein. Also described are: (1) fragments of mutant BAD protein. Also described are: (1) fragments of mutant BAD with a heterologous polypeptide that increases intracellular delivery. Mutant BAD proteins are used to treat or prevent diseases associated with reduced apoptosis, e.g. cancer, viral infection, lymphoproliferation, arthritis, infertility, inflammation and autoimmune disease. Polynucleotide sequences encoding mutant BAD proteins can be used similarly by gene therapy or to produce transgenic animals for use as disease models or in drug screening. BAD proteins phosphorylated at specified Ser are used to screen for enhancers and inhibitors of serine-phosphatase. Inhibitors are potentially useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein; serine substituted mutant; apoptosis; cancer; viral infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in treatment of excessive apoptosis such as AIDS, neurodegeneration, aging or ischaemic cell death. The apoptotic status of cells is determined by measuring relative amounts of phosphorylated and non-phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have phosphorylated on the specified Ser, forming a product that does not heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family proteins in the cytosol, thus promoting cell survival. The mutants with ser substituted cannot bind 14-3-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                            New mutant BAD polypeptide with phosphorylatable serine replaced useful for, e.g. treating reduced apoptosis such as in cancer or viral infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96.5%; Score 138; DB 19; Length 204; 100.0%; Pred. No. 4e-13; tive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mutant BCL-XL/BCL-2 associated cell death regulator #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         140 NLWAAQRYGRELRRMSDEFEGSFKGL 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 NLWAAORYGRELRRMSDEFEGSFKGL 27
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                                                                                                                                                                                                                                                                                                                                          Claim 7; Page 59; 95pp; English.
                                                                                           96US-0733505.
                                                      97WO-US19175.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                (UNIW ) UNIV WASHINGTON
                                                                                                                                                                                                           WPI; 1998-261422/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      204 AA;
                                                                                                                                                                                                                            N-PSDB; AAV27834
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                                                                                                                                                                       Korsmeyer SJ;
                                                      17-0CT-1997;
                                                                                           18-OCT-1996;
                   30-APR-1998
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Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell death regulator) proteins, having an amino acid other than Ser at cath regulator) proteins, having an amino acid other than Ser at position 112 and/or 136, relative to the murine BAD 204 aa sequence. The present sequence represents a mutant BAD protein. Also described are: (1) fragments of mutant BAD protein able to decrease cell viability; (2) fusion proteins of mutant BAD proteins are used to treat or prevent diseases associated with reduced apoptosis, e.g. cancer, or prevent diseases associated with reduced apoptosis, e.g. cancer, or prevent diseases associated with reduced apoptosis, e.g. cancer, or inflammation and autoimmune disease. Polynucleotide sequences encoding mutant BAD proteins can be used similarly by gene therapy or to produce transgenic animals for use as disease models or in drug screening. BAD corteins phosphorylated at specified Ser are used to screen for enhancers and inhibitors of serine-phosphatase. Inhibitors are potentially useful in treatment of excessive apoptosis such as AIDS, neurodegeneration, aging or ischaemic cell death. The apoptotic status of cells is caping or ischaemic cell death. The apoptotic status of cells is greater death-promoting activity than wild-type BAD which can become phosphorylated on the specified Ser, forming a product that does not phosphorylated with BCL-2 or BCL-XI but instead binds to 14-3-3 family proteins in the cytosol, thus promoting cell survival. The mutants with two services are substituted cannot bind 14-3-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                           New mutant BAD polypeptide with phosphorylatable serine replaced useful for, e.g. treating reduced apoptosis such as in cancer or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 138; DB 19; Length 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96.5%; Scc...
100.0%; Pred. No. ...
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 NLWAAQRYGRELRRMSDEFEGSFKGL 27
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97WO-US19175
                                                                                    96US-0733505
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Best Local Similarity 100.
Matches 26; Conservative
                                                                                                                                                                     (UNIW ) UNIV WASHINGTON
                                                                                                                                                                                                                                                                                                                                    WPI; 1998-261422/23.
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                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAV27835
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Mus musculus.
Synthetic.
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                                                                                                                         Korsmeyer SJ;
                                        09-SEP-1997;
                                                                   09-SEP-1996;
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               12-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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  dath regulator) proteins, having a mino acid other than Ser at position 112 and/or 136, relative to the murine BAD 204 as sequence. The position 112 and/or 136, relative to the murine BAD 204 as sequence. The present sequence represents a mutant BAD protein. Also described are: (1) fragments of mutant BAD protein. BAD proteins are used to treat increases intracellular delivery. Mutant BAD proteins are used to treat or prevent diseases associated with reduced apoptosis, e.g. cancer, viral infection, lymphoproliferation, arthritis, infertility, inflammation and autoimmune disease. Polynuclectide sequences encoding mutant BAD proteins as disease. Polynuclectide sequences encoding mutant BAD proteins can be used similarly by gene therapy or to produce transgenic animals for use as disease models or in drug screening. BAD proteins phosphatates. Inhibitors are potentially useful in treatment of excessive apoptosis such as AIDS, neurodegeneration, aging or ischaemic cell death. The apoptotic status of cells is determined by measuring relative amounts of phosphated and non-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                               present invention describes mutant BAD (BCL-XL/BCL-2 associated cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have greater death-promoting activity than wild-type BAD which can become phosphorylated on the specified Ser, forming a product that does not heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family proteins in the cytosol, thus promoting cell survival. The mutants with Ser substituted cannot bind 14-3-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BAD protein; Bcl-XL/Bcl-2 associated cell death regulator; 14-3-3; serine phosphorylation; post-translational modification; apoptosis; signal transduction regulator; phosphoserine phosphatase; senescence; immunodeficiency disease; neurodegenerative disease; infertility; cancer, viral infection; lymphoproliferative condition; arthritis; inflammation; autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                               New mutant BAD polypeptide with phosphorylatable serine replaced useful for, e.g. treating reduced apoptosis such as in cancer or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96.5%; Score 138; DB 19; Length 204; 100.0%; Pred. No. 4e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           140 NLWAAQRYGRELRRMSDEFEGSFKGL 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 NLWAAQRYGRELRRMSDEFEGSFKGL 27
                                                                                                                                                                                                                    Claim 7; Page 60-61; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW58832 standard; protein; 204 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96.0%,
100.0%; Pre-
             97WO-US19175.
                                        960S-0733505
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                   (UNIW ) UNIV WASHINGTON
                                                                                                                        WPI; 1998-261422/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Murine BAD protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            204 AA;
                                                                                                                                     N-PSDB; AAV27836
                                                                                                                                                                                          viral infection
                                                                                             Korsmeyer SJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9809643-A1
             17-OCT-1997;
                                        18-OCT-1996;
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This sequence represents a novel serine-phosphorylated protein, BAD

(Bcl-XI/Bcl-2 associated cell death regulator). The serine residue is
phosporylated in a post-translational modification and allows binding
to the 14-3-3 protein which is a signal transduction regulator.

Modulators of phosphorylated BAD, which act through inhibition/activation
of a phosphoserine phosphatase, are useful for preventing/treating
increased/decreased apoptosis in a cell. The increased apoptosis may
result from immunodeficiency diseases, senescence, neurodegenerative
disease, ischaemic cell death, reperfusion cell death, infertility and
wound-healing. Decreased apoptosis may result from cancer, viral
infection, lymphoprolificative conditions, arthritis, infertility,
inflammation and autoimmune diseases. Measuring the amount of
this mannament of autoimmune diseases. Measuring the amount of
BAD in a cell is useful for determining the apoptotic state of a cell.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                            Serine-phosphorylated Bcl.X-1/Bcl-2 Associated cell Death regulator polypeptide - useful for modulation of apoptosis associated with, e.g. cancer and immunodeficiency diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           140 NIWAAQRYGRELRRMSDEFEGSFKGL 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 NLWAAQRYGRELRRMSDEFEGSFKGL 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB70369 standard; protein; 204 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 3; Fig 8; 61pp; English
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                                                                         96US-0707868.
97WO-US15871
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                                                                                                                                                           (UNIW ) UNIV WASHINGTON.
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WFI; 2001-218343/22.
N-PSDB; AAS00248.
                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
es 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                     204 AA;
N-PSDB; ABZ81201
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Chimeric - C
Chimeric - S
                                                                                                                                                                                                                                                                                                                                                                         Seguence
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
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                                                                                                                                                                                                                            The present invention describes an isolated or synthetic polypeptide

(I) comprising a less than full length amino acid sequence of a mutant

BC1-XL/BC1-2 associated cell death regulator polypeptide (BAD) or its

fragment, which contains amino acid substitutions at Serl18 of a human

C fragment, which contains amino acid substitutions at Serl18 of a mutine

BAD, Ser155 of a mutine BAD). (I) has immunostimulant, neuroprotective,

CC BAD (shorter murine BAD). (I) has immunostimulant, neuroprotective,

CC antiarthritic, antiinflammatory and immunosuppressive activities, and

CC can be used as an apoptosis inducer or inhibitor. BAD polypeptides and

CC polynucleotides can be used for screening candidate compounds and drugs

CC polynucleotides can be used for screening candidate compounds and drugs

CC polynucleotides can be used for screening candidate compounds

inducing or inhibiting apoptosis in a cell. Candidate compounds

cidentified and (mutant) BAD polypeptides are useful in treating

immunodeficiency diseases, neurodegenerative diseases, ischemic cell

cdeath, reperfusion cell death, wound healing, cancer, viral infections,

lymphoproliferative conditions, arthritis, infertility inflammation and

cutoimmune diseases. The present sequence represents a specifically

condimination and sequence represents a specifically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Murine; BAD; herpes simplex virus; HSV; US3; herpes virus; apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                        New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide, useful for screening for candidate compounds which induce or inhibit apoptosis, comprises amino acid substitutions at Serli8, Serl55 or Serl13 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 138; DB 22; Length 204; Pred. No. 4e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96.5%; Scc.
100.0%; Pred. No.
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            140 NLWAAORYGRELRRMSDEFEGSFKGL 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 NEWAAQRYGRELRRMSDEFEGSFKGL
                                                                                                                                                                                                   Claim 4; Page 148; 157pp; English.
               (APOP-) APOPTOSIS TECHNOLOGY INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABR39082 standard; Protein; 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Murine BAD protein SEQ ID NO:4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-JUL-2001; 2001US-308929P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-JUL-2002; 2002WO-US24177.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Roizman B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYCH-) UNIV CHICAGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-248168/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  virucide; infection.
                                                                                 WPI; 2001-138734/14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       204 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2003012049-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-FEB-2003.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                    Zhou X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Loc
Matches
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The present invention describes a method (MI) for inducing apoptosis in a cell infected with herpes simplex virus (HSV), which comprises administering to the cell, a composition having an agent that inhibits phosphorylation of pro-apoptotic polypeptide BAD by HSV US3. Also described is a method (M2) for treating a patient infected with HSV, by administering to the patient, a composition comprising a peptide comprising a sequence of 4-100 continuous amino acids of a 168 residue amino acid sequence (see ABR39081), where the peptide comprises seril2, setil5, or seril5, or their combinations. BAD has viruoide activity. MI is useful for inducing apoptosis in a cell infected with HSV, where the cell is in a human. M2 is useful for treating a patient infected with HSV. The present sequence represents murine BAD, which is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse; Bad-DTTR; apoptosis; cancer; spinal muscular atrophy; diphtheria toxin receptor binding domain; DTR; neoplasm; tumour; hyper-proliferation; Alzheimer's disease; neurodegenerative disorder; transient ischaemic neuronal injury; stroke; spinal cord injury;
Inducing apoptosis in a cell infected with herpes simplex virus, HSV, by administering to the cell, a composition comprising an agent that inhibits phosphorylation of pro-apoptotic polypeptide BAD by HSV US3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bad-DTTR apoptosis-modifying fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "10x histidine tag'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 138;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HARD ) HARVARD COLLEGE.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 NLWAAQRYGRELRRMSDEFEGSFKGL 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Corynebacterium diptheriae.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU00220 standard; Protein; 567 AA.
                                                                                                                                                Claim 15; Page 168; 192pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96.5%; Sco.
100.0%; Pred
0; M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-MAY-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Huntington's disease
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Novel fusion protein for modifying apoptosis in target cell and reducing apoptosis after transient ischaemic neuronal injury, has two domains which targets protein to a cell and modifies apoptotic response of cell
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Claim 4; Page 59-61; 65pp; English

The sequence represents the amino acid sequence of Bad-DTTR apoptosismodifying fusion protein comprising Bad gene sequence fused via a short
linker to diphtheria toxin translocation domain (DTTR). The
functional apoptosis-modifying fusion protein is capable of binding a
c target cell and integrating into or crossing a cellular membrane of the
target cell. The apoptosis-modifying fusion protein comprises at least
two domains: the DTR domain, which targets the fusion protein to the
target cell. The BCI-XL domain, which modifies an apoptotic response
of the target cell. The fusion protein is useful for modifying
c finhibiting or enhancing) apoptosis in a target cell, such as neuron,
lymphocyte, cancer, neoplasm, macrophage, epithelial, stem, tumour or
hyper-proliferative cell or an adipocyte. It is also useful for reducing
apoptosis in a subject after transient ischaemic neuronal injury.
c apoptosis in a subject after transient ischaemic neuronal injury.
c specially spinal cord injury. The fusion protein may be used to treat
various diseases and injury conditions through inhibition or enhancement
of apoptotic cellular response, including neurodegenerative disorders
c such as Alzheimer's disease, including neurodegenerative disorders
c atrophy, stroke episodes and unregulated cell growth as in tumours and
various cancers. The apoptosis-modifying fusion protein can be delivered
effectively throughout the body and targeted to selective tissue and

567 AA; Sequence

Gaps 0; Query Match 96.5%; Score 138; DB 22; Length 567; Best Local Similarity 100.0%; Pred. No. 1.2e-12; Matches 26; Conservative 0; Mismatches 0; Indels 0

2 NLWAAQRYGRELRRMSDEFEGSFKGL 27

161 NLWAAQRYGRELRRMSDEFEGSFKGL 186 g

Search completed: September 15, 2003, 17:22:14 Job time: 38.1857 secs

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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CLASSIFICATION NUMBER: US/08/33,565
FILING DATE: 31-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
REGISTRATION WINIBER: 15726A-000700
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFRA: (415) 326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 204 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) NAME/KEY: Protein

) LOCATION: 1.204

) OTHER INFORMATION: CHER INFORMATION: US-08-333-565-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 26; Conserv
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                                                                                                                                                                                                                                                                                        US-08-333-565-2
                                                                                            RESULT 1
APPLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                 September 15, 2003, 17:22:21; Search time 14.0786 Seconds (without alignments) 81.144 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 69,
Sequence 69,
Sequence 40,
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Sequence 1, b
Sequence 12,
Sequence 13,
Sequence 14,
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Sequence 55,
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Sequence 14,
Sequence 3,
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Sequence 7,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
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Sequence 2
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Sequence
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                                                                                                                                                                                                                                                                                                                                                            /cgg2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/pcTuS_COMB.pep:*
              GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-733-505A-1
US-08-733-505A-12
US-08-733-505A-14
US-08-717-123-3
US-08-717-123-3
US-08-717-123-2
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US-08-333-505A-55
US-08-333-505A-55
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US-08-333-505A-55
US-08-333-505A-55
US-08-333-505A-55
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US-08-706-741B-69
US-08-924-695A-69
US-08-867-087B-40
                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                  328717 segs, 42310858 residues
                                                                                                                                             143
1 KNLWAAQRYGRELRRMSDEFEGSFKGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                             protein search, using sw model
                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                   Issued_Patents_AA:*
                                                                                                                                                                                                                                                                 Minimum DB seq length: 0 Maximum DB seq length: 2000000000
                                                                                                                                 US-09-544-664-56
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Match Length DB
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                                                                                                                                                                                 Scoring table:
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                                                                                    Run on:
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Gaps

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96.5%; Score 138; DB 1; Length 204; 100.0%; Pred. No. 1e-13; iive 0; Mismatches 0; Indels

/note= "Deduced amino acid sequence of mouse BAD."

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Sequence 3, Appli
Sequence 3, Appli
Sequence 1, Appli
Sequence 31458, A
Sequence 23807, A
Sequence 5164, Ap
                                                                                                                             Sequence 4, Appli
Sequence 17508, A
Sequence 28775, A
Sequence 27, Appl
Sequence 27, Appl
Sequence 27, Appl
Sequence 28581, A
                 Sequence 1
Sequence 3
                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08333565
; Sequence 2, Application US/08333565
; Patent No. 5622852
; GENERAL INFORMATION:
    APPLICANT: KORSMEYER, Stanley J.
    TITLE OF INVENTION: Bcl.*/Bcl.2 ASSOCIATED CELL DEATH
    TITLE OF INVENTION: REGULATOR
    NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
    ADDRESSEE: Townsend and Townsend Khourie and Crew
    STREET: 379 Lytton Avenue
    CITY: Palo Alto
    STATE: California
    CONTRY: US
US-09-328-352-4656
US-09-074-579-3
US-09-074-579-3
US-09-388-774-3
US-09-546-153-1
US-09-252-991A-31458
US-09-252-991A-31458
US-09-328-352-5164
US-09-328-352-5164
US-09-235-103-2
US-09-252-991A-17508
US-09-252-991A-17508
US-09-252-991A-17508
US-09-252-991A-17508
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US-09-252-991A-17508
US-09-252-991A-17508
US-09-252-991A-17508
US-09-252-991A-17508
                                                                                                                                                                                                  US-09-650-855-27
US-09-252-991A-28581
US-09-206-551-20
                                                                                                                                                                                                                                             US-09-252-991A-18729
   904
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322
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107
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us-09-544-664-56.rai

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Patent No. 5965703
GENERAL INFORMATION:
APPLICANT: Horne, William A.
APPLICANT: Oltersdorf, Tilman
TITLE OF INVENTION: Human BAD Polypeptides, Encoding Nucleic NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4770 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                     79.7%; Score 114; DB 1; Length 165; 91.7%; Pred. No. 4e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79.7%; Score 114; DB 2; Length 168; 91.7%; Pred. No. 4e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Indels
                                                                                                                                                                                                                                                                                                                                                                               2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPOSIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/717,123
FILING DATE: 20-SEP-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                              101 NLWAAQRYGRELRRMSDEFVDSFK 124
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                                                                                                                                                                                                                                                                                                                                                                                                                         2 NLWAAQRYGRELRRMSDEFEGSFK 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 NLWAAQRYGRELRRMSDEFEGSFK 25
                            NAME: Saliwanchik, David R. REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: CL-8
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEZ/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-I
TELECOMMUNICATION INFORMATION:
                                                                                                         TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 166 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 168 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 91.73
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 91.73
Matches 22; Conservative
                                                                                                                                                                                                                                     single
                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-08-665-617-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                           LENGTH: 166 amino TYPE: amino acid
                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-717-123-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-717-123-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENCODING NUCLEIC
                                                                                                                                                                                                                                 Length 204;
                                                                                                                                                                                                                               Score 135, DB 2; Length 20
Pred. No. 2.9e-13;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,617
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/09375257; Patent No. 6504022; GENERAL INFORMATION:
APPLICANT: Horne, William A.
APPLICANT: OlterSoorf, Tilman
TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCORTILE REFERENCE: 480140,428D1
CURRENT APPLICATION NUMBER: US/09/375,257
CURRENT APPLICATION NUMBER: 1999-08-16
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Xudong, Yin
TITLE OF INVENTION: Gene and Protein for Re
NUMBER OF SEQUENCES: 2
CORRESPONDENCE SA
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                     140 NIWAAQRYGRELRRWIDEFEGSFKGL 165
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; Sequence 2, Application US/08665617
; Patent No. 5663316
REFERENCE/DOCKET NUMBER: P-ID TELECOMMUNICATION INFORMATION: (619) 535-9001 TELEFAX: (619) 535-9949 INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                               94.48;
96.28;
                                                                                                                            I: 204 amino acids amino acid
                                                                                                                                                                                                                            Query Match
Best Local Similarity 96.29
Matches 25; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 25; Consery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION: APPLICANT: Xudong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 32606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE
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SEQ ID NO 3
LENGTH: 204
                                                                                                                                                                ; TOPOLOGY:
US-08-717-123-3
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US-09-375-257-3
                                                                                                                            LENGTH:
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us-09-544-664-56.rai

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Query Match 79.7%; Score 114; DB 3; Length 168; Best Local Similarity 91.7%; Pred. No. 4e-10; Matches 22; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
APPLICANT: Lal, Preeti
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                COMPUTE READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SISTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,335
FILING DATE: Filed Herewith
APPLICATION NUMBER:
FILING DATE: Filed Herewith
FILING DATE:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/410,372
FILING DATE:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Dr. CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PF-0421 US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECHAUNICATION INFORMATION:
TELEPHONE: 650-855-0555
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LIBRARY: GenBank
CLONE: 1683637
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                                              STREET: 3174 POI CITY: Palo Alto
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COUNTRY:
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                                                                                                                        GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Yue, Henry
APPLICANT: Lal, Preeti
APPLICANT: Shah, Purvi
APPLICANT: Shah, Purvi
APPLICANT: Orley, Neil C.
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
TITLE OF INVENTION: PROLIFERATION
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROTEINS ASSOCIATED WITH CELL PROLIFERATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM COMPALLALL
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,335
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
RECISTRATION NUMBER: 36,749
RECISTRATION INPORMATION:
TELECOMONICATION INPORMATION:
TELECHONE: 650-855-0555
TELECHONE: 650-845-4166
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                103 NIWAAQRYGRELRRMSDEFVDSFK 126
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Patent No. 6080847
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: PROLIFERATION
TITLE OF INVENTION: PROLIFERATION
                                                                                  ; Sequence 1, Application US/08985335; Patent No. 6080847
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LIBRARY: SYNORAB01
CLONE: 358673
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IMMEDIATE SOURCE:
LIBRARY: SYNORA
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US-08-985-335-7
                                            RESULT 11
US-08-985-335-1
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;; LIBRARY: GenBank
; CLONE: 1683637
US-09-410-372-7
   TOPOLOGY: linear IMMEDIATE SOURCE:
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US-09-375-257-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL TITLE OF INVENTION: PROLIFERATION NUMBER OF SEQUENCES: 9 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: ISM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/410,372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Dr. CITY: Palo Alto
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PRIOR APPLICATION DAFA:
APPLICATION NUMBER: 08/985,335
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                     PF-0421 US
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/985,335
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                             NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0.
TELECOMNUNICATION:
TELEPHONE: 650-855-0555
TELEPHONE: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 7, Application US/09410372; Patent No. 6281334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
APPLICANT: Lal, Preeti
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGIH: 168 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 168 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                         SYNORAB01
                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                        ; LIBRARY; SYNOI
; CLONE: 358673
US-09-410-372-1
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COUNTRY: US
ZIP: 94304
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US-09-410-372-7
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Sequence 2, Application US/09375257

Patent No. 6504022

GENERAL INFORMATION:

APPLICANT: Horne, William A.

APPLICANT: Oltersdorf, Tilman

TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC

TITLE OF INVENTION: ACIDS AND METHODS OF USE

FILE REFERENCE: 480140.428D1

CURRENT APPLICATION NUMBER: US/09/375,257

CURRENT FILING DATE: 1999-08-16

NUMBER OF SEQ ID NOS: 15

SEQ ID NO 2

LENGTH: 168
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                                               0,
Score 114; DB 3; Length 168; Pred. No. 4e-10;
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                                                 2; Indels
                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: September 15, 2003, 17:45:07 Job time : 15.0786 secs
                                                                                                                     103 NLWAAQRYGRELRRMSDEFVDSFK 126
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                                                                                           2 NIWAAQRYGRELRRMSDEFEGSFK 25
  79.78;
Query Match
Best Local Similarity 91.73
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM; Homo sapiens
US-09-375-257-2
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Page 1

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September 15, 2003, 17:25:56 ; Search time 21.4071 Seconds (without alignments) 184.034 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
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1 KNIWAAQRYGRELRRMSDEFEGSFKGL 27
                                                                                                                                                                                                                        541936 segs, 145912426 residues
                                                  OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                  Published_Applications_AA:*
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Maximum Match 1008
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                          Minimum DB seq length: 0 Maximum DB seq length: 2000000000
                                                                                                                             US-09-544-664-56
                                                                                                                              Title:
Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 3, Appli Sequence 3, Appli Sequence 2, Appli Sequence 2, Appli Sequence 1, Appli Sequence 1, Appli Sequence 107, Appli Sequence 107, Appli Sequence 115, Appli Sequence 1, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 1, Appli
SUMMARIES	US-09-922-378-3 US-10-066-179-3 US-09-922-378-3 US-09-894-657-1 US-09-894-657-1 US-10-174-1058-147 US-10-174-1058-147 US-10-1058-145 US-10-156-761-9145 US-10-092-750-1 US-10-156-761-9145 US-10-156-761-9145 US-10-156-761-9145 US-10-156-761-9145 US-10-156-761-9145 US-10-156-761-9145 US-10-156-761-9145 US-10-156-761-9145
	40 400000 0 04400001111111111111111111111111111111
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Score	
Result No.	0 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2

Sequence 8, Appli Sequence 12463, Appli Sequence 12, Appli Sequence 18, Appli Sequence 18, Appli Sequence 238, Appli Sequence 2, Appli Sequence 23, Appli Sequence 188, Appli Sequence 188, Appli Sequence 501, Appli Sequence 5	
US-10-008-355-8 US-09-815-242-12463 US-09-815-242-12463 US-10-369-294-20 US-10-369-294-20 US-09-843-846-18 US-09-817-52A-238 US-09-814-55-162 US-10-166-357-2 US-10-166-357-2 US-10-166-357-2 US-10-166-357-2 US-10-166-357-2 US-10-166-357-2 US-10-166-357-2 US-10-166-357-2 US-10-166-357-2 US-10-16-377-2 US-10-251-385-62 US-10-251-385-62 US-10-251-385-62 US-10-251-385-62 US-10-251-385-62 US-09-981-272-501 US-09-981-727-501 US-09-981-727-501 US-09-981-727-501 US-09-991-727-501 US-09-991-737-501 US-09-991-737-501 US-09-991-737-501 US-09-991-737-501 US-09-991-335-601 US-09-991-335-601 US-09-991-335-601	
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APPLICANT: HORNE, William A. APPLICANT: HORNE, William A. APPLICANT: OlterStorf, Tilman TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC TILE REPRENDE: 480140, 428D3 CURRENT APPLICATION NUMBER: US/09/922,378 CURRENT FILING DATE: 2001-08-03 NUMBER OF SEQ ID NOS: 15 SOPTWARE: EastSeQ for Windows Version 4.0 SEQ ID NO 3 Length 204; Sequence 3, Application US/09922378; Patent No. US20020037869A1; GENERAL INFORMATION:) ORGANISM: Mus musculus US-09-922-378-3 204 RESULT 1 US-09-922-378-3 TYPE: PRT LENGTH

ALIGNMENTS

ő 94.4%; Score 135; DB 9; Length 20 96.2%; Pred. No. 5.5e-12; tive 1; Mismatches 0; Indels 2 NLWAAQRYGRELRRMSDEFEGSFKGL 27 Query Match
Best Local Similarity 96.2
Matches 25; Conservative ò

6

Gaps

US-10-066-179-3
Sequence 3, Application US/10066179
Sequence 3, Application WS/10066179
Sequence 3, Application No. US20020115631a1
GENERAL INPORMATION:
APPLICANT: Oltersdorf, Tilman, APPLICANT: Oltersdorf, Tilman, TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC TITLE OF INVENTION: ACIDS AND METHODS OF USE 140 NLWAAQRYGRELRRMTDEFEGSFKGL 165 RESULT 2 qq

us-09-544-664-56.rapb

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; ORGANISM: Homo sapiens US-09-922-378-2
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US-09-894-657-7
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Sequence 258, Application US/10059261

Publication No. US20030077826A1

GENERAL INFORMATION:

APPLICANT: EDELMAN, LENA

APPLICANT: EDELMAN, LETIENNE DANIEL FRANCOIS

APPLICANT: BRIAND, JEAN-PAUL

TITLE OF INVENTION: CHIMERIC MOLECULES CONTAINING A MODULE ABLE TO TARGET

TITLE OF INVENTION: SPECIFIC CELLS AND A MODULE REGULATING THE APOPTGENIC

TITLE OF INVENTION: (PIPC)

TITLE OF INVENTION: (PIPC)

TITLE OF INVENTION: (PIPC)

FILE REFERENCE: 2003-08-29

PRIOR APPLICATION NUMBER: 60/265,594

PRIOR FILING DATE: 2001-02-02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Horne, William A.
APPLICANT: Horne, William A.
APPLICANT: Oltersdorf, Tilman
TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC
TITLE OF INVENTION: ACIDS AND METHODS OF USE
FILE REPERENCE: 480140, 42803
CURRENT APPLICATION NUMBER: US/09/922,378
CURRENT APPLICATION NUMBER: US/09/922,378
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PSSESSQ for Windows Version 4.0
; SEQ ID NO 2
LENGTH: 168
                                                                                                                                                                                                                                              94.4%; Score 135; DB 14; Length 204; 96.2%; Pred. No. 5.5e-12;
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                                                                                                                                                                                                                                                                                           0; Indels
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                                                                                                                                                                                                                                                                                         1; Mismatches
FILE REFERENCE: 480140.428C1
CURRENT APPLICATION NUMBER: US/10/066,179
CURRENT FILING DATE: 2002-02-01
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 204
                                                                                                                                                                                                                                                                                                                                                               2 NLWAAQRYGRELRRMSDEFEGSFKGL 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 NLWAAQRYGRELRRMSDEFEGSFK 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 325
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Unknown Organism
                                                                                                                                                                                                                                              Query Match
Best Local Similarity 96.23
Matches 25; Conservative
                                                                                                                                                                              ) ORGANISM: Mus musculus US-10-066-179-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-922-378-2
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                                                                                                                                                           TYPE: PRT
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                                           Gaps
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                                         0
Query Match 79.7%; Score 114; DB 9; Length 168; Best Local Similarity 91.7%; Pred. No. 5.1e-09; Matches 22; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79.7%; Score 114; DB 9; Length 168; 91.7%; Pred. No. 5.1e-09; Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                       PPLICANT: HILLMAN,
Yue, Hebry
Lal, Preeti
Shah, Purvi
Corley, Neil C.
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT AIRL.

COMBUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTEED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/894,657
FILING DATE: 28-Jun-2001
PRIOR APPLICATION NUMBER: 09/410,372
ATTORING DATE: CURROWIN
ATTORING PATE: CURROWIN
ATTORING PATE: CURROWIN
                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: FF-0421 US
TELECOMMUNICATION INFORMATION:
TELEPRONE: 650-855-0555
TELEPRONE: 67-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLONE: 358673
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              103 NLWAAQRYGRELRRMSDEFVDSFK 126
                                                                                                     103 NLWAAQRYGRELRRWSDEFVDSFK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 NLWAAQRYGRELRRMSDEFEGSFK 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749
                                                                            2 NLWAAQRYGRELRRMSDEFEGSFK 25
                                                                                                                                                                                                               LENGTH: 168 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIBRARY: SYNORAB01
CLONE: 358673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: US.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 22; Conserv
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Gaps

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2; Indels

Length 168;

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APPLICANT: Cell Signaling Technology, Inc.,
APPLICANT: Cell Signaling Technology, Inc.,
APPLICANT: Cell Signaling Technology, Inc.,
APPLICANT: Coll Signaling Technology, Inc.,
TITLE OF INVENTION: CONTEXT-INDEPENDENT ANTIBODIES COUPLED WITH DATABASE SEARCH:
TITLE OF INVENTION: CONTEXT-INDEPENDENT ANTIBODIES COUPLED WITH DATABASE SEARCH:
TITLE OF INVENTION NUMBER: US 09/148,712
PRIOR FILING DATE: 2002-06-18
PRIOR FILING DATE: 1998-09
PRIOR FILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 193
SOFTWARE: Patentin version 3.1
SEQ ID NO 147
LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1077, Application US/10238075

Publication No. US20030148324A1

GENERAL INFORMATION:
APPLICANT: I.N.S.E.R.W.

TITLE OF INVENTION: B.Coll, and biological uses of these polynucleotides and of t
FILE REPERENCE: BLANDINE
CURRENT APPLICATION NUMBER: US/10/238,075

CURRENT APPLICATION NUMBER: 0003145

PRIOR PRIOR FILING DATE: 2002-09-10

PRIOR FILING DATE: 2000-03-10

SEQ ID NOS: 1576

SEQ ID NO 1077

LENGTH: 682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHER INFORMATION: (8) OTHER INFORMATION: Serine at position 8 is phosphorylated US-10-174-105A-147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
49.7%; Score 71; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0008;
Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                      79.7%; Score 114; DB 14;
91.7%; Pred. No. 5.1e-09;
tive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                              103 NIWAAQRYGRELRRMSDEFVDSFK 126
                                                                                                                                                                                                                                                                                                         2 NIWAAQRYGRELRRMSDEFEGSFK 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 147, Application US/10174105A Publication No. US20030068652A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Synthetic Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 GRELRRMSDEFEGS 23
                                                                                                                                                      Query Match
Best Local Similarity 91.78
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Escherichia coli
                 ; TYPE: PRT
) ORGANISM: Homo sapiens
US-10-066-179-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: MOD_RES
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US-10-174-105A-147
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Sequence 2, Application US/10066179

Sequence 2, Application US/10066179

Publication No. US20020115631A1

GENERAL INFORMATION:

APPLICANT: Horne, William A.

APPLICANT: Olversdorf, Tilman

TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC

TITLE OF INVENTION: ACIDS AND METHODS OF USE

FILE REFERENCE: 480140.42861

CURRENT APPLICATION NUMBER: US/10/066,179

CURRENT FILING DATE: 2002-02-01

NUMBER OF SEQ ID NOS: 15

SOUTHWARE: RASISEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 79.7%; Score 114; DB 9; Length 168; Best Local Similarity 91.7%; Pred. No. 5.1e-09; Matches 22; Conservative 0; Mismatches 2; Indels
                                                                                                             APPLICANT: HILLING.,
Yue, Henry
Lal, Preeti
Sahah, Puri C.
COTLEY, Neil C.
TILLE OF INVENTION: PROLIFERATION
PROLIFERATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA

LIP: 94304

COMPUTER EADABLE FORM:
MUDIUM TYPE: Diskette
COMPUTER: LBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FastSeQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/894,657
FILING DATE: 28-Jun-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/410,372
FILING DATE: CUNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/COCKET NUMBER: 36,749
REFERENCE/C
                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Dr. CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE DESCRIPTION: SEQ ID NO: 7: US-09-894-657-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            103 NLWAAQRYGRELRRMSDEFVDSFK 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 168 amino acids
TYPE: amino acid
STRANDEDNESS: single
Sequence 7, Application US/09894657
Patent No. US20020098569A1
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer
                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERIST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLONE: 1683637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMMEDIATE SOURCE:
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LENGTH: 168
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32.9%; Score 47; DB 15; Length 138; 45.5%; Pred. No. 24;
                                                                                                                             US-10-02-750-241
; Sequence 241, Application US/10092750
; Publication No. US20030032157A1
; GENERAL INFORMATION:
; APPLICANT: Hammond, Philip W.
; APPLICANT: Wright, Martin C.
; TITLE OF INVENTION: Polypeptides Interactive with BCL-X1
; FILE REFERENCE: 50036/050002
; CURRENT FILING DAIR: 2002-03-07
; PRIOR APPLICATION NUMBER: US 60/274,526
; PRIOR FILING DAIR: 2001-03-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INHIBITOR HEAVY CHAIN PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Guegler, Karl J.
Patterson, Chandra
TITLE OF INVENTION: GROWTH-ASSOCIATED TRYPSIN-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Word Perfect 6.1/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/828,423
FILING DATE: 05-Apr-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: PF-0505 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 253
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 241
LENGTH: 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/388,774
FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86 IWIAQ----ELRRIGDEFNAYY 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Hillman, Jennifer L.
                             3 LWAAQRYGRELRRMSDEFEGSF 24
3 LWAAQRYGRELRRMSDEFEGSF 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 3, Application US/09828423
; Patent No. US20020099178A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 45.5°
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CIIY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapiens
US-10-092-750-241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
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                                            Query Match 35.7%; Score 51; DB 12; Length 682; Best Local Similarity 40.7%; Pred. No. 32; Matches 11; Conservative 5; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32.9%; Score 47; DB 15; Length 35; 45.5%; Pred. No. 5.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STEERAL INFORMATION: Philip W.

APPLICANT: Hammond. Philip W.
APPLICANT: Alpin, Julia
APPLICANT: Alpin, Julia
APPLICANT: Wright, Martin C.
TITLE OF INVENTION: Polypeptides Interactive with BCL-X1
FILE REFERENCE: 50036/050002
CURRENT APPLICATION NUMBER: US/10/092,750
CURRENT PILING DATE: 2002-03-07
PRIOR APPLICATION NUMBER: US 60/274,526
PRIOR FILING DATE: 2001-03-08
NUMBER OF SEQ ID NOS: 253
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                     PUDLICALION NO. USZOJOLIZOJORAL

APPLICANT: NEURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: IKEDA, HARUO
APPLICANT: SHIRAWA, JUN
APPLICANT: SHIRAWA, JUN
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: APATORI, WASAHIRA
TITLE OF INVENTION: NOWEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 9145
                                                                                                                                                               1 KNLWAAQRYGRELRRMSDEFEGSFKGL 27
                                                                                                                                                                                                                                                      RESULT 10
US-10-156-761-9145
; Sequence 9145, Application US/10156761
; Publication No. US20030119018A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Streptomyces avermitilis US-10-156-761-9145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-092-750-1; Sequence 1, Application US/10092750; Publication No. US20030032157A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 ORYGRELRRMSDEFEG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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Best Local Similarity
Matches 9; Conserv
    US-10-238-075-1077
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Search completed: September 15, 2003, 17:47:53 Job time : 21.4071 secs
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.core 46; DB 9; Length 945;
Pred. No. 2.4e+02;
5; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 30.8%; Score 44; DB 15; Length 27 Best Local Similarity 53.3%; Pred. No. 1.3e+02; Matches 8; Conservative 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: IRBLA, HARUON
APPLICANT: IRBIKAMA, JUN
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIXUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT PILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR PILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 11541
                                                                                                                                : | || | |:
.LHVPDTFEGHFDGV 237
                                                                                                   SDEFEGSFKGL 27
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APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Tawick, John D.
APPLICANT: Yamamoto, Robert T.
                                                                                                                                                                                                                                                                     Sequence 11541, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Streptomyces avermitilis US-10-156-761-11541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | | :| |||| :|
29 WIAAAHGAELRRAAD 43
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US-09-815-242-5704
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                                                  CORRENT FILLING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PAPLICATION NUMBER: 60/206,848
PRIOR PELING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-110-27
PRIOR PELING DATE: 2000-112-27
PRIOR FILING DATE: 2000-112-22
PRIOR FILING DATE: 2001-12-22
PRIOR FILING DATE: 2001-12-22
PRIOR FILING DATE: 2001-12-22
PRIOR FILING DATE: 2001-02-16
NUMBER: 05 EQU ID NOS: 14110
SOFTWARE: FASLSEQ for Windows Version 4.0
SEQ ID NO 5704
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
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386 FGGSLRRQDENFDGKIKAI 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 YGRELRRMSDEFEGSFKGL 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
COGANISM: Staphylococcus aureus
US-09-815-242-5704
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

US-09-544-664-56 143 1 KNLWAAQRYGRELRRMSDEFEGSFKGL 27 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 seqs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	bad protein - mous	inter-alpha-trypsi	hypothetical prote	inter-alpha-inhibi	2-dehydro-3-deoxy-	floral homeotic pr	spermidine/putresc	probable threonine	conserved hypothet	Ig kappa chain - h	annexin P35 - maiz	transforming prote	oxidoreductase, so	threonine synthase	Antho-RFamide neur	oxaloacetate decar	oxoglutarate dehyd	14	- 1	Antho-RFamide prec		orin	probable polyamine	inter-alpha-trypsi	hypothetical prote	DNA-directed RNA p	othe	neuropeptide Pol-R	conserved hypothet
	ai.	A55671	5	9	S54354	S38185	A42095	C84338	A96753	E83517	S40376	T02975	C36365	F72289	T08545	A39172	G82308	F82668	B96695	T02961	A44308	T09486	829899	T35440	IYHU2	T24806	81	69	38	AF2859
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	Score	138	54	53	53	52	51	50	50	49	ω.	48.5	48	48	48	47.5	47	47	47	ė.	46.5	Ġ.	46	46	46	46	46	S)	45.5	
Result	No.	7.	7 Q	m	4	ιΩ	9	7	∞	O	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

30 45.5 31.8 327 2 D97636 31 45.5 31.8 562 2 C71473 32 45.5 31.8 562 2 C71473 34 45 31.5 273 2 S06736 45 31.5 295 2 F83201 36 45 31.5 295 2 F83201 37 45 31.5 291 2 AB0509 40 45 31.5 591 2 AB0509 41 45 31.5 591 2 AB0509 42 45 31.5 591 2 AB0609 43 45 31.5 591 2 AB0609 44 45 31.5 1199 2 T23005 45 31.5 1199 2 T23005
45.5 31.8 327 45.5 31.8 562 45 31.8 562 45 31.5 273 45 31.5 273 45 31.5 295 45 31.5 591 45 31.5 591 45 31.5 596 45 31.5 1199 45 31.5 1199
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ALIGNMENTS

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A550L1 1
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bad protein - mouse
C; Species: Mus musculus (house mouse)
C; Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 05-Nov-1999
C; Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 05-Nov-1999
C; Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 05-Nov-1999
C; Date: 03-Mar-1995 #sequence_revision 0.B.; Korsmeyer, S.J.
Cell 80, 285-291, 1995
A; Title: Bad, a heterodimeric partner for Bcl-x-L and Bcl-2, displaces Bax and promot A; Reference number: A55671; MUID:95136361; PMID:7834748
A; Reference number: A55671; MUID:95136361; PMID:7834748
A; Catus: preliminary; not compared with conceptual translation
A; Molecule type: mRNA
A; Residues: 1-204 < VAN>
A; Cross-references: GB:L37296; NID:9639778; PIDN:AA64465.1; PID:9639779
C; Keywords: heterodimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     140 NEWAAQRYGRELRRMSDEFEGSFKGL 165
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RESULT

C.Suncarfamily inter-alpha-tropsin inhibitor component T
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Score 54; DB 2; Length 946; Pred. No. 9.9;

37.8%; 34.6%;

Query Match Best Local Similarity

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A: Title: The complete sequence of a 6794 bp segment located on the right arm of chrom A: Reference number: S38185; MUID: 94078675; PMID: 8256522
A: Accession: S38185
A: Status: translation not shown A: Molecule type: DNA
A: Residues: 1-370 < COI>
A: R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Molecule type: DNA
A, Residues: 1-370 < ALG>
A, Cross references: EMBL: Z36118; NID: 9536664; PIDN: CAA85212.1; PID: 9536665; MIPS: YBR2
R, Kuenzler, M.; Paravicini, G.; Egli, C.M.; Irniger, S.; Braus, G.H.
Gene 113, 67-74, 1992
A, Title: Cloning, primary structure and regulation of the ARO4 gene, encoding the tyr
A, Reference number: JN0322; MUID: 92225349; PMID: 1348717
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-370 <ALJ>
A; Cross-references: EMBL: Z36118; NID: 9536664; PIDN: CAA85212.1; PID: 9536665; MIPS: YBR2
R; Aigle, M.; Baclet, M.C.; Barthe, C.; Biteau, N.; Crouzet, M.; Doignon, F.
submitted to the Protein Sequence Database, August 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A, Title: Cloning, primary structure, and regulation of the HIS7 gene encoding a bifun A, Reference number: A48651; MUID:93374850; PMID:8366040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Comment: This enzyme catalyzes the condensation of phosphoenolpyruvate and D-erythr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Description; aldehyde-lyase; carbon-carbon lyase
A; Pathway; aromatic amino acid biosynthesis; shikimate pathway
A; Note: first step in shikimate pathway
C; Superfamily; phospho-2-dehydro-3-deoxyheptonate aldolase
C; Keywords: aldehyde-lyase; aromatic amino acid biosynthesis; carbon-carbon lyase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ó;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A Accession: JN0322
A; Molecule type: DNA
A; Residues: 1-204,208-370 < KUE>
A; Cross-references: EMBL:X61107
B; R; Ruenzler, M.; Balmelli, T.; Egli, C.M.; Paravicini, G.; Braus, G.H.:
J; Bacteriol. 175, 5548-5558, 1993
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Best Local Similarity 47.6
Matches 10; Conservative
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A, Molecule type: DNA
A, Residues: 352-370 - KU2>
A, Cross-references: GB: X61107
C; Comment: This enzyme catalyz
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A; Accession: $46130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Reference number: $45906
A;Accession: $46126
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A42095
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                                                                                                                                                                                                                                                                                                                                                                                               Dypothetical protein Rv2014 - Mycobacterium tuberculosis (strain H37RV)

C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: D70760

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Barrell, B.G.
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A)0500; MUID:98295987; PMID:9634230
A;Accession: D70760
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-223 <COL>
A;Cols-references: GB:Z74025; GB:AL123456; NID:g3261586; PIDN:CAA98415.1; PID:e1299911;
A;Experimental source: strain H37RV
C;Genetics:
A;Gene: Rv2014
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2-dehydro-3-deoxy-phosphoheptonate aldolase (EC 4.1.2.15) ARO4 - yeast (Saccharomyces ce 2-dehydro-3-deoxy-phosphoheptonate aldolase (EC 4.1.2.15) ARO4 - yeast (Saccharomyces C.5.Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 03-Jun-2002
C;Aocession: S38185; S46126; S46130; JN0322; B48651
R;Doignon, F.; Biteau, N.; Aigle, M.; Crouzet, M.
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Pred. No. 14;
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              Indels
         12;
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Pred. No. 3.2;
1; Mismatches
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         5; Mismatches
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                                                                                                                                                                                                              212 NVWIVELQGMRFLHVPDTFEGHFQGV 237
                                                                                                              2 NLWAAQRYGRELRRMSDEFEGSFKGL 27
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34.68;
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58.8%;
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         Conservative
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         Matches
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C; Species: Pseudomonas aeruginosa
C; Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C; Accession: E83517
R; Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L.; Lory, S.; Olson, M.Y.
Nature 406, 959-964, 2000
A; Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa A; Reference number: A82950; MUID: 20437337; PMID: 10984043
A; Reference preliminary
A; Molecule type: DNA
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-453 <STO>
A; Cross-references: GB: AE004691; NID: 99946936; PIDN: AAG04420.1; GSFDB:GN
A; Genetics:
A; Genetics:
A; Genetics:
                   Clacesion A96753

Ritheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L. Raul, S.; White, O.; Alon Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L. Raul, S.; Khan, S.; Khaykin, E.; Kim, A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

Rizzo, M.; Rooney, T.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Tu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A; Fitle: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A; Reference number: A86141; MUID:21016719; PMID:11130712

A; Status: preliminary

A; Molecule type: DNA

A; Residues: 1-516 (STO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 conserved hypothetical protein PA1031 [imported] - Pseudomonas aeruginosa (strain PA0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:AE005173; NID:g5903070; PIDN:AAD55628.1; GSPDB:GN00141
C;Genetics:
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C;Species: Homo sapiens (man)

C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C;Accession: 34036

R;Riein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A;Title: Expressed human immunoglobulin chi genes and their hypermutation.

A;Reference number: $40312; M(ID):94080891; PMID:8258341

A;Accession: $40376

A;Status: preliminary; translation not shown
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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21;
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25;
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Pred. No. 25;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 NLWAAQRYGRELRRMSD-----EFEGSFKGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 50;
Pred. No. 2
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55.6%;
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Best Local Similarity 55.6
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12; Conservative
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Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Map position: 1
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E83517
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C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: C84338
F;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabld Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A;Itle: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
                      A)Cross-references: GB.M86357; NID:9166607; PIDN:AAA32740.1; PID:9166608
A)Experimental source: petals, stamens
A)Note: sequence extracted from NCBI backbone (NCBIN:82520, NCBIP:82521)
R)Okamoto, H.; Yano, A.; Shiraishi, H.; Okada, K.; Shimura, Y.
Plant Mol. Biol. 26, 465-472, 1994
A)Title: Genetic complementation of a floral homeotic mutation, apetala3, with an Arabid A):Reference number: S52633; MUID:95036018; PMID:7948893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Mary POSTION (1972) 139/3; 153/3; 168/3
A; Note: T12E18.30
C; Superfamily: transcription factor squa; serum response factor DNA-binding domain homol C; Keywords: DNA binding; nucleus; transcription regulation
F; 2-57/Domain: serum response factor DNA-binding domain homology <SRF>
                                                                                                                                                                                                                                                                                         A; Residues: 1-63 < CKA>
A; Cross references: GB:D21125
A; Cross references: GB:D21125
A; Diecker, H.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Quetier, F.; Salanoubat M.Mewes, submitted to the Protein Sequence Database, March 2000
A; Reference number: Z24469
A; Accession: T47593
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Pred. No. 15;
1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
A;Molecule type: DNA
A;Rosidues: 1-232 <&LD>
A;Cross-references: EMBL;AL132971
A;Experimental source: cultivar Columbia; BAC clone T12E18
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35.7%; Score 51; DB 2; ilarity 44.4%; Pred. No. 6.5; Conservative 3; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | | | | : | | : | | 107 QRLGECLDELDIQELRRLEDEMENTFK 133
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76.9%;
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Matches 12; Conserv
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A, Status: preliminary
A, Molecule type: DNA
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Tue Sep 16 09:28:59 2003

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Nature 399, 323-329, 1999
A) Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome A) Reference number: A72200; MUID:99287316; PMID:10360571
A) Accession: F72289
A) Status: preliminary
A) Molecule type: DNA
A) Residues: 1-220 <ARN>
A) Residues: 1-220 <ARN>
A) Experimental source: SB:AE001772; GB:AE000512; NID:g4981693; PIDN:AAD36230.1; PID:g498
C) Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Curien, G.; Dumas, R.; Ravanel, S.; Douce, R. FEBS Lett. 390, 85-90, 1996 A;Title: Characterization of an Arabidopsis thaliana cDNA encoding an S-adenosylmethi A;Reference number: S71362; MJID:96314555; PMID:8706836
                                                                                                                                                                                                                                                            RiNelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hic Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Threonine synthase (EC 4.2.3.1) precursor - Arabidopsis thaliana

N.Alternate names: protein F27B13.80

C.Species: Arabidopsis thaliana (mouse-ear cress)

C.Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 03-Jun-2002

C.Accession: T08545. S71862; S74307

R.Bevan, M.; Zimmermann, W.; Grueneisen, A.; Wambutt, R.; Bancroft, I.; Mewes, H.W.;

Submitted to the Protein Sequence Database, May 1999

A; Reference number: Z16442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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A;Accession: S74307
                                                                                                                                                                        C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: F72289
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A;Residues: 1-526 <BEV>
A;Cross-references: EMBL:AL050352; GSPDB:GN00062; ATSP:F27B13.80
A;Experimental source: cultivar Columbia; BAC clone F27B13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33.6%; Score 48; DB 2; Length 220; ilarity 34.8%; Pred. No. 17; Conservative 8; Mismatches 7; Indels
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Pred. No. 42;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 AAQRYGRELRRMSDEFEGSFKGL 27
169 REIRRMNKEOEGRSKG 184
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C;Superfamily: yeast SOL3 protein
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A; Residues: 40-54 <CUI>
C; Genetics:
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Matches 8; Conserv
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A; Molecule type: mRNA
A; Residues: 'L',3-526
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C;Species: Rhizomucor racemosus
C;Species: Rhizomucor racemosus
C;Species: Rhizomucor racemosus
C;Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 19-Jan-2001
C;Accession: C36365
R;Casale, W.L.; McConnell, D.G.; Wang, S.Y.; Lee, Y.J.; Linz, J.E.
Mol. Cell. Biol. 10, 6654-6663, 1990
A;Title: Expression of a gene family in the dimorphic fungus Mucor racemosus which A;Recence number: A36365; MUID:91061774; PMID:1701021
A;Recence number: A36365; MUID:91061774; PMID:1701021
A;Recence cumber: A36365, MUID:91061774; PMID:1701021
A;Recence cumber: A36365
A;Status: preliminary
A;Mesidues: 1-206 c.CAS>
A;Cross-references: GB:M55177
C;Superfamily: ras transforming protein; translation elongation factor Tu homology
C;Reywords: GTP binding; nucleotide binding; P-loop
F;11-126/Domain: translation elongation factor Tu homology
C;Reywords: GTP binding motif A (P-loop)
F;123-126/Region: GTP-binding SAK/L motif
F;153-125/Region: GTP-binding site: Mg-GTP (Lys, Ser, Thr, Asn, Lys, Asp, Ser) #sta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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A.Residues: 1.314 <BAT>
A.Residues: 1.314 <BAT>
A.Residues: 1.314 <BAT>
A.Residues: DIBL:X98245; NID:g1370602; PIDN:CAA66901.1; PID:g1370603
A.Experimental source: cultivar clipper; root tip
C.Superfamily: annexin I; annexin repeat homology
F:14-85/Domain: annexin repeat homology <AXR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Zea mays (maize)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jul-2000
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jul-2000
C;Accession: T02975
R;Battey, N.H.; James, N.C.; Greenland, A.J.
Plant Physiol. 112, 1391-1396, 1996
A;Title: CDNA isolation and gene expression of maize annexins P33 and P35.
A;Reference number: Z14796; MUID:97092863; PMID:8938425
A;Accession: T02975
                                                   A; Cross references: EMBL:X72486; NID:g441440; PIDN:CAA51154.1; PID:g441441
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 34-113/Domain: immunoglobulin homology <IMM>
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Pred. No. 8.6;
1; Mismatches 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                      WFRQRPGRSPRRLIYNVSKRDSGVSDRFSGSGS 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 48.5; DE Fred. No. 21; 4; Mismatches
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54 AEAYGKELLRALGDEIHGKFE 74
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38.2%;
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Local Similarity 47.6%;
Les 10; Conservative
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                           A; Residues: 1-134 <KLE>
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Best Local S:
Matches 10
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Anthore remaide neuropeptide 19 repeat precursor - sea anemone (Calliactis parasitica)
Anthore remaide neuropeptide 19 repeat precursor - sea anemone (Calliactis parasitica
C; Decies: Calliactis parasitica
C; Date: 07-Feb-1992 #sequence_revision 07-Feb-1992 #text_change 21-Jul-2000
C; Accession: A39172
R; Darmer, D.; Schmutzler, C.; Diekhoff, D.; Grimmelikhuijzen, C.J.P.
R; Darmer, D.; Schmutzler, C.; Diekhoff, D.; Grimmelikhuijzen, C.J.P.
R; Darmer, D.; Schmutzler, C.; Diekhoff, D.; Grimmelikhuijzen, C.J.P.
A; Title: Primary structure of the precursor for the sea anemone neuropeptide Antho-RFamil A; Reference number: A39172
A; Accession: A39172
A; Accession: A39172
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Cross-references: GB:M59166; NID:g156133; PIDN:AAA27878.1; PID:g156134
C; Keywords: neuropeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 33.2%; Score 47.5; DB 2; Length 334; Best Local Similarity 44.0%; Pred. No. 31; Matches 11; Conservative 3; Mismatches 10; Indels 1; Gaps
| : ||||| : | |||:| |
89 KRRYVPGRYGREFQGRFGREFQGRF 113
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A39172
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Search completed: September 15, 2003, 17:27:04 Job time : 13.15 secs

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September 15, 2003, 17:16:55; Search time 6.36429 Seconds (without alignments) 199.507 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                   OM protein - protein search, using sw model
                                                                                                                                                            Run on:
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US-09-544-664-56 143 1 KNLWAAQRYGRELRRMSDEFEGSFKGL 27 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 seqs, 47026705 residues Searched:

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

	Description		. 035147 rattus norv	Q92934 homo sapien		Q61703 mus musculu			062991 rhododendro		P35632 arabidopsis		Q9i4u3 pseudomonas					Q01133 calliactis				P10419 anthopleura					kluyvero					Yf5 .	18823	Q95gj0 gaultheria
SUMMARIES	QI	BAD_MOUSE	BAD_RAT	BAD_HUMAN	ITH2_MESAU	ITH2_MOUSE	MATK_LEDPA	MATK_RHOFR	MATK_RHOTS	AROG_YEAST	AP3_ARATH	CE05_MOUSE	RMUC_PSEAE	RAS3_RHIRA	6PGL_THEMA	THRC_SOLTU	THRC_ARATH	FMRA_CALPA	MATK_LOIPR	BIM_HUMAN	FMR2_ANTEL	FMR1_ANTEL	ITH2_HUMAN	RPOB_CAMJE	PRFA_POLPE	PSBO_ANASP	SNF4_KLULA	DCOA_SALTY	DCOA_KLEPN	HT2A_HUMAN	ENV_SIVAT	CE05_HUMAN	LML1_CAEEL	MATK_GAUPR
	latch Length DB	1																334 1																
ď	Query Match	96.5	96.5	79.7	37.8	37.1	36.7	36.7	36.7	36.4	35.7	35.7	34.3	33.6	33.6	33.6	33.6	33.2	33.2	32.9	32.5	32.5	32.2	32.2	31.8	31.5	31.5	31.5	31.5	31.5	31.5	31.5	31.5	31.1
	Score	13	138	114	54	53	52.5	52.5	52.5	52	51	51	49	48	48	48	48	47.5	47.5	47	46.5	46.5	46	46	45.5	45	45	45	45	45	45	45	45	44.5
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512	907 196	196	262	262	262	262	629	768	877
31.1	31.1 30.8	30.8	30.8	30.8	30.8	30.8	30.8	30.8	30.8
44.5	44.5 44	44	44	44	44	44	44	44	44
34 35	36	38	39	40	41	42	43	44	45

ALIGNMENTS

ALLGWADNIO		VOI-NOV-1997 (Rel. 35, Created) OI-NOV-1997 (Rel. 35, Last sequence update) 28 FEB-2003 (Rel. 41, Last annotation update)		BAD OR BBC6. Mus musculus (Mouse)			TISSUE=BI	Tang E., Zha J., Jockel J., Boise L.H., Thompson C.B., Korsmey	<pre>bau, a metriculmente partmen for bullah and bull, unspraces bax promotes cell death.";</pre>	Cell 8	PHOSPHORYLATION, AND MUTAGENESIS	MEDLINE=98022383; Pubmed≈93811/8; Del Peso L., Gonzalez-Garcia M., Page C.,	"Interleukin-3-induced phosphorylation of BAD through the pro	K W	(3) MITAGENESTS OF SERTINE RESTRIFES	MEDLINE=20403302; PubMed=10949026; Parts C Par	Greenberg M.E.; Au D., Felics A., Fesin S.W.,		BH3 domain phosphorylation."; Mol. Cell 6:41-51(2000).	- -	of heterodimerization of these proteins with BAX. Can re		and the apoptotic pathways.	x(L), Bcl-2 and Bcl-w, Also binds protein 100410 (By similar)	! :	-	BAX for their pro-apoptotic activity and for their with activity and for their with activity and for their formation of the policy and formation of the policy formation of th	!	Subsequent phosphorylation on Ser-136 promotes het with 14-3-3 proteins. This interaction then facili	phosphorylation at Ser-155, a site within the BH3 domain, leading to the release of Bcl-x(L) and the promotion of cell survival.
	REAL		E E	S S	888	R S	7. 2. 5. 5. 5. 5. 5. 5. 5. 5. 5. 5. 5. 5. 5.	Z Z Z	R	E E	잠.	X &	E E	퉕	N G	XX	RA	RT	R.F.	88	ŭ	ರ ರ	ರ ೮	ŏŏò	3 8	ပ္ပ င	3 8 8	388	38	88

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hsu S.Y., Kaipia A., Zhu L., Hsueh A.J.W.; "Interference of BAD (Bcl-xL/Bcl-2-associated death promoter)-induced apoptosis in mammalian cells by 14-3-3 isoforms and Pll."; Mol. Endocrinol. 11:1858-1867(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D'Agata V., Magro G., Travali S., Musco S., Cavallaro S.; "Cloning and expression of the programmed cell death regulator BAD in the rat brain.";
                                                                                                                                                                                                                                                                         S->A: NO PHOSPHORYLATION.
S->A: NO PHOSPHORYLATION; INTERACTS WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
Ser-136 is the major site of AKT/PKB phosphorylation, Ser-155 the
                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                           PKB).
PKB).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Bcl2-antagonist of cell death (BAD) (Bcl-2 binding component
                                                                                                                                                                                                                                                                                                                              Length 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND MUTAGENESIS OF SER-113 AND SER-137
         major site of protein kinase A (CAPK) phosphorylation. SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain. SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                                                                                                               PHOSPHORYLATION (BY PKA AND PHOSPHORYLATION (BY PKA AND PHOSPHORYLATION (BY PKA AND S->A: NO PHOSPHORYLATION.
                                                                                                                                                                                                                                                                                                                             Score 138; DB 1; Length 20.
Pred. No. 1.8e-13;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                        6C2BA910205053F7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Bcl-xL/Bcl-2 associated death promoter).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   205 AA
                                                                                                                                                                                                                                                                                                                                                                                   140 NIWAAQRYGREIRRMSDEFEGSFKGL 165
                                                                                                                                                                                                                                                                                                                                                                         2 NLWAAQRYGRELRRMSDEFEGSFKGL 27
                                                                                                                                                                                                                                                                                                 BCL-X(L)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21109372; PubMed=11161472;
                                                                                                                                                                        MGD; MGI:1096330; Bad.
InterPro; IPR000712; Bc12_BH.
PROSITE; PS01259; BH3; FALSE_NEG.
Apoptosis; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=98194755; PubMed=9535132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neurosci. Lett. 243:137-140(1998)
                                                                                                                                                                                                                                                                                                                                100.0%; Fr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98034386; PubMed=9369453;
                                                                                                                                                                                                                                                                                                          22080 MW;
                                                                                                                                           EMBL; L37296; AAA64465.1; -.
                                                                                                                                                                                                                                                                                                                               96.5%;
                                                                                                                                                                                                                                                                                                                                                   Conservative
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Rattus norvegicus (Rat)
                                                                                                                                                                                                                             1136
1136
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1136
                                                                                                                                                                                                                                                                                                          204 AA;
                                                                                                                                                                                                                                                                                                                                      Local Similarity
es 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  BAD_RAT 5 035147; 070256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Brain;
                                                                                                                                                   PIR; A5567
                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                               MOD_RES
                                                                                                                                                                                                                                                     MOD RES
                                                                                                                                                                                                                                                               MUTAGEN
                                                                                                                                                                                                                                                                          MUTAGEN
                                                                                                                                                                                                                                                                                    MUTAGEN
                                                                                                                                                                                                                     DOMAIN
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Matches
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration
Hamner S., Arumae U., Yu L.-Y., Sun Y.-F., Saarma M., Lindholm D.;

"Functional characterization of two splice variants of rat BAD and
their interaction with Bcl-w in sympathetic neurons.";

Mol. Cell. Neurosci. 17:97-106(2001).

L. Gell. Neurosci. 17:97-106(2001).

Mol. Cell. Serion serion of these proteins with BAX. Can reverse the binding to Bcl-x(L), Bcl-2 and Bcl-w, thereby affecting the level of heterodimerization of these proteins with BAX. Can reverse the death repressor activity of Bcl-x(L), but not that of Bcl-2 (By similarity). Appears to act as a link between growth factor receptor signaling and the apoptotic pathways.

C. SUBUNIT: Forms heterodimers with the anti-apoptotic proteins, Bcl-x(L), Bcl-2 and Bcl-w. Also binds protein slowalo. The Ser-137 phosphorylated form binds 14-3-3 proteins.

C. SUBCELLULAR LOCATION: Outer mitochondrial membrane. Upon phosphorylation, locates to the cytoplasm (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /FITG=VSP_000534.
S->A: NO EFFECT ON HETERODIMERIZATION
WITH 14-3-3 PROTEINS.
S->A: NO HETERODIMERIZATION WITH 14-3-3
PROTEINS. NO BEFECT ON HETERODIMERIZATION
WITH BCLS. NOR WITH PROTEIN P11.
SDAGGR -> ERRORK (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                    Bcl-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -> EELTYSVEFLPVRAIAMEGWPLLWSFQSFPHTLPPTPP
EVAMFPLRYWTALRRLC (in isoform Beta).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ISOId=035147-2; Sequence=VSP_000534;
TISSUE SPECIFICITY: Expressed in all tissues tested, including brain, liver, spleen and heart. In the brain, restricted to epithelial cells of the choroid plexus. Isoform alpha is the more abundant form.

DOMAIN: Intact BH3 domain is required by BIK, BID, BAK, BAD AND BAX for their pro-apoptotic activity and for their interaction with anti-apoptotic members of the Bcl-2 family.

PMM: Phosphorylated on Ser-113 in response to survival stimuli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Subsequent phosphorylation on Ser-137 promotes heterodimerization with 14-3-3 proteins. This interaction then facilitates the phosphorylation at Ser-156, a site within the BH3 domain, leading to the release of Bcl-x(L) and the promotion of cell survival. Ser-137 is the major site of ArX/PKB phosphorylation, Ser-156 the major site of protein kinase A (CAPK) phosphorylation (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BY SIMILARITY).
LPRPKSAGTATQMRQSASWTRIIQSWWDRNLGKGGSTPSQ
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PHOSPHORYLATION (BY PKA AND PKB)
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PHOSPHORYLATION (BY PKA AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain. SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Event-Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Phosphorylation; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId=035147-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000712; Bc12_BH.
PROSITE; PS01259; BH3; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF003523; AAC53374.1; -. EMBL; AF031227; AAC15100.1; -. EMBL; AF279910; AAF91427.1; -. EMBL; AF279911; AAF91428.1; -.
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22228 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALTERNATIVE PRODUCTS
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205 AA;
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RA Altschul S.F., Zeeberg B.A. Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Bottchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong I.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong I.,
Rapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Brownstein M.J., Workernan K.J., Malek J.A., Gunaratne P.H.,
Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Richards S., Worley K.C., Feren E.J., Lu X., Gibbs R.A.,
Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rhiting W., Maran J.W., Green E.D., Dickson M.C.,
Schein J.E., Jones S.J.M., Marra M.A.,
Schnerthen J.E., Jones S.J.M., Marra M.A.,
Represention and initial analysis of more than 15,000 full-length
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Yin D.X., Li Z., Huang B., Chen S., Zhou H.;
"A human protein that interacts with Bcl-2 and have homology to mouse
                                                                                                                                                                                                                                                                                                                                                                         Bcl2-antagonist of cell death (BAD) (Bcl-2 binding component 6) (Bcl-XL/Bcl-2 associated death promoter) (BCL2-like B protein).
BAD OR BBC6 OR BCL2L8.
                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wang Y., Wilson G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND PHOSPHORYLATION BY RAF-1.
MEDLINE=97083574; PubMed=8929532;
Wang H.-G., Rapp U.R., Reed J.C.;
"Bcl-2 targets the protein kinase Raf-1 to mitochondria.";
Cell 87:629-638(1996).
                   Length 205;
                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Takayama S., Reed J.C.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases
                DB 1; L
1.8e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98049554; Pubmed=9388232;
Ottilie S., Diaz J.-L., Horne W., Chang J., Wan Chang S., Titz L.C., Oltersdorf T.;
Linerization properties of human BAD.";
J. Biol. Chem. 272:30866-30872(1997).
                                                                                                                                                                                                                                                                                     092934; 014803; 01-NOV-1997 (Rel. 35, Created) 16-0CT-2001 (Rel. 40, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                      168 AA.
            Score 138; DB s; Pred. No. 1.86 0; Mismatches
                                                                                                                                   2 NLWAAQRYGRELRRMSDEFEGSFKGL 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND DIMERIZATION.
                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Lung;
MEDLINE=22388257; PubMed=12477932;
              96.5%;
                                                             26; Conservative
                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Bone marrow;
              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606
                                                                                                                                                                                                                                                                      BAD_HUMAN
                                                               Matches
                                                                                                                                                                                                                                               BAD_HUMAN
                                                                                                                                                                                                                         RESULT 3
                                                                                                                                                                                                                                                                      REPARTED TO THE SECOND OF THE 
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**Resin S.W.;

**Rationale for Bcl-xL/Bad peptide complex formation from structure,

**T mutagenesis, and biophysical studies.";

**Protein Sci. 9:2528-2534(2000).

**L Protein Sci. 9:2538-2534(2000).

**L Protein Sci. 9:254(2000).

**C death repressor activity of Bcl-x(L), but not that of Bcl-z (By Similarity). Appears to act as a link between growth factor receptor signaling and the apoptotic pathways.

**C complex sci. 10:2528-253 proteins Sci. 10:2528-253 proteins (By similarity).

**C complex sci. 10:2528-253 proteins (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are ho restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ser-99 is the major site of ART/PKB phosphorylation, Ser-118 the major site of protein kinase A (CAPK) phosphorylation (by similarity).

SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.

SIMILARITY: BELONGS TO THE BCL-2 FAMILY.

CAUTION: Ref.1 sequence differs from that shown due to frameshifts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            phosphorylation, locates to the cytoplasm.

TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.

DOMAIN: Inteact BH3 domain is required by BHX, BID, BAK, BAD AND
BAX for their pro-appoptotic activity and for their interaction
with anti-apoptotic members of the Bcl-2 family.

PTM: Phosphorylated on Ser-75 in response to survival stimuli.
Subsequent phosphorylation on Ser-99 promotes heterodimerization
with 14-3-3 proteins. This interaction then facilitates the
phosphorylation at Ser-118, a site within the BH3 domain, leading
to the release of Bcl-x(L) and the promotion of cell survival
                       MEDLINE=21073561; Pubmed=11206074; Petros A.M., Netteshaim D.G., Wang Y., Olejniczak B.T., Meadows R.P., Mack J., Swift K., Matayoshi E.D., Zhang H., Thompson C.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PKB) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PHOSPHORYLATION (BY PKA AND PKB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Outer mitochondrial membrane. Upon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 168;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polymorphism; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A -> S (in dbSNP:3729933)
/FTId=VAR_015380.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79.7%; Score 114; DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A -- S
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PROSITE; PS01259; BH3; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, AF021792; AAB72092.1; -.
EMBL, AF031523; AAB88124.1; -.
EMBL; BC001901; AAH01901.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18392 MW;
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STRUCTURE BY NMR OF 103-127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in position 64 and 91.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PDB; 1G5J; 07-FEB-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        168 AA;
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ITH2 MOUSE
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CARBOHYD
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                                                                                                                                                                                                                                                                                                        CONFLICT
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CHAIN
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                                                                               SIGNAL
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ITH2_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nakatani T., Suzuki Y., Yamamoto T., Sinohara H.; "Molecular cloning and sequencing of cDNAs encoding three heavy-chain precursors of the inter-alpha-trypsin inhibitor in Syrian hamster: implications for the evolution of the inter-alpha-trypsin inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBDUIT: 1-ALPHA-I PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN, BIKUNIN. INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2 AND BIKUNIN, INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN. AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN. PTM: HEAYY CHAINS ARE INTERLINED WITH BIKUNIN VIA A CHONDROITIN 4-SULFATE BRIDGE TO THE THEIR C-TERMINAL ASPARTATE (BY
                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Biochem. 120:145-152(1996).

-!- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN, INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yamamoto T., Yamamoto K., Sinohara H.; "Inter-alpha-trypsin inhibitor and its related proteins in Syrian hamster urine and plasma.";
                                                                                                                                                                                                                                             15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Inter-alpha-trypsin inhibitor heavy chain H2 precursor (III heavy chain H2) (Inter-alpha-inhibitor heavy chain 2) (HC2).
                                                                                                                                                                                                                                                                                                                                        Mesocricetus auratus (Golden hamster).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 55-64; 140-146; 151-156; 424-447; 500-528 AND 577-605
                     0;
                      Indels
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   5.8e-10;
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-!- SIMILARITY: Contains 1 VWFA domain.
                                                                                                                                                                                            946 AA.
                     Mismatches
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Ю
                                                                               103 NLWAAQRYGRELRRMSDEFVDSFK 126
                                                         2 NLWAAQRYGRELRRMSDEFEGSFK 25
                                                                                                                                                                                            PRT;
     Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-97420688; PubMed-9276673;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=97018241; PubMed=8864857;
                 0,
                                                                                                                                                                                                                             (Rel. 36, Created)
91.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biochem. 122:71-82(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; D89286; BAA13939.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR006587; VIT.
InterPro; IPR002035; VWF_A.
Pfam; PF00092; vwa; 1.
SMART; SM00609; VIT; 1.
                      22; Conservative
                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; JC5575; JC5575.
   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            heavy chain family
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AND SUBUNITS.
TISSUE=Plasma;
                                                                                                                                                                                                                                                                                                                                                                                                      Mesocricetus.
                                                                                                                                                                                                                               15-JUL-1998
                                                                                                                                                                                          ITH2 MESAU
                                                                                                                                                     RESULT 4
ITH2 MESAU
                      Matches
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SECURINE # 125/181/6N; TISSUE=Liver;

MEDLINE # 95194326; PubMed # 7534067;

MEDLINE # 95194326; PubMed # 7534067;

An P., Risler J.-L., Raquenez G., Salier J.-P.;

An P., Risler J.-L., Raquenez G. the inter-alpha-inhibitor

The three heavy-chain precursors for the inter-alpha-inhibitor

family in mouse: new members of the multicopper oxidase protein group

AT family in mouse: new members of the multicopper oxidase protein group

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                                                                                                                                                                                                     BY SIMILARITY.
INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CROSS-LINK SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                precursor (ITI heavy 2).
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N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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0
                                                                             Repeat; Signal; Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 54; DB 1; Length 946;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              106580 MW; CA8BF565458E7B2E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHONDROITIN 4-SULFATE, (BY SIMILARITY). V -> Y (IN REF. 2). E -> I (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUL-1998 (Rel. 36, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Inter-alpha-trypsin inhibitor heavy chain H2 givain H2) (Inter-alpha-inhibitor heavy chain 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Mismatches
                                                                                                                                                                                                                                                                                                                            SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      212 NVWIVELQGMRFLHVPDTFEGHFQGV 237
                                                                                                                                                                  POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 NLWAAQRYGRELRRMSDEFEGSFKGL 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                        BY SI
VWFA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37.8%;
                                                                             Serine protease inhibitor;
                                      VWFA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 36, C
(Rel. 36, L
(Rel. 41, L
SMART; SM00327; VWA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 510
                                                                                                                                                              18
54
702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              946 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                      PS50234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               445
578
702
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                                                                                                                                                                                                     19
55
                                                                                                                       Glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5-JUL-1998
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                                                                                                                                                                                                                                                                                         INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                  WWFA.

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

CHONDROITIN 4-SULFATE, CROSS-LINK SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chloroplast.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Asteridae; Ericales; Ericaceae; Ericoideae; Rhodoreae; Rhododendron.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Investigation of sectional relationships in the genus Rhododendron (Ericaceae) based on matK sequences."; Shokubutsu Kenkyu Zasshi 73:143-154(1998).
-:- FUNCTION: Probably assists in splicing chloroplast group II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              introns (By similarity).
-!- SIMILARITY: BELONGS TO THE INTRON MATURASE FAMILY 2. MATK
                                                                                                                                                                                                                         Serine protease inhibitor; Repeat; Signal; Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 946; 5.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. Kobayashi N., Handa T., Takayanagi Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  Y SIMILARITY).
40DB6716433ED9DC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Rel. 42, Last sequence update) (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            506 AA.
                                                                                                                                                                                                                                                                                                                      SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37.1%; Score 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            212 NVWIIEPQGMRFLHVPDTFEGHFQGV 237
                                                                                                                                                                                                                                                          POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 NLWAAQRYGRELRRMSDEFEGSFKGL 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                     ΒY
                                                                                                                                                                                                                                                                                                                      BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ledum palustre (Wild rosemary).
                                                                                                                                                                                                                                                                                                                                                                                                                                     MM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last seq
15-SEP-2003 (Rel. 42, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Maturase K (intron maturase).
                                                                                           PIR; S54354; S54354.
MGD; MGI:96619; Itih2.
InterPro; IPR006587; VIT.
InterPro; IPR002035; VWE_A.
Pfam; PF00092; VWA; 1.
SMART; SM00327; VWA; 1.
PROSITE; PS50234; VWA; 1.
                                                                              EMBL; X70392; CAA49842.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                  105927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best_Local Similarity 34.63
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                     946
468
118
263
702
                                                                                                                                                                                                                                                                                                                                                                                                                                  946 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=75583;
                                                                                                                                                                                                                                                                      19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBFAMILY
                                                                                                                                                                                                                                          Glycoprotein.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MATK_LEDPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yukawa T.;
                                                                                                                                                                                                                                                                                                                                     DOMAIN
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                    BINDING
                                                                                                                                                                                                                                                                         PROPEP
CHAIN
                                                                                                                                                                                                                                                                                                                     PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 6
MATK_LEDPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; endicotyledons; core eudicots; Asteridae; Ericales; Ericaceae; Ericoideae; Rhodoreae; Rhododendron. NCBI_TaxID=49622;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- FUNCTION: Probably assists in splicing chloroplast group II introns (By similarity).
-!- SIMILARITY: BELONGS TO THE INTRON MATURASE FAMILY 2. MATK
                                                                                                                                                                           7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7;
                                                                                                                                     Score 52.5; DB 1; Length 506; Pred. No. 3.1; S; Mismatches 8; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 506;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [1]
SEQUENCE FROM N.A.
Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AB012741; BAA25862.1; -.
InterPro; IPR000442; Intron_maturse2.
InterPro; IPR002866; Matk_N.
Pfam; PF01348; Intron_maturas2; 1.
Pfam; PF01824; Matk_N; 1.
mRNA PF02824; Matk_N; 1.
ERQUENCE 506 AA, 60534 MW; ADA44B25E92436E8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Invastigation of sectional relationships in the genus Rhododendron (Ericaceae) based on matk sequences."; Shokubutsu Kenkyu Zasshi 73:143-154(1998).
                                                                                                        CFEA926307DAC85E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36.7%; Score 52.5; DB 1; 37.5%; Pred. No. 3.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                  | :||| :||| | :|| | | :|| | 391 KPVWAALSDSDIIERFGRIYRNLSHYYSGSLK 422
                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | :||| :||| | 391 KPVWAALSDSDIIERFGRIYRNLSHYYSGSLK 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 KNLWAA-----QRYGRELRRMSDEFEGSFK 25
                                                                                                                                                                                                              1 KNLWAA-----QRYGRELRRMSDEFEGSFK 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rhododendron ferrugineum (Alpenrose).
EMBL; AB012751; BAA25872.1; -.
InterPro; IPR000442; Intron_maturse2.
InterPro; IPR002866; MatK_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                               Prem: PF01348; Intron_maturas2; 1. Pfam; PF01848; Intron_maturas2; 1. MFAm; PF01824; Matk N. 1. MRNA processing; Chloroplast. SEQUENCE 506 AA; 60412 MW; CFE
                                                                                                                                                                                                                                                                                                                                                                                                                                 Maturase K (Intron maturase).
                                                                                                                                          36.7%;
37.5%;
                                                                                                                                  Suery Match
Best Local Similarity 37.59
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12; Conservative
                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MATK_RHOTS
062991;
                                                                                                                                                                                                                                                                                                                                        MATK RHOFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MATK_RHOTS
ID MATK_RI
AC 062991
                                                                                                                                                                                                                                                                                                                        MATK_RHOFR
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Kuenzler
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Matches
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             NAMES OF A COLOR OF A 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δŏ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; Ericales; Ericaceae; Ericoideae; Rhodoreae; Rhododendron
NCBI_TaxID-49629;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1994 (Rel. 28, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Phospho-2-dehydro-3-deoxyheptonate aldolase, tyrosine-inhibited
(EC 4.1.2.15) (Phospho-2-keto-3-deoxyheptonate aldolase) (DAHP
synthetase) (3-deoxy-D-arabino-heptulosonate 7-phosphate synthase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                       "Investigation of sectional relationships in the genus Finododendron (Ericaceae) based on matK sequences."; Shokubutsu Kenkyu Zasshi 73:143-154(1998).
-!- FUNCTION: Probably assists in splicing chloroplast group II introns (By similarity).
-!- SIMILARITY: BELONGS TO THE INTRON MATURASE FAMILY 2. MATK SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 ;
                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36.7%; Score 52.5; DB 1; Length 506; 37.5%; Pred. No. 3.1; Live 5; Mismatches 8; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chloroplast.
A; 60569 MW; AEE12FF8809C223E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomycetales; Saccharomycetaceae; Saccharomyces
(Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 KNLWAA-----QRYGRELRRMSDEFEGSFK 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000442; Intron_maturse2.
InterPro; IPR002866; Matk_N.
Pfam; PF01348; Intron_maturas2; 1.
Pfam; PF01824; Matk_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1993 (Rel. 27, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AB012750; BAA25871.1; -.
                                                                            Maturase K (Intron maturase).
                                                                                                                              Rhododendron tsusiophyllum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ARO4 OR YBR249C OR YBR1701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 37.55
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gene 113:67-74(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               506 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mRNA processing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=4932;
                        28-FEB-2003
28-FEB-2003
                                                                                                                                                       Chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AROG_YEAST
                                                                                                                                                                                                                                                                                                                                                   Yukawa T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AROG_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QΥ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X61107; CAA43419.1; -.
EMBL; L20296; AAA65607.1; -.
EMBL; 236118; CAA85212.1; -.
PIR; 539185; S18185.
PIR; S9086; 10R7.
SGD; S0000453; ARO4.
GO; GO:0003849; F:2-dehydro-3-deoxyphosphoheptonate aldolase . . .; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                             Aljinovic G., Pohl F.M., Pohl T.M.;
Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: STEREOSPECIFIC CONDENSATION OF PHOSPHOENOLPYRUVATE (PEP)
AND D-ENTIHROSE-4-PHOSPHATE (E4P) GIVING RISE TO 3-DBCXY-D-
ARABINO-HEPPULOSONATE-7-PHOSPHATE (DAHP).
-!- CATALXTIC ACTIVITY: 2-dehydro-3-deoxy-D-arabino-heptonate 7-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
                                                                                                                                            Doignon F., Biteau N., Aigle M., Crouzet M.;
"The complete sequence of a 6794 bp segment located on the right arm of chromosome II of Saccharomyces cerevisiae. Finding of a putative Admins in a veset ".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AP3_ARATH STANDARD; PRT; 232_AA.
P35632; Q39003; Q8LB79; Q9S7Q3; Q9SQ14; Q9SQ15; Q9SQ16; Q9SQ17; Q9SQ18; Q9SQ19; Q9SQ20; Q9SQ21; Q9SQ22; Q9SX13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  phosphate + phosphate = phosphoenolpyruvate + D-erythrose phosphate + H(2)0. ENZYME REGULATION: INHIBITED BY TYROSINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PP00793; DAHP, synth_1; 1.
ProDom; PD005060; AroFGH; 1.
TIGRFAMS; TIGR00034; aroFGH; 1.
Aromatic amino acid biosynthesis; Lyase; Multigene family.
SEQUENCE 370 AA; 39749 MW; 594ED48F24175979 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 52; DB 1; Length 370; Pred. No. 2.7; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- INDUCTION: By amino acid starvation.
-!- SIMILARITY: BELONGS TO CLASS-I DAHP SYNTHETASE FAMILY.
Submitted (NOV-1993) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Floral homeotic protein APETALA3.
AP3 OR AT3654340 OR T12E18_30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80 DLEAAQEYALRIKKLSDELKG 100
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                                                                                                                                PubMed=8256522;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR006219; ArorGH.
InterPro; IPR006218; DAHP1/KDSA.
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47.68;
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                                                                                                                                                                                                                                                     dUTPase in a yeast.";
Yeast 9:1131-1137(1993).
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mes 10; Conserv
                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                             MEDLINE=94078675;
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                                                                                                STRAIN=S288C;
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                                                                                                                                                                                                                                                        dUTPase
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ID AP3_A
AC P3563_A
AC P3563
AC P3563
DT 01-JU
DT 15-SE
DE Flora
GN Arabi
OC Sperm
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DAY BERKER BY SERVER BY SE
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RA BALANDUBELVILO/20; RIGHEGER M., ABSOTGE W., Unseld M.,
RA Fartmann B., Valle G., Bloecker H., Perez-Alonso M., Obermaier B.,
Belseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,
Belseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,
RA De Simone V., Choisne N., Artiquenave F., Robert C., Brottier P.,
RA Mincker P., Cattolico L., Weissenbach D., Saurin W., Ouetier F.,
RA Wincker P., Cattolico L., Weissenbach C., Fuchs M., Benes V.,
Wurmbach B., Drzonek H., Erfle H., Jordan N., Bangert S.,
Wurmbach B., Drzonek H., Erfle H., Jordan N., Bangert S.,
RA Wiedelmann R., Krann H., Voss H., Holland R., Brandt P., Nyakatura G.,
RA Wezzi A., Hornischer K., Kauer G., Loehnert T.-H., Nordsiek G.,
RA Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,
RA Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,
RA Mavarro P., Collado C., Perez-Perez A., Ottenwælder B., Masuy D.,
Cooke R., Laudie M., Berger-Llauro C., Purnelle B., Masuy D.,
A de Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,
RA Monhaupt G., Haase D., Schoof H., Rudd L., Tallon L.J., Jenkins J.,
RA Manhaupt G., Hass B., Maiti R., Wu D., Peterson J., Van Aken S.,
RA Manhaupt G., Militscher J., Sellers P., Gill J.E., Feldblyum T.V.,
RA Pai G., Militscher J., Sellers P., Gill J.E., Feldblyum T.V.,
RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,
RA Sasamoto S., Kimura T., Idesawa R., Rawashima K., Rishida Y.,
RA Stowawa C., Kohara M., Matsumoto M., Matsumo A., Wada T.,
Nakayama S., Nakazaki N., Shingo S., Takeuchi C., Wada T.,
Haliana M., Matsumoto M., Tabata S.;
RA Watanabe A., Yamada M., Tasuda M., Tabata S.;
RA Watanabe A., Yamada Malandus S., Ether P., Tabata S.,
Ra Matanabe A., Yamada M., Tasuda S., fthe plant Arabidopsis
                                                                                                                                                                                    MEDLINE=92154682; PubMed=1346756; Jack T., Brockman L.L., Meyerowitz B.M.; "The homeotic gene APETALA3 of Arabidopsis thaliana encodes a MADS box and is expressed in petals and stamens."; Cell 68:683-697(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Purugganan M.D., Suddith J.I.;

"Molecular population genetics of floral homeotic loci: departures from the equilibrium neutral model at the APETALA3 and PISTILLATA genes of Arabidopsis thaliana.";

Genetics 151:839-848(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Okamoto H., Yano A., Shiraishi H., Okada K., Shimura Y.; "Genetic complementation of a floral homeotic mutation, apetala3, with an Arabidopsis thaliana gene homologous to DEFICIENS of Antirrhinum majus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=cv. Bla-1, cv. Bretagny, cv. Bs-1, cv. Bu-0, cv. Bu-2, cv. Chi-1, cv. Co-1, cv. Columbia, cv. Corsacalla-1, cv. Cvi-0, cv. Gr-3, cv. Jl-1, cv. Ras-1, cv. Kent, cv. Landsberg erecta, cv. Li-3, cv. Li-8, and cv. Lisse;
MEDLINE=99126449; PubMed=9927474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SECURNCE FROM N.A.

Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R., Feldmann K.;
"Full-length cDNA from Arabidopsis thaliana.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
eurosids II; Brassicales; Brassicaceae; Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=cv. Columbia;
MEDLINE-21016720; PubMed=11130713;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=cv. Landsberg erecta;
MEDLINE=95036018; PubMed=7948893;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plant Mol. Biol. 26:465-472(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND VARIANTS.
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STRAIN=cv. Columbia;
                                                                                                               SECUENCE FROM N.A.
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                                           NCBI_TaxID=3702;
                                                                                                                                                          rissum-petal
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between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 409:525-529(2001).

Nature 409:525-529(2001).

-I- FUNCTION: Probable transcription factor involved in the genetic control of flower development. Is required for normal development of petals and stamens in the wild-type flower. Forms an heterodimer with PISTILLATA that is required for autoregulation of both AP3 and PI genes. AP3/PI heterodimer interacts with APETALAI or SEPALLAIA3 to form a ternary complex that could be responsible for the regulation of the genes involved in the flower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed-8643482;
Riechmann J.L., Krizek B.A., Meyerowitz E.M.;
"Dimerization specificity of Arabidopsis MADS domain homeotic proteins
APETALA1, APETALA3, PISTILLATA, and AGAMOUS.";
Proc. Natl. Acad. Sci. U.S.A. 93:4793-4798(1996).
                                                                                                                                                                                                                                                          STRAIN-cv. Columbia;
MEDLINE-99311297; PubMed-10382288;
Brunel D., Froger N., Pelletier G.;
"Development of amplified consensus genetic markers (ACGM) in Brassica
napus from Arabidopsis thaliana sequences of Known biological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Krizek B.A., Meyerowitz E.M.; "The Arabidopsis homeotic genes APETALA3 and PISTILLATA are sufficient to provide the B class organ identity function.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -:- TISSUE SPECIFICITY: Expressed in petals and stamens.
-:- INDUCTION: Positively regulated by the meristem identity proteins APETALA1 and LEAFY with the cooperation of UFO.
-:- MISCELLANEOUS: Mutations in AP3 cause transformation of petals into sepals and stamina into carpels.
-:- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT: Forms an heterodimer with PISTILLATA, capable of binding to CArG-box sequences. AP3/PI heterodimer binds AP1 or SEP3 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Honma T., Goto K.; "Complexes of MADS-box proteins are sufficient to convert leaves into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NG M., Yanofsky M.F.; "Activation of the Arabidopsis B class homeotic genes by APETALA1.";
Shinozaki K., Davis R.W., Ecker J.R., Theologis A.; "RIXEN Arabidopsis full length cDNA clones (RAFLs) sequenced by the SSP consortium (Salk/Stanford/PGEC)."; Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: Contains 1 K-box dimerization domain.
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EMBL; D21125; BAA04665.1; -.
EMBL; AF115798; AAD51887.1; -.
EMBL; AF115799; AAD51888.1; -.
                                                                                                                                                                                                                         SEQUENCE OF 36-128 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Development 122:11-22(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genome 42:387-402(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=11283333;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           function
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NCBI_TaxID=287;
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Q914U3;
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MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Xlausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
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Eukaryota, Metazoa, Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi; Muridae, Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 51; DB 1; Length 232;
Pred. No. 2.3;
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15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
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K-BOX.

COLLED C

K -> R

M -> T

N -> D

N -> D

C -> S

C -> 
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                                                                                                                    AAD51892.1;
AAD51893.1;
AAD51894.1;
AAD51895.1;
AAD51896.1;
AAD51897.1;
AAD51898.1;
AAD51809.1;
AAD51900.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, AFILS813; AAD51902.1; --
EMBL, AFILS814; AAD51903.1; --
EMBL, AL132971; CAB81799.1; --
EMBL, AX087369; AAM64919.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AY070397; AAL49893.1;
EMBL; AY142590; AAN13159.1;
EMBL; AF056541; AAD41557.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 44.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein C5orf5 homolog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR, A42095; A42095.
HSSP; P11746; 1MNM.
TRANSFAC; T01776; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                        AF115803; PAF115804; P
                                                                                                                                                                                                                                                                                                                               AF115808; AF115809;
                                                                                                                                                                                                          EMBL; AF115805;
EMBL; AF115806;
                                      AF115801;
AF115802;
                                                                                                                                                                                                                                                                                                EMBL; AF115807;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AF115811;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AF115812;
                                                                                                                                                                                                                                                                                                                                                                                                                        AF115810;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CE05_MOUSE
AC 08K2H3;
DT CE05 MOUSE
OF 15-SEP-2003
DT 15-SEP-2003
DT 15-SEP-2003
DT 15-SEP-2003
DE POTEIN CSOT
GN MUS MUSCULUS
OC MUSMALIS; EN
OC MAMMALIS; EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                       EMBL;
EMBL;
                                                                                                                        EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Loc
Matches
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ODR ROOM REAL MANAGEMENT OF THE PROPERTY OF TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
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Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Blatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshlyuki S., Carninci F., Prange C.,

Raba S.S., Loquellano N.A., Peters G.J., Malek J.A., Gunarathe P.H.,

Robark S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A. Villalon D.K., Muzuy D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rabey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Rodriguez A.C., Grimwood J.W., Jones S.J.W., Marra M.A.,

Generation and initial analysis of more than 15,000 full-length

Human and mouse CDNA sequences.",

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

-I. SIMIJARITY: Gontains 1 Rho-GAP domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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STRAIN-ATCC 15692 / PAO1;
MEDLINE-20437337; PubMed=10984043;
MEDLINE-20437337; PubMed=10984043;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith X.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pseudomonas aeruginosa.
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ·,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          189 256 GLU-RICH.
851 AA; 97054 MW; C2B2669FB6DB2CE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
DNA recombination protein rmuc homolog.
RMUC OR PA1031.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      453 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    782 EQLWKARAEKKKLRKMLREFEEAF 805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RHO-GAP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 KNLWAAQRYGRELRRMSDEFEGSF 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; BC031465; AAH31465.1; -. InterPro; IPR000198; RhoGAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pseudomonadaceae; Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PP00620; RhoGAP; 1.
SMART; SM00324; RhoGAP; 1.
PROSITE; PS50238; RHOGAP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 41.7 ses 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             opportunistic pathogen."; Nature 406:959-964(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTPase activation.
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PRINTS; PR00449; RASTRNSFRMNG.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6PGL_THEMA
Q9X0N8;
                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6PGL_THEMA
                                                                                                                                                                                                                                                                                        Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                      Db
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDINE-91061774; PubMed=1701021;

Casale W.L., McConnell D.G., Wang S.-Y., Lee Y.-J., Linz J.E.;

Casale W.L., McConnell D.G., Wang S.-Y., Lee Y.-J., Linz J.E.;

"Expression of a gene family in the dimorphic fungus Mucor racemosus which exhibits striking similarity to human ras genes.";

Wol. Cell. Biol. 10:6664-6663(1990).

-!- ENZYME REGULATION: ALTERNATE BETWEEN AN INACTIVE FORM BOUND TO GDP AND AN ACTIVE FORM BOUND TO GTP. ACTIVATED BY A GUANINE NUCLEOTIDE-EXCHANGE FACTOR (GEF) AND INACTIVATED BY A GTPASE-ACTIVATING PROTEIN (GAP).

-!- SUBCELLULAR LOCATION: Plasma membrane.

-!- BUYELLOPMENTAL STAGE: IN SPORULATING MYCELIUM AND MUCH LESS IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GERMLING AND YEAST. SIMILARITY: BELONGS TO THE SMALL GIPASE SUPERFAMILY. RAS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rhizomucor racemosus (Mucor circinelloides f. lusitanicus).
Eukaryota, Fungi, Zygomycota, Zygomycetes, Mucorales, Mucoraceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2
FUNCTION: Involved in DNA recombination (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Indels
                                                                                                                                                                                                                                                                                                                             Pfam; PF02646; RmuC; 1.

DNA recombination; Coiled coil; Complete protecme.

DOMAIN 16 201 COILED COIL (POTENTIAL).

SEQUENCE 453 AA; 51539 MW; 1E7EA97E82EG5E4B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    205 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 9.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                        SIMILARITY: BELONGS TO THE RMUC FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP; P01112; 1PLL.
InterPro; IPR003577; GTPase_Ras.
InterPro; IPR001806; Ras_trnsfrmng.
InterPro; IPR005225; Small_GTP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 WAAQRYGR--ELRRMSDE 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65 WASEROGREEELRRLASE 82
                                                                                                                                                                                                                                                         EMBL; AE004535; AAG04420.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      34.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M55177; AAA83379.1; -.
                                                                                                                                                                                                                                                                               PIR; E83517; E83517.
InterPro; IPR003798; DUF195.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00071; ras; 1.
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HSSP; P01112; 1PLL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ras-like protein 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN=ATCC 1216B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=4841;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RAS3_RHIRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 13
RAS3_RHIRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mucor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
  q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEATH TO SECOND CONTRACTOR SERVING CONTRACTOR SERVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99287316; PubMed=10360571;
Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.,
"Evidence for lateral gene transfer between Archaea and Bacteria from
genome sequence of Thermotoga maritima.";
Nature 399:323-329(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- PATHWAY: Pentose phosphate pathway; second step.
-!- SIMILARITY: BELONGS TO THE GLUCOSAMINE/GALACTOSAMINE-6-PHOSPHATE.
ISOMERASE FAMILY. 6-PHOSPHOGLUCONOLACTONASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHOSPHOGLUCONAIE.
-:- CATALYTIC ACTIVITY: 6-phospho-D-glucono-1,5-lactone + H(2)0 = 6-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thermotoga maritima.
Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
                                                                                                                                                                                                                                                                                                                                                                                                                .,
                                                                                                                                                                                                                                                                                                                                       33.6%; Score 48; DB 1; Length 205; 62.5%; Pred. No. 5.6; tive 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VACULE 373:343-343(1939).
                                                               GTP-binding; Prenylation; Lipoprotein.

NP_BIND
16 23 GTP (BY SIMILARITY).

NP_BIND
12 125 GTP (BY SIMILARITY).

NP_BIND
12 125 GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

SEQUENCE 202 PERCYOR REGION (PROBABLE).

LIPID
202 202 FARRESYL (BY SIMILARITY).

SEQUENCE 205 AA; 23408 MW; DBF086466F090F50 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MaY-2000 (Rel. 39, Created)
30-MaY-2000 (Rel. 39, Last sequence update)
38-FEB-2003 (Rel. 41, Last annotation update)
6-phosphogluconolactonase (EC 3.1.1.31) (6PGL).
PGL OR DEVB OR TM1154.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
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Pred. No. 6
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Interpro; IPR005900; Phosphogluconlac.
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SMART; SM00173; RAS; 1.
TIGRFAMS; TIGR00231; small_GTP; 1.
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SEQUENCE 220 AA; 25325 MW;
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                                                                                                                                                                                                                                                                                                                                                                          Local Similarity ....
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
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EMBL; AFUGLOST.

R HSSP: Q957B5; IBEX.

DR InterPro; IPR001926; B6_enzyme_beta.

DR InterPro; IPR000634; S/T_dehydrtse.

DR InterPro; IPR000634; S/T_dehydrtse.

DR TIGRAMA: T
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"Expression of threonine synthase from Solanum tuberosum L. is not metabolically requlated by photosynthesis-related signals or by nitrogenous compounds.";
Plant Sci. 157:43-50(2000).
-:- CATALYTIC ACTIVITY: O-phospho-L-homoserine + H(2)O = L-threonine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
Threonine synthase, chloroplast precursor (EC 4.2.3.1) (TS).
Solanum tuberosum (Podato).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; lamids; Solanales; Solanaceae; Solanum.
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Best Local Similarity 35.3%; Pred. No. 15;
Matches 12; Conservative 6; Mismatches 8; Indels
7; Indels
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8; Mismatches
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                                                                                                                                  5 AAQRYGRELRRMSDEFEGSFKGL 27
8; Conservative
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SEQUENCE FROM N.A.
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NCBI_TaxID=4113;
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AC QGMT28;

DT 28-FBB-2003

DT 28-FBB-2003

DT 28-FBB-2003

DS Solanum tubes;

OS Solanum tubes;

OS Solanum tubes;

OS Solanum tubes;

OS SOLANUM TO SOLAND=4

RN SEQUENCE FRO

RC ASCETIGAC;

OX NCBL_TAXTD=4

RN SEQUENCE FRO

RC TSSUB-LEASI;

RY EXPRESSION

RT TSSUB-LEASI;

RY TSSUB-LEASI;

RY TSSUB-LEASI;

RY TSSUB-LEASI;

RY TSSUB-LOSTICALI

CC -1- CATALYTI

CC -1- CATALYTI

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CC -1- SUBCELLI

CC -1
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Matches
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us-09-544-664-56.rspt

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September 15, 2003, 17:17:31 ; Search time 29.3143 Seconds
(without alignments)
237.680 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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1 KNIMAAQRYGRELRRMSDEFEGSFKGL 27
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Maximum Match 1008
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Q8Vjs3 mycobacteri Q10843 mycobacteri Q8K016 mus musculu Q4K149 menziesia c 047149 rhododendro 047171 rhododendro 062982 rhododendro 062972 rhododendro 062972 rhododendro 062978 rhododendro 062978 rhododendro 062978 rhododendro 047155 rhododendro 047155 rhododendro 047155 rhododendro 047155 rhododendro Q919n2 brachydanio Description Q919N2 Q8VJS3 Q8VJ63 Q10843 Q10843 Q47148 Q47149 Q47171 Q62982 Q62975 Q62975 Q62975 062978 047155 047152 047173 Query Match Length DB 11146 22296 22296 22296 23206 23206 23206 23206 23206 23206 837.1 837.1 837.1 837.1 837.1 837.1 837.1 847.1 857.1 86 Score

196 AA.

PRT;

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Q8VJS3, Q8VJS3,

RESULT 2 Q8VJS3 ID Q8 AC Q8

17 52.5 36.7 506 8 062974 18 52.5 36.7 506 8 062974 20 52.5 36.7 506 8 062974 21 52.5 36.7 506 8 062981 22 52.5 36.7 506 8 062981 23 52.5 36.7 506 8 062981 24 52.5 36.7 506 8 062981 25 52.5 36.7 506 8 062981 25 52.5 36.7 506 8 062981 25 52.5 36.7 506 8 062981 25 52.5 36.7 506 8 062981 25 52.5 36.7 506 8 062981 25 52.5 36.7 506 8 062981 25 52.5 36.7 506 8 062981 25 52.5 36.7 506 8 062981 25 52.5 36.7 506 8 062891 31 52.5 36.7 506 8 062891 32 52.5 36.7 506 8 062891 33 52.5 36.7 506 8 062891 34 52.5 36.7 506 8 062891 35 52.5 36.7 506 8 062891 35 52.5 36.7 506 8 062891 36 52.5 36.7 506 8 062891 37 52.5 36.7 506 8 062891 38 52.5 36.7 506 8 062891 39 52.5 36.7 506 8 062891 30 52.5 36.7 506 8 062891 31 52.5 36.7 506 8 062891 32 52.5 36.7 506 8 062891 34 52.5 36.7 506 8 062891 35 52.5 36.7 506 8 062891 36 52.5 36.7 506 8 062891 37 52.5 36.7 506 8 062891 38 52.5 36.7 506 8 062891 39 52.5 36.7 506 8 062891 44 51.5 36.0 506 8 044160 52 53 6.7 506 8 062891 50 52 5 36.7 506 8 062891 50 52 5 36.7 506 8 062891 50 7	062990 rhododendro 062974 rhododendro 062993 menziesia m 04717 rhododendro 062983 rhododendro 062981 rhododendro 062981 rhododendro 062981 rhododendro 062981 rhododendro 062981 rhododendro 062973 rhododendro 062973 rhododendro 062982 ledum palus 047175 rhododendro 062982 rhododendro 08hsp1 rhododendro 08hsp1 rhododendro 08hsp1 rhododendro 08hsp1 rhododendro 08hsp1 rhododendro 08hsn7 rhododendro 062985 rhododendro 062996 rhododendro 062971 rhododendro			e) ate)	ata; Buteleostomi; physi; Cypriniformes;	regulators identified in	CRC64;	Length 146; ; Indels 0; Gaps 0;	
11 12.52.5 36.7 506 52.5 36.7	062990 062974 062993 062993 047174 062980 062981 062981 062988 062988 062977 04716 0681SNP 0681SNP 0681SNP 0681SNP 0681SNP 0681SNP 0681SNP 0681SNP 062985 062985 062985 062985 062985 062985 062985 062985 062985	ALIGNMENTS	. 146	quence u	(Danio : Craniata Teleoste:	8; n apoptosis	(2000). - : 28A56	Score 87; DB 13; Pred. No. 5.9e-05; Mismatches	25
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11.52.55 52.55	<i>~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~</i>		PRE	(Tr (Tr (Tr	rer feta jii; Dan 7955	N MC 7379 Nun hom)117;)17; 1; 1	Llar Con	4AQR ::
RESULT OF THE RE			LT 1 N2 Q919N2	USISNZ; 01-0CT-2000 01-DEC-2001 01-0CT-2002	BAD. BRAD. Brachydanio Eukaryota; N Actinopteryg Cyprinidae;	Lij MEDLINE=2037 Inohara N., "Genes with	zebrafish."; Cell Death I EMBL; AF231(HSSP; Q92934 ZFIN; ZDB-GE	Matc]	e 0
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Indels
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 Mismatches
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                                          2 NLWAAQRYGRELRRMSD
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Best Local Similarity 34.6
Matches 9; Conservative
10; Conservative
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SEQUENCE FROM N.A.
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01-MAR-2003
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Q8K016;
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                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Alland B., Eisen J.A., Haft D., Hickey E.,
Kolonay J.F., Melson W.C., Umayam E.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                             Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacterium.
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                                                                                                                                                                                                                                                                                                                                                                              6; Indels
                                                                                                                                                                                                                                         laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AE007058; AAK46348.1; -.
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Pfam; PR02371; Transposase_20; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 223 AA; 24132 MW; 70456750017FEF37 CRC64;
                                                                                                                                                                                                                                                                                                            Pfam; PF02371; Transposase_20; 1.
SEQUENCE 196 AA; 21349 MW; C145A8D836FD9C2D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Corynebacterineae; Mycobacteriaceae; Mycobacterium
                                                                                                                                                                                                                                                                                                                                                 37.1%; Score 53; DB 16; 58.8%; Pred. No. 8.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 53; DB 16;
Pred. No. 9.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complete genome sequence.";
Nature 393:537-544(1998).
-!- SIMILARITY: TO M.PARATUBERCULOSIS IS900.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   223 AA.
                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                              InterPro; IPR003346; Transposase_20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
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                                                                                                                                                                                                                                                                                                                                                                          1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1998 (TrEMBLrel. 08, 01-MAR-2002 (TrEMBLrell. 20, HYPOTHEIGAL PROTOLEIR RV2014 OR MTCX39.03C.
                                                                  Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 58.88
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                      IS1607, transposase.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [1]
SEQUENCE FROM N.A.
STRAIN=H37Rv;
                                                                                                         NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                 TIGE; MT2070;
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-!- SINIRUNS (B: SIMILARIII).
-!- SINIRUNS (B: SIMILARIII).
AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED IMICCHONDRIAL INTRONS.
EMBL; UG1331; AAC15245.2; -.
Interpro: IPR000442; Intron_maturse2.
Interpro: IPR002866; Matk_N.
Pfam; PF01348; Intron_maturas2; 1.
Pfam; PF01349; Matk_N. 1.
  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata; Vertebrata, Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Phylogenetics of Rhododendroideae (Ericaceae).";
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
INTRONS (BY SIMILARITY).
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01-JUN-1998 (TrEMBLrel. 06, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Ribosomal maturase (Introm maturase) (Maturase K) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 53; DB 11; Length 946;
Pred. No. 48;
5; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.;
Strausberg R.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC034341; AAH34341.1; -.
MGD; MGI:96619; Itih2.
InterPro: IPR006587; VIT.
InterPro: IPR002035; VWF_A.
SWART; SM00609; VIT; 1.
SWART; SW00327; VWA; 1.
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Chloroplast.
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O62982
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-!- SIMILARITY: WITH CORRESPONDING ORF IN CTHER PLANT CHLOROPLASTS,
AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY
MITOCHONDRIAL INTRONS.

EMBL; U61332; AAB93753.1; -...
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                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots;
Asteridae, Ericales, Ericaceae, Ericoideae, Rhodoreae, Rhododendron.
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Asteridae, Ericales, Ericaceae, Ericoideae, Rhodoreae, Rhododendron.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kron K.A.;
"Phylogenetics of Rhododendroideae (Ericaceae).";
submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 ;
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                                                                                         Length 505;
                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA processing; chloroplast.
SEQUENCE 506 AA; 60502 MW; 0009EA88CD28549F CRC64;
                                          60233 MW; EE5F927AD2E57DE5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-1998 (TrEMBLrel. 06, Last sequence update) 01-OCT-2002 (TrEMBLrel. 22, Last annotation update) Ribosomal maturase (Intron maturase) (Naturase K).
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                                                                                         DB 8;
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                                                                                                                                                                                                     390 KPVWAALSDSDIIERFGRIYRNLSHYYSGSLK 421
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                                                                                                                                                                              1 KNLWAA-----QRYGRELRRMSDEFEGSFK 25
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                                                                                                                                                                                                                                                                                                                                     AA.
                                                                                   36.7%; Score 52.5; I
37.5%; Pred. No. 28;
tive 5; Mismatches
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InterPro; IPR002866; MatK_N.
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01-JUN-1998 (TrEMBLrel. 06, Last seq
01-OCT-2002 (TrEMBLrel. 22, Last ann
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mRNA processing; Chloroplast.
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                                                                                                           Local Similarity 37.5 hes 12; Conservative
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                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rhododendron kiusianum.
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Best Local Similarity
The 12; Conserve
                                          505 AA;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Asteridae; Erica.
NCBI_TaxID=49167
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                      NON_TER
SEQUENCE
                                                                                       Query Match
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047149
1D 047149
DT 01-J
DT 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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-:- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS, AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED MITOCHONDRIAL INTRONS.
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"Phylogenetics of Rhododendroideae (Ericaceae).";
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7;
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Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 8; Length 506;
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PROJECT STATE ST
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Ribosomal maturase (Intron maturase) (Maturase K).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 KNLWAA-----QRYGRELRRMSDEFEGSFK 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36.7%; Score 52.5; 37.5%; Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 52.5;
Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AB012749; BAA25870.1; -.
EMBL; AB012745; BAA25866.1; -.
InterPro; IPR000442; Intron_maturse2.
InterPro; IPR002866; Matk_N.
                                                                                                                                                                                                                                                                                                                               EMBL, U61354; AAB93748.1; -
Interpro; IPR000442; Intron_maturse2.
Interpro; IPR002866; MatK_N.
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01-AUG-1998 (TrEMBLrel. 07, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF01348; Intron maturas2; 1. Pfam; PF01824; MatK_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mRNA processing; Chloroplast.
SEOUENCE 506 AA; 60389 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36.7%;
37.5%;
                                                                                                                                           INTRONS (BY SIMILARITY)
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Best Local Similarity 37.5
Matches 12, Conservative
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nes 12; Conservative
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Chloroplast.
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Matches
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                                                                                                                                    RESULT 11
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A NULASHIPS....

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RT "INVESTIGATION of Sectional Relationships in the Genus
RT "Abdodendron(Ericaceae) based on matK Sequences.";

RL J. Jpn. Bot. 0:0-0(1998).

CC -!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II

CC -!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II

CC -!- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,

CC AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY

CC MITOCHONDRIAL INTRONS.

CC MATOCHONDRIAL INTRONS.

DR MITOCHONDRIAL INTRONS.

DR MITOCHONDRIAL INTRONS.

DR MITOCHONDRIAL INTRONS.

DR INTERPRO: IPR000442; Intron_maturse2.

DR InterPro: IPR002866; MatK.N.

InterPro: IPR002866; MatK.N.
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-!- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,
AND REGIONS OF SIMILARITY TO MATCRASE-LIKE POLYPEPTIDES ENCODED
MITOCHONDRIAL INTRONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; Ericales; Ericaceae; Ericoideae; Rhodoreae; Rhodorean
                                                                 Chloroplast.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; Ericales; Ericaceae; Ericoideae; Rhodoreae; Rhododendron.
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                                                                                                                                            CLJUENCE FROM N.A.
Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
                                                                                                                                                                                                                                                                                                                                                                                                     Score 52.5', DB 8; Length 506;
Pred. No. 28;
5; Mismatches 8; Indels '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [1]
SEQUENCE FROM N.A.
Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi
Yukawa T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF01348; Intronmaturas2; 1.
Pfam; PF01824; MatK_N; 1.
mRNA processing; Chloroplast.
SEQUENCE 506 AA; 60449 MW; 21DFF700B071B5B8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Investigation of Sectional Relationships in the Genus
                                                                                                                                                                                                                                                                                                                                                               Chloroplast.
A; 60419 MW; 1F95132CCF4F6B40 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
01-AUG-1998 (TIEMBLIE). 07, Last sequence update) 01-OCT-2002 (TIEMBLIE). 22, Last annotation update) Ribosomal maturase (Intron maturase) (Maturase K).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rhododendron(Ericaceae) based on matK Sequences.";
J. Jpn. Bot. 0:0-0(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 KNLWAA------QRYGRELRRMSDEFEGSFK 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      506 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AB012732; BAA25853.1; -.
InterPro; IPR000442; Intron_maturse2.
InterPro; IPR002866; Matk_N.
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                                                                                                                                                                                                                                                                                                                                    Pfam; PF01348; Intron_maturas2; 1. Pfam; PF01824; Matk_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                      36.7%;
37.5%;
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 37.55
Matches 12; Conservative
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                                                   Rhododendron nipponicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rhododendron ponticum.
                                                                                                                                                                                                                                                                                                                                                                             506 AA;
                                                                                                                        NCBI_TaxID=75577;
                                                                                                                                                                                                                                                                                                                                                                mRNA processing;
SEQUENCE 506 AA
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062975
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J. Jpn. Bot. 0:0-0(1998).
-!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
INTRONS (BY SIMILARITY).
-!- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,
AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES BNCODED BY
MITCHCHONDRIAL INTRONS.
EMBL, AB012729; BAA25850.1; -.
InterPro; IPR00442; Intron_maturse2.
InterPro; IPR002666; Matk_N.
Pfam; PF01348; Intron_maturas2; 1.
Pfam; PF01348; Intron_maturas2; 1.
                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; Ericales; Ericaceae; Ericoideae; Rhodoreae; Rhododendron. NCBI_TaxID=49169;
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                                                                       7;
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Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
Yukawa T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [1]
SEQUENCE FROM N.A.
Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
Yukawa T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 8; Length 506;
                   Length 506;
                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                               01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Ribosomal maturase (Intron maturase) (Maturase K)
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                      DB
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                                                                                                                           1 KNLWAA-----QRYGRELRRMSDEFEGSFK 25
                   Score 52.5; DE
Pred. No. 28;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          506 AA
                                                                                                                                                                                                                                                                                                                506 AA.
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37.5%; Pred. No. 28;
ive 5; Mismatches
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                                                                                                                                                                                                                                                                                                                PRT;
36.7%; Scur
37.5%; Pred
5;
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                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rhododendron ovatum.
                      Query Match
Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA processing;
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                      mRNA processing;
          01-JUN-1998
01-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chloroplast.
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                                                                                                                                                      Kron K.A.;
                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
047152
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                                                                                                                                                                                                           Ä
         Rhododendron(Ericaceae) based on matK Sequences.";
J. Jpn. Bot. 0:0-0(1998).
-!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
INTRONS (BY SIMILARITY).
-!- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,
AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY
MITOCHONDRIAL INTRONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INTRONS (BY SIMILARITY).

-!- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,

AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY

MITOCHONDRIAL INTRONS.
                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                          Chloroplast.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Magnoliophyta; endicotyledons; Core eudicots;
Asteridae; Ericales; Ericaceae; Ericoideae; Rhodoreae; Rhododendron.

NCBL_TaxID=49465;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rhododendron(Ericaceae) based on matK Sequences.";
J. Jpn. Bot. 0:0-0(1998).
-!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7;
                                                                                                                                                                                                           1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
Yukawa T.;
                                                                                                                                                                                   36.7%; Score 52.5; DB 8; Length 506; 37.5%; Pred. No. 28; Live 5; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 506;
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"Investigation of Sectional Relationships in the Genus
                                                                                                                                                              6D38A1D4D6FEC9BF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Investigation of Sectional Relationships in the Genus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60350 MW; 5E832589ED64EA25 CRC64;
                                                                                                                                                                                                                                                                                                                                      01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                             01-0CT-2002 (TrEMBLrel. 22, Last annotation update
Ribosomal maturase (Intron maturase) (Maturase K)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 KNLWAA-----QRYGRELRRMSDEFEGSFK 25
                                                                                                                                                                                                                                  1 KNLWAA-----QRYGRELRRMSDEFEGSFK 25
                                                                                                                                                                                                                                                                                                                  506 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 52.5; Pred. No. 28;
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InterPro; IPR000442; Intron_maturse2.
InterPro; IPR002866; MatK_N.
                                                                                         EMBL; AB012747; BAA25868.1; -.
InterPro; IPR000442; Intron_maturse2.
InterPro; IPR002866; MatK_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                   PRT;
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Pfam; PF01824; Matk_N; 1.
mRNA processing; Chloroplast.
SEQUENCE 506 AA; 60350 WW; 5E8
                                                                                                                           Pfam; PF01348; Intron maturas2; 1. Pfam; PF01824; MatK_N; 1.
                                                                                                                                                  mRNA processing; Chloroplast.
SEQUENCE 506 AA; 60489 MW;
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37.5%;
                                                                                                                                                                                               Local Similarity 37.5%;
nes 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                  Rhododendron canadense,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12;
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Best Local S
                                                                                                                                                                                    Query Match
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047155
ID 04715
AC 04715
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-!- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,
AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY
MITOCHONDRIAL INTRONS.

EMBL, U61335, AAB93757.1; -
InterPro, IPR000442; Intron_maturse2.

InterPro; IPR002866; Matk_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INTRONS (BY SIMILARITY).
-!- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,
AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                  Chloroplast.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; Ericales; Ericaceae; Ericoideae; Rhodoreae; Rhododendron.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; Ericales; Ericaceae; Ericoideae; Rhodoreae; Rhododendron. NCBI_TaxID=49170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Phylogenetics of Rhododendroideae (Ericaceae).";
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
                                                                                                                                                                                                                                                                                                                                                                                         "Phylogenetics of Rhododendroideae (Ericaceae).";
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-1998 (TrEMBLrel. 06, Last sequence update) 01-OCT-2002 (TrEMBLrel. 22, Last annotation update) Ribosomal maturase (Intron maturase) (Maturase K).
                            (TrEMBLrel. 06, Last sequence update) (TrEMBLrel. 22, Last annotation update)
                                                                                     Ribosomal maturase (Intron maturase) (Maturase K)
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Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36.7%; Score 52.5; 37.5%; Pred. No. 28
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EMBL; U61338; AAB93751.1; -,
InterPro; IPR000442; Intron_maturse2.
InterPro; IPR002866; MatK_N.
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506 AA; 60406 MW;
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37.5%;
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06,
22,
(TrEMBLrel. 06, TrEMBLrel. 06,
                                                                                                                                      Rhododendron hongkongense.
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Matches 12; Conservative
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SEQUENCE 506 AA;
                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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7; Gaps
  8; Indels
Matches 12; Conservative 5; Mismatches
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-1

1 KNLWAA------QYRGRELRRWSDEFEGSFK 25 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 391 KPVWAALSDSDIIERFGRIYRNLSHYSGSLK 422

OD δÿ

Search completed: September 15, 2003, 17:25:50 Job time: 29.3143 secs

Page 6

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
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OM protein - protein search, using sw model

September 15, 2003, 17:16:01; Search time 22.6286 Seconds (without alignments) 112.231 Million cell updates/sec Run on:

US-09-544-664-28 84 1 QRYGRELRRMSDEFEG (16) Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1107863 seqs, 158726573 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_19Jun03:* Database :

| SIDSI/gogdata/geneseqy/geneseqy embl/Ah1990.DAT:*
| SIDSI/gogdata/geneseqy/geneseqy-embl/Ah1990.DAT:*
| SIDSI/gogdata/geneseqy/geneseqp-embl/Ah1991.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		c				
Result No.	Score	% Query Match	% Query Match Length DB	DB	ID	Description
;	84	100.0	16	707	AAY05422	Mouse BAD BH3 doma
7	84	100.0	16	21	AAB37028	Bcl2 polypeptide B
m	84	100.0	23	17	AAR95166	bcl-x(L)/bcl-2 ass
4	84	100.0	26	21	AAB37001	Bcl2 polypeptide B
·	84	100.0	36	21	AAB37002	Bcl2 polypeptide B
9	84	100.0	27	21	AAB37003	Bcl2 polypeptide B
7	84	100.0	27	21	AAB37056	Bcl2 polypeptide B
8	84	100.0	28	21	AAB37055	Bcl2 polypeptide B
6	84	100.0	162	22	AAB70370	Shorter murine BAD

bcl-x(L)/bcl-2 ass	Murine BCL-XL/BCL-	Mutant BCL-XL/BCL-	u	Mutant BCL-XL/BCL-	Murine BAD protein	Longer murine BAD	Murine BAD protein	Bad-DITR apoptosis	Human BAD BH3 doma	Bcl2 polypeptide B	Human Bcl2 fluores	Ba	Mutant Bcl2 compet	Human Bad peptide	й П	Ba	Human Bad peptide	Ba(Bã	Human Bcl2 fluores	Human Bad peptide	1 Bad	PTPC-interacting T	Human Bcl2 fluores	^1	t Bcl2	t Bc12	~	Mutant Bc12 compet	Δ.	ο,	E Bcl2	c12	ant Bcl2	C)	
516	131	AAW61316	131	131	383	336	908)22	AAY05421	702	48	360	349	362	350	860	863	362	362	348	860	362	ABP56161	348	348	848	848	848	84	ABG78489	7849	7849	7849	37849	7849	
17	19	19	19	19	19	22	24	22	20	21	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	
\bigcirc	\Diamond	204	\circ	0	0	\circ	0	w	16	16	18	18	20	20	21	21	21	22	23	24	24	24	25	25	25	25	25	25	25	25	25	25	25	25	25	
100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	86.9	86.9	86.9	86.9	86.9	86.9	86.9	86.9	86.9	86.9	86.9	86.9	86.9	86.9	86.9	86.9	86.9	86.9	86.9	86.9	86.9	86 9	86.9	86.9	86.9	80. 80.	86.9	
84	84	84	84	84	84	84	84	84	73	73	73	73	73	73	73	73	73	73	73	73	.73	73	73	73	73	73	73	73	73	73	73	73	73	73	73	
10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

AAY05422 standard; peptide; 16 AA RESULT 1 AAY05422

AAY05422;

(first entry) 02-JUL-1999

Mouse BAD BH3 domain.

BH3 domain; cell death agonist; bcl homology domain; BCL-2 family; apoptosis promoter; cancer cell; virus infected cell; inflammation; autoantibody producing cell; cancer; lymphoproliferative condition; arthritis; autoimmune disease; therapy.

Mus sp

W09916787-A1

(0)(e) (1 km ft. tr. 10) 08-APR-1996.

98WO-US19765.

22-SEP-1998;

97US-0946039. 97US-0060133. 07-OCT-1997; 26-SEP-1997;

(UNIW) UNIV WASHINGTON

Korsmeyer SJ;

WPI; 1999-255058/21.

us-09-544-664-28.rag

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Best Loca
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a peptide conjugate having the formula: (R-X)n-peptide where n=1-10; X=C=0, when the R-X group is attached to the N-terminus of the peptide, or a side chain of the peptide where the functional group of the side chain is NH2 or OH; or X=0 or NH, when the R-X group is attached to the C-terminus of the peptide, or a side chain of the peptide, where the side chain functional group is COOH or CONH2; and R=2\cdot18C alkyl or alkoxy, 2\cdot14C alkylenyl containing one or two double bonds, exclobutyl, cyclopentyl, cyclohexyl optionally
                                                                 This sequence represents the BH3 domain of mouse BAD. The invention relates to a bcl homology domain 3 (BH3 domain), derived from a proapoptotic member of the BCL-2 family. The BH3 polypeptide can be used in a method for promoting apoptosis in a target cell, especially where the cell. is a cancer cell a virus infected cell or an autoantibody producing cell. The BH3 polypeptide can be used in therapeutic compositions for treating disease including cancer, other lymphoproliferative conditions, arthritis, inflammation, and autoimmune diseases, which may result from the down regulation of cell death
                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective; cardiant; Bc1-2 superfamily; BH3 domain; cell death agonist; Bad; apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate; colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma; melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS; stroke; myocardial infarction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New peptide conjugates for modulating apoptosis or for inhibiting cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for treating neurodegenerative disorders, stroke, or cancer -
                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                            Length 16;
                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                           Score 84; DB 20;
Pred. No. 2.6e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lu Z;
                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bcl2 polypeptide BH3 domain peptide #28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Huang Z, Wang J, Zhang Z, Shan S,
                                                                                                                                                                                                                                                                                          100.0%; Scor
100.0%; Pred
0; }
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB37028 standard; peptide; 16 AA
Bcl homology domain 3 polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 18; Page 18; 74pp; English.
                                      Example 1; Fig 4; 104pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYJE-) UNIV JEFFERSON THOMAS.
                                                                                                                                                                                                                                                                                                                                                                                1 ORYGRELRRMSDEFEG 16
                                                                                                                                                                                                                                                                                                                                                                                                      1 QRYGRELRRMSDEFEG 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-APR-2000; 2000WO-US09352.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0128202.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-679325/66.
                                                                                                                                                                                                                                                                                                                     Local Similarity
hes 16; Conserv
                                                                                                                                                                                                                                                                     16 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200059526-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-FEB-2001
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                                                                                                                                                                                                                                       requlation.
                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB37028;
                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 2
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monosubstituted with a 1-5c straight or branched chain alkyl group,

phenyl optionally monosubstituted with a 1-5c straight or branched chain

alkyl group, or benzyl. The peptides AAB37001-B37058 represent examples

of the peptide portion of the conjugate. The peptides represent analogues

of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of

the BH3 domain of the cell death agonist Bad. The peptide conjugate is

useful for modulating apoptosis in the cells of a subject, or for

reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of

apoptosis in cancer cells. It is also useful for inhibiting Bcl-2

c apoptosis in cancer cells. It is also useful for inhibiting as

c subject afflicted with a cancer characterized by cancer cells that

express Bcl-2. The cancer includes prostate, colorectal, gastric,

non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or

acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide

c conjugate is also useful for treating disorders characterized by

increased apoptosis, e.g. neurodegenerative disorders, acquired

immunodeficiency syndrome (AIDS), stroke or myocardial infarction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Epitope; murine, bcl-x(L)/bcl-2 associated death promoter; Bad; stroke, polypeptide; bcl-x; cell death; regulate; BH1; BH2; apoptotic cell death; cytokine deprivation; IL-3 dependent cell line; immunodeficiency; AIDS; neurodegenerative disease; senescence; ischaemia; neoplasia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequences given in AAR95155-67 represent epitopes derived from the murine bcl-x(L)/bcl-2 associated death promoter (Bad) polypeptide (see also AAR95168). Bad is a 22.1 kD protein which interacts with bcl-2 and bcl-x proteins and regulates cell death. It has homology to the bcl-z-related family clustered in the BH1 and BH2 domain. Bad has been found to hybridise to bcl-x(L) and bcl-z in yeast two-hybrid assays and in vivo in mammalian cells. Overexpressed Bad counters the death
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bcl-x(L)/bcl-2 associated death promoter epitope, residues 138-160.
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les 16; Conserva
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inhibitory activity of bcl-x(L), but is much less effective at countering the death inhibitory activity of bcl-2. Bad expression can accelerate apoptotic cell death induced by cytokine deprivation in an IL-3 dependent cell line expressing bcl-x(L), and its also counters the death repressor activity of bcl-x(L). Bad competes with Bax for binding to bcl-x(L). Bad may be used to identify agents which inhibit its binding to bcl-2 or bcl-x(L) to form heterodimers. Such agents may be used to treat neurodegenerative diseases, immunodeficiency diseases, e.g. AIDS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a peptide conjugate having the formula: (R-X)n-peptide where n = 1-10; X = C-0, when the R-X group is attached to the N terminus of the peptide, or a side chain of the peptide where the functional group of the side chain is NH2 or OH; or X = 0 or NH, when the R-X group is attached to the C-terminus of the peptide, or a side chain of the peptide, where the side chain is OH; or COMH2; and R = 2-18C alkyl or alkoxy, 2-14C alkylenyl containing one or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally monosubstituted with a 1-5C straight or branched chain alkyl group, phenyl optionally monosubstituted with a 1-5C straight or branched chain alkyl group, or benzyl. The peptides AAB37001-B37058 represent examples of the peptide portion of the conjugate. The peptides represent analogues of the BCl-2 superfamily polypeptide corresponding to amino acids 72-97 of
                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cytostatic, neuroprotective, anti-HIV; virucide, cerebroprotective, cardiant, Bcl-2 superfamily, BH3 domain, cell death agonist, Bad; apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate, colorectal; gastric, non-small lung; renal; thyroid; neuroblastoma; melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS; stroke; myocardial infarction.
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                                                                                                                                                                                                                                                                   Score 84; DB 17;
Pred. No. 3.7e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB37001 standard; peptide; 26 AA.
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                                                                                                                                                                                                                                                                                                              16; Conservative
                                                                                                                                                                                senescence or ischaemia.
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Best Local Similarity
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The invention relates to a peptide conjugate having the formula: (R-X)n-peptide where n=1-10; X=C=0, when the R-X group is attached to the N-terminus of the peptide, or a side chain of the peptide where the functional group of the side chain is NH2 or OH; or X=0 or NH, when the R-X group is attached to the C-terminus of the peptide, or a side chain of the peptide, where the side chain functional group is COOH or CONH2; and R=2-18C alkylor alkoxy, 2-14C alkylenyl containing one or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally monosubstituted with a 1-5C straight or branched chain alkyl group, phenyl optionally monosubstituted with a 1-5C straight or branched chain alkyl group,
the BH3 domain of the cell death agonist Bad. The peptide conjugate is useful for modulating apoptosis in the cells of a subject, or for reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of apoptosis in cancer cells. It is also useful for inhibiting Bcl-2 function. In particular, the peptide conjugate is useful for treating a subject afflicted with a cancer characterized by cancer cells that express Bcl-2. The cancer includes prostate, colorectal, gastric, non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide conjugate is also useful for treating disorders characterized by increased apoptosis, e.g. neurodegenerative disorders, acquired immunodeficiency syndrome (AIDS), stroke or myocardial infarction.
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                                                                                                                                                                                                                                                                                                               100.0%; Score 84; DB 21; Length 26; 100.0%; Pred. No. 4.2e-07;
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Best Local Similarity 100.
Matches 16; Conservative
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alkyl group, or benzyl. The peptides AAB37001-B37058 represent examples of the peptide portion of the conjugate. The peptides represent analogues of a Bc1-2 superfamily polypeptide corresponding to amino acids 72-97 of the BH3 domain of the cell death agonist Bad. The peptide conjugate is useful for modulating apoptosis in the cells of a subject, or for reversing B cell lymphoma/leukemia 2 (Bc1-2)-mediated blockage of apoptosis in cancer cells. It is also useful for inhibiting Bc1-2 function. In particular, the peptide conjugate is useful for treating a cubject afflicted with a cancer characterized by cancer cells that supject afflicted with a cancer characterized by cancer cells that express Bc1-2. The cancer includes prostate, colorectal, gastric, non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide conjugate is also useful for treating disorders characterized by increased apoptosis, e.g. neurodegenerative disorders, acquired immunodefliciency syndrome (AIDS), stroke or myocardial infarction.
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is COOH
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or two double bonds, cyclobutyl, cyclopentyl, cyclobexyl optionally monosubstituted with a 1-5c straight or branched chain alkyl group, phenyl optionally monosubstituted with a 1-5c straight or branched chain alkyl group, or benzyl. The peptides AAB37001-B37058 represent examples of the peptide portion of the conjugate. The peptides represent analogues of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of the BH3 domain of the cell death agonist Bad. The peptide conjugate is useful for modulating apoptosis in the cells of a subject, or for reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of apoptosis in cancer cells. It is also useful for inhibiting Bcl-2 function. In particular, the peptide conjugate is useful for treating a subject afflicted with a cancer characterized by cancer cells that express Bcl-2. The cancer includes prostate, colorectal, gastric, on-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or courte or chronic lymphocytic and non-lymphocytic leukemia. The peptide conjugate is also useful for treating disorders characterized by increased apoptosis, e.g. neurodegenerative disorders acquired immunodeficiency syndrome (AlDS), stroke or myocardial infarction.
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100.0%; Pred. No. 4.4e-07;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB37056 standard; peptide; 27 AA.
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Best Local Similarity 100.
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                             27 AA;
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when the R-X group is attached to the C-terminus of the peptide, or a side chain of the peptide, where the side chain functional group is COOH or COONE2; and R = 2-18C alkyl or alkoxy, 2-14C alkylenyl containing one or two double bonds, cyclobutyl, cyclobentyl, cyclohexyl optionally monosubstituted with a 1-5C straight or branched chain alkyl group, phenyl optionally monosubstituted with a 1-5C straight or branched chain alkyl group, or benzyl. The peptides AAB37001-B37056 represent analogues of the peptide portion of the conjugate. The peptides represent analogues of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of the BH3 domain of the cell death agonist Bad. The peptide conjugate is useful for modulating apoptosis in the cells of a subject, or for reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of apoptosis in cancer cells. It is also useful for inhibiting Bcl-2 function. In particular, the peptide conjugate is useful for treating a cutte or chronic lymphocytic and non-lymphocytic leukemia. The peptide conjugate is also useful for treating disorders characterized by increased apoptosis, e.g. neurodegenerative disorders, acquired immunodeficiency syndrome (AIDS), stroke or myocardial infarction.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New peptide conjugates for modulating apoptosis or for inhibiting
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB37055 standard; peptide; 28 AA.
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100.0%;
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Best Local Similarity 100.(
Matches 16; Conservative
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the functional where n = 1-10; X = C=O, when the R-X group is attached to the N-terminus of the peptide, or a side chain of the peptide where the functional group of the side chain is NH2 or OH; or X = O or NH, when the R-X group is attached to the C-terminus of the peptide, or a side chain of the peptide, where the side chain functional group is COCH or COCHA; and R = 2-18C alkyl or alkxyk, 2-14C alkylenyl containing one or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally monosubstituted with a 1-5C straight or branched chain alkyl group, phenyl optionally monosubstituted with a 1-5C straight or branched chain alkyl group, or benzyl. The peptides AAB37001-B37058 represent analogues of the peptide portion of the conjugate. The peptides represent analogues of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of the BH3 domain of the cell death agonist Bad. The peptide conjugate is useful for modulating apoptosis in the cells of a subject, or for reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of suppticing in cancer cells. It is also useful for inhibiting Bcl-2 conversed by cancer cells that
                                                                                                                                                                                                                                                                                                                                                                                      express Bc1-2. The cancer includes prostate, colorectal, gastric, non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide conjugate is also useful for treating disorders characterized by increased apoptosis, e.g. neurodegenerative disorders, acquired immunodeficiency syndrome (AIDS), stroke or myocardial infarction.
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Matches 16; Conservative
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In prostiting a less than full length amino acid sequence of a mutant BC1-XL/BC1-2 associated cell death regulator polypeptide (BAD) or its fragment, which contains amino acid substitutions at Seril8 of a human BAD (and a murine BAD) or Seril3 of a murine BAD (and a murine BAD) or Seril3 of a murine BAD (and a murine BAD) or Seril3 of a murine BAD (shorter murine BAD). (I) has immunostimulant, neuroprotective, nootropic, antiinflammatory and immunosupprosesive activities, and antiarthritic, antiinflammatory and immunosuppressive activities, and can be used as an apoptosis inducer of inhibitor. BAD polypeptides and ofruge for activity that promote cell survival or apoptosis. Other uses include inducing or inhibiting apoptosis in a cell. Candidate compounds inducing or inhibiting apoptosis in a cell. candidate compounds immunodeficiency diseases, neurodegenerative diseases, ischaemic cell death, wound healing, cancer, viral infections, lymphoproliferative conditions, arthritis, infertility, inflammation and cutoimmune diseases. The present sequence represents a specifically claimed shorter murine BAD mutant amino acid sequence from the present
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apoptosis, comprises amino acid substitutions at Ser118, Ser155 or
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Pred. No. 2.7e-06;
Mismatches 0; Indels
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147..149
/note= "BH1 conserved amino acids"
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1111..130
/note= "PEST sequence"
                                                                                                                                                                         Claim 7; Page 148-149; 157pp; English.
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191..19
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38..61
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This sequence represents the murine bcl-x(L)/bcl-2 associated death promoter (Bad) gene. Bad is a 22.1 kD protein which interacts with bcl-2 and bcl-x proteins and requilates cell death. It has homology to the bcl-2-related family clustered in the BHI and BHI domain. Bad assays and in vivo in mammalian cells. Overexpressed Bad counters the death inhibitory activity of bcl-x(L), but is much less effective at countering the death inhibitory activity of bcl-x(L), but is much less effective at countering the death inhibitory activity of bcl-x(L), and its also counters the accelerate apoptotic cell death induced by cytckine deprivation in an IL-3 dependent cell line expressing bcl-x(L), and its also counters the death repressor activity of bcl-x(L). Bad competes with Bax for binding to bcl-x(L). Bad may be used to identify agents which inhibit its binding to bcl-z or bcl-x(L) to form heterodimers. Such agents may be used to ideaeses, immunodeficiency diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Murine, mouse, BCL-XL/ECL-2 associated cell death regulator; BAD protein; serine substituted mutant; apoptosis; cancer; viral infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                Polynucleotide encoding bcl-x(L)/bcl-2 associated death promoter useful to treat neoplasia and apoptosis and to identify agents inhibiting its binding to bcl-2 or bcl-x(L) to form heteromultimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New mutant BAD polypeptide with phosphorylatable serine replaced - useful for, e.g. treating reduced apoptosis such as in cancer or viral infection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Murine BCL-XL/BCL-2 associated cell death regulator.
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                                                                                                                                                                                                                                                                                                                                                                                                                            e.g. AIDS, senescence or ischaemia.
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                                                                                                                                                     Claim 3; Fig 1; 130pp; English.
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Matches 16; Conservative
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                                WPI; 1996-251465/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              204 AA;
                                                 N-PSDB; AAT29479
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Korsmeyer SJ;
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                                                                                                                                                                                                                                           phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have greater death-promoting activity than wild-type BAD which can become phosphorylated on the specified Ser, forming a product that does not heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family proteins in the cytosol, thus promoting cell survival. The mutants with Ser substituted cannot bind 14-3-3.
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N-PSDB; AAV27834.
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death regulator) proteins, having an amino acid other than Ser at death regulator) proteins, having an amino acid other than Ser at death regulator) proteins, having an amino acid other than Ser at position 112 and/or 136, relative to the murine BAD 204 as sequence. The present sequence represents a mutant BAD protein. Also described are: (1) fragments of mutant BAD protein. Also described are: (2) fusion proteins of mutant BAD with a heterologous polypeptide that correases intracellular delivery. Mutant BAD proteins are used to treat or prevent diseases associated with reduced apoptosis, e.g. cancer, viral infection, lymphoproliferation, arthritis, infertility, infammation and autolimnum disease. Polynucleotide sequences encoding mutant BAD proteins can be used similarly by gene therapy or to produce transgenic animals for use as disease models or in drug screening. BAD proteins phosphorylated at specified Ser are used to screen for enhancers and inhibitors of serine-phosphatase. Inhibitors are potentially useful in treatment of excessive apoptosis such as AIDS, neurodegeneration, aging or ischaemic cell death. The apoptotic status of calls is determined by measuring relative amounts of phosphorylated and non-phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have greater death-promoting activity than will-type BAD which can become phosphorylated on the specified Ser, forming a product that does not heterodimerise with BCL-2 or BCL-XL forming a product that does not become broteins in the cytosol, thus promoting cell survival. The mutants with Xxx
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present invention describes mutant BAD (BCL-XL/BCL-2 associated cell
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useful for, e.g. treating reduced apoptosis such as in cancer or
viral infection
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death regulator) proteins, having an amino acid other than Ser at position 112 and/or 136, relative to the murine BAD 204 as sequence. The present sequence represents a mutant BAD protein. Also described are: (1) fragments of mutant BAD protein. Also described are: (2) fragments of mutant BAD protein about preptide that increases intracellular delivery. Mutant BAD proteins are used to treat or prevent diseases associated with reduced apoptosis, e.g. cancer, viral infection, lymphoproliferation, arthritis, infertility, infammation and autoimmune disease. Polynucleotide sequences encoding mutant BAD proteins can be used similarly by gene therapy or to produce transgenic animals for use as disease models or in drug screening. BAD proteins phosphorylated at specified Ser are used to screen for enhancers and inhibitors of serine-phosphatase. Inhibitors are potentially useful intratument of excessive apoptosis such as AIDS, neurodegeneration, ading or ischaemic cell death. The apoptotic status of cells is determined by measuring relative amounts of phosphorylated and non-phosphorylated on the specified Ser forming a product that does not betterodimenise with BCL-2 or BCL-XI but instead blids to 14-3-3 family better substituted cannot bind 14-3-3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein; serine substituted mutant; apoptosis; cancer; viral infection.
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N-PSDB; AAV27836.
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position 112 and/or 136, relative to the murine BAD 204 aa sequence. The present sequence represents a mutant BAD protein. Also described are: (1) fragments of mutant BAD protein able to decrease cell viability; (2) fusion proteins of mutant BAD with a heterologous polypeptide that increases intracellular delivery. Mutant BAD proteins are used to treat or prevent diseases associated with reduced apoptosis, e.g. cancer, viral infection, lymphoproliferation, arthritis, infertility, ancert, inflammation and autoimmune disease. Polynucleotide sequences encoding mutant BAD proteins can be used similarly by gene therapy or to produce transgenic animals for use as disease models or in drug screening. BAD proteins phosphorylated at specified Ser are used to screen for enhancers or inhibitors of serine-phosphatase. Inhibitors are potentially useful in treatment of excessive apoptosis such as AIDS, neurodegeneration, determined by measuring relative amounts of phosphorylated and non-phosphorylated mathypromoting relative amounts of phosphorylated and non-phosphorylated on the specified Ser, forming a product that does not heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family conteins in the cytosol, thus promoting cell survival. The mutants with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BAD protein; Bcl-XL/Bcl-2 associated cell death regulator; 14-3-3; serine phosphorylation; post-translational modification; apoptosis; signal transduction regulator; phosphoserine phosphatase; senescence; immunodeficiency disease; neurodegenerative disease; infertility; cancer, viral infection; lymphoproliferative condition; arthritis; inflammation; autoimmune diseases.
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CC (Bc1-x1/Bc1-2 associated cell death regulator). The serine residue is phosporylated in a post-translational modification and allows binding cc to the 14-3-3 protein which is a signal transduction regulator. CC Modulators of phosphorylated BAD, which act through inhibition/activation cc of a phosphoserine phosphotase, are useful for preventing/treating increased/decreased apoptosis in a cell. The increased apoptosis may result from immunodeficiency disease, senescence, neurodegenerative cd disease, ischaemic cell death, repertuis on cell death, infertility and wound-healing. Decreased apoptosis may result from cancer, viral infection, lymphoproliferative conditions, arthritis, infertility, cc inflammation and autoimmune diseases. Measuring the amount of phosphorylated compared to unphosphorylated BAD polypeptide and/or total cc phosphorylated compared to unphosphorylated BAD polypeptide and/or total XXX

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

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Total number of hits satisfying chosen parameters:

Title: Perfect score: Sequence:

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Scoring table:

Searched:

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
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Sequence 69, Appl Sequence 7, Appl Sequence 7, Appl Sequence 21995, A Sequence 28443, A Sequence 27256, A Sequence 26270, A Sequence 26351, A Sequence 26867, A Sequence 26967, A Sequence 26977, A Sequence 29777, A Sequence 25977, A Sequence 259777, A Sequence 25977, A Sequence 259777, A Sequence 259777, A Sequence 259777, A Sequence 2598, Ap Sequence 25989,		E
US-08-706-741B-69 US-08-924-695A-69 US-09-359-161-7 US-09-328-352-4656 US-09-252-991A-21995 US-09-252-991A-21995 US-09-252-991A-28443 US-09-252-991A-28443 US-09-252-991A-26270 US-09-252-991A-26270 US-09-252-991A-26867 US-09-252-991A-31458 US-09-252-991A-31458 US-09-252-991A-31458 US-09-252-991A-31458 US-09-252-991A-31458 US-09-252-991A-31458 US-09-252-991A-31458 US-09-252-991A-31458 US-09-252-991A-31458 US-09-252-991A-31458 US-09-252-991A-31458	ALIGNMENTS	S/08333565 Stanley J. 1-x/Bcl-2 ASSOCIATED CELL DEATH GULATOR 9 and Townsend Khourie and Crew venue -DOS/MS-DOS elease #1.0, Version #1.25 elease #1.0, Version #1.25 US/08/333,565 110N: M 30,223 ER: 15726A-000700 MATION: -2400 422 5: 635
50.0 50.0 48.8 48.8 48.2 48.2 48.2 46.4 46.4 46.4 46.0		tion US/0: "ETER, Sta N: Bc1-x, N: REGUL, Ses: 59 DORESS: 59 DORESS: 100 Tha "Into Aven, The Rele DORESS: 100 The Rel DOR
28 29 30 30 30 30 30 40 40 40 41 40 41 40 41 40 41 40 41 40 40 40 40 40 40 40 40 40 40		RESULT 1 US-08-33-565-10 Sequence 10, Application Patent No. 5622852 GENERAL INFORMATION: APPLICANT: KORSMENT ITILE OF INVENTION: NUMBER OF SEQUENCES CORRESPONDENCE ADDR ADDRESSEE: TOWNS STREET: 379 LYLL CORPESSEE: TOWNS STREET: 379 LYLL COUNTRY: US ZIP: 94301 COMPUTER READABLE FOR EDIUGATION MEDIUM PREADABLE FOR EDIUGATION MEDIUM PREPIECATION APPLICATION NUMBER CURSENT APPLICATION ATTORNEY/AGENT INFO NAME: Smith, WHINER REGISTRATION NUMBER REGISTRATION NUMBER ATTORNEY/AGENT INFO NAME: Smith, WHINER REGISTRATION NUMBER REGIS

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CTHER INFORMATION: /note= "Deduced amino acid sequence CTHER INFORMATION: of mouse BAD."
US-08-333-565-2
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Sequence 2, Application US/08661479
Patent No. 5834209
GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
TITLE OF INVENTION: REGULATOR
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/661,479
FILING DATE: 11-JUN-1995
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/333,565
FILING DATE: 31-OCT-1994
ATTORNEY/AGENT INFORMATION:
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 84; DB 1; I Best Local Similarity 100.0%; Pred. No. 5.5e-07; Matches 16; Conservative 0; Mismatches 0;
                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/33,565
FILING DATE: 31-CT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 35-23
REFERENCE/DOCKET NUMBER: 15726A-000700
TELEPHONE: (415) 326-2400
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REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726A-000700
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                    LENGTH: 204 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94301
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STATE: Ca
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US-08-661-479-2
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                                                                                  GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICAMT: KORSMETER, Stanley J.
TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
TITLE OF INVENTION: RECULATOR
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: Galifornia
COUNTEX: US
ZIP: 94301
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Sequence 2, Application US/08333565
Fatent No. 5622852
GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: REGULATOR
TITLE OF INVENTION: REGULATOR
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Townsend and Townsend Khourie and Crew 379 Lytton Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT ARELICATION DATA:
APPLICATION NUMBER: US/08/661,479
FILING DATE: 11-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION OBTA:
APPLICATION OBTA:
APPLICATION OBTA:
APPLICATION NUMBER: US 08/33,565
FILING DATE: 31-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
RESISTRATION NUMBER: 35,223
REFERENCE/DOCKET NUMBER: 15726A-000700
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (415) 326-2420
TELEFRAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                US-08-661-479-10; Sequence 10, Application US/08661479; Patent No. 5834209
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CITY: Palo Alto
STATE: California
COUNTRY: US
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Best Local Similarity
Matches 16; Conserv
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COUNTRY:
                                                                                                                                                          CITY:
STATE:
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                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: KORSMERS, STANLEY J.
APPLICANT: KORSMERSER, STANLEY J.
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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                                                                                                                                                                                             Length 204;
                                                                                                                       /note= "Deduced amino acid sequence of mouse BAD." \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                              0; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
COMPUTER: IBM PC COMPALIBLE
SOFTWARE: PATENTIN PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
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100.0%; Pred. No. 5.5e-07;
tive 0; Mismatches 0;
                                                                                                                                                                                             Score 84; DB 2; 1 Pred. No. 5.5e-07;
                                                                                                                                                                                                                                 Mismatches
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FILING DATE:
CLASSIFICATION: 530
ATTONEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 965458
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-733-505A-12
; Sequence 12, Application US/08733505A
                                                                                                                                                                                                                                                                                                                                                                           US-08-733-505A-1; Sequence 1, Application US/08733505A; Patent No. 5856445; GENERAL INFORMATION:
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                                                                                                                                                                                             100.0%;
100.0%;
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                                                                                                                                                                                                                                                                                      1 ORYGRELRRMSDEFEG 16
                                                                                                                                                                                                                                                                  1 QRYGRELRRMSDEFEG 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0
Matches 16; Conservative
                                                                                                                                                                                             Query Match
Best Local Similarity 100.1
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
                               TOPOLOGY: linear MOLECULE TYPE: protein
              STRANDEDNESS: single TOPOLOGY: linear
                                                                                 ; NAME/KEY: Protein
; LOCATION: 1.204
; OTHER INFORMATION: /
; OTHER INFORMATION: o
US-08-651-479-2
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP:
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Gaps
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Patent No. 5856445
GENERAL INFORMATION:
APPLICANT: KORSNEYER, STANLEY J.
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
                                            APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
NUMBER OF SEQUENCES: 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPOTER: PATEM: PC-DOS/MS-DOS
SOFTWARE: PATEMIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 84; DB 2; 100.0%; Pred. No. 5.5e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: USA
                                                                                                                                                       ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/733,505A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                         AFFILICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND DONALD R.
REFERENCE/DOCKET NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 9654
TELECOMMUNICATION INFORMATION:
TELEPAN: (314) 727-5188
TELEPAN: (314) 727-5188
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: peptide US-08-733-505A-12
                                                                                                             NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                             MISSOURI
Patent No. 5856445
GENERAL INFORMATION:
APPLICANT: KORSME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63105
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SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
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Best Local Similarity 93.8
Matches 15; Conservative
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Best Local Similarity 93.8
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) ORGANISM: Mus musculus US-09-375-257-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear
US-08-717-123-3
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US-09-375-257-3
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                   RESULT 9
US-08-717-123-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Вþ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 14, Application US/08733505A
Patent No. 5856445
GENERAL INFORMATION:
APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .,
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                                                                                                                                                                                                                                                                                                     100.0%; Score 84; DB 2; Length 204; 100.0%; Pred. No. 5.5e-07;
                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/733,505A
                                                                                                                                                                                                                                                                                                                                            0; Mismatches
         RECISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 965458
TELECOMMUNICATION INFORMATION:
TELEFAN: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 13: SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           965458
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CLASSIFICATION: 530
ATTORNEY FAGENT INFORMATION:
NAME: HOLLAND, DONALD R.,
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 96545
TELEFONNUNCATION INFORMATION:
TELEFONNE (314) 727-5188
TELEFAX: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                             145 QRYGRELRRMSDEFEG 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    145 ORYGRELRRMSDEFEG 160
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HOLLAND, DONALD R.
                                                                                                                                                         LENGTH: 204 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                              16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-733-505A-14
                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 16; Conserv
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Best Local Similarity
Matches 16; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 63105
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Patent No. 6504022

GENURAL INFORMATION:

APPLICANT: Horne, William A.

APPLICANT: Oltersdorf, Tilman

TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC

TITLE OF INVENTION: ACIDS AND METHODS OF USE

FILE REFERENCE: 480140,42801

CURRENT APPLICATION NUMBER: US/09/375,257

CURRENT FILING DATE: 1999-08-16

NUMBER OF SEQ ID NOS: 15

SOFTWARE: FASLSEQ for Windows Version 4.0
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                                               GENERAL INFORMATION:
APPLICANT: Horne, William A.
APPLICANT: Oltersdorf, Tilman
TITLE OF INVENTION: Human BAD Polypeptides, Encoding Nucleic
TITLE OF INVENTION: Acids and Methods of Use
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96.4%; Score 81; DB 4; Length 204; 93.8%; Pred. No. 1.8e-06; Live 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96.4%; Score 81; DB 2; Length 204
93.8%; Pred. No. 1.8e-06;
tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                               STREET: 4370 La JOLLA .....
STREET: 4370 La JOLLA .....
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/717,123
FILING DATE: 20-SEP-1996
77 ASSIFICATION: 435
                                                                                                                                                                                                                                          ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/ACENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-ID 1929
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFRAX: (619) 535-8049
INFORMATION FOR SEQ ID NO: 3:
Sequence 3, Application US/08717123
Patent No. 5965703
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us-09-544-664-28.rai

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1 QRYGRELRRMSDEF 14
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TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLEOULE TYPE: peptide
US-08-733-505A-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59 amino acids
                                                                                                                                                                                                                                                                                                                                              LENGTH: 59 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 86.9
Best Local Similarity 100.
Matches 14; Conservative
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; MOLECULE TYPE: peptide
US-08-733-505A-56
                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63105
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Patent No. 5856445
GENERAL INFORMATION:
APPLICANT: KORSMETER: STANLEY J.
TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERRAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
                                                                                                                                                                                 GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
NUMBER OF SEQUENCES:
ADDRESSE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
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                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: ELAPPY disk
COMPUTER: ELAPPY disk
COMPUTER: ELAPPY disk
COMPUTER: DATE:
CONTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 36,497
REFERENCE/DOCKET NUMBER: 965458
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEPHONE: (314) 727-6092
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 59 amino acids

"WATE: AMINO Acids
"WATE: AMINO Acids
"WATE: AMINO Acids
                                                                                                                          US-08-733-505A-55; Sequence 55, Application US/08733505A; Patent No. 5856445
                         1 ORYGRELRRMSDEFEG 16
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Matches 14; Conservative
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: US
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Gaps
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Patent No. 5856445

GENERAL INFORMATION:
APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
INTHER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERRAMP, L.C.
STREET: ST. LOUIS
STATE: MISSOURI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 59;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DAR: US/08/733,505A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 73; DB 2; L
Pred. No. 1.1e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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APPLICATION NUMBER: US/08/733,505A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 965458
TELECOMMUNICATION INFORMATION:
                                                                                                                       FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION WUBER: 35,197
REFERENCE/DOCKET NUMBER: 96545
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 56: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86.9%,
100.0%; Pre
0;
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US-08-665-617-2
; Sequence 2, Application US/08665617
; Patent No. 5663316
; GENERAL INFORMATION:
    APPLICANT: Audong, Yin
; TITLE OF INVENTION: Gene and Protein for Regulation of Cell Death
NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
. CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                 Gaps
                                                                                                                                                                                                                                                                            Patent No. JOURNAL STANLEY J.
GENERAL INFORMATION:
GENERAL INFORMER, STANLEY J.
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
TITLE OF INVENTION: 60
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Query Match 86.9%; Score 73; DB 2; Length 59; Best Local Similarity 100.0%; Pred. No. 1.1e-05; Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF ENVIRONS: 60
CORRESPONDENCE: 60
CORRESPONDENCE, ADDRESS:
ADDRESSE: HOWELL & HAPERKAMP, L.C.
STREET: 7733 FORSTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUMTRY: USA
ZIP: 63105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 965458
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 59 amino acids
                                                                                                                                                                                                                                             Sequence 58, Application US/08733505A Patent No. 5856445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: HOLLAND, DONALD R. REGISTRATION NUMBER: 35,197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46 QRYGRELRRMSDEF 59
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                                                                                                                    46 ORYGRELRRMSDEF 59
                                                                                             1 ORYGRELRRMSDEF 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
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                                                                                                                                                                                                       RESULT 14
US-08-733-505A-58
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COMPUTER: 132606

COMPUTER: TREADBLE FORM:
MEDIUM TYPE: RIOPPY disk
COMPUTER: INP PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/665,617
FILING DATE:
CLASSIFICATION NUMBER: US/08/665,617
FILING DATE:
CLASSIFICATION NUMBER: US/08/665,617
FILING DATE:
CLASSIFICATION NUMBER: 31.794
REGISTRATION NUMBER: 31.794
REGISTRATION NUMBER: 31.794
REGISTRATION NUMBER: 31.794
REGISTRATION NUMBER: 31.794
REFERENCE/COCKET NUMBER: 31.794
REGISTRATION NUMBER: 3.794
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Sequence 241, App Sequence 570, App Sequence 122, App

Sequence 1813, App Sequence 197, Appl Sequence 197, Appl Sequence 10435, App Sequence 12, Appl Sequence 8, Appli Sequence 8, Appli Sequence 704, Appli Sequence 10045, Appli Sequence 2, Appli Sequence 10, Appli Sequence 10,

0 US-09-971-980-64 0 US-09-971-980-62 5 US-10-092-750-241 5 US-10-102-806-570 5 US-10-102-806-570 6 US-10-146-772-122 US-09-815-242-11813 US-09-841-132-583 US-09-841-132-583 US-10-186-761-10435 5 US-10-198-070-69 5 US-10-198-070-69 5 US-09-738-626-4812 US-09-738-626-4812 US-09-738-626-4812 US-09-738-626-4812 US-09-815-242-5704 US-09-815-242-5704 US-09-815-242-5704 US-09-819-136-10 US-09-813-136-10 US-09-813-124-12463 US-09-813-136-10 US-09-813-136-10 US-09-813-124-12463 US-09-813-136-10 US-09-813-136-10 US-09-813-136-10 US-09-912-481-4

Sequence 4, Appli Sequence 1577, Ap Sequence 1237, Ap Sequence 5539, Ap Sequence 1433, Ap Sequence 1788, Ap

US-10-083-357-1237 US-10-106-698-5539

US-09-925-300-1788 US-09-925-300-1789 US-09-925-301-1433

ALIGNMENTS

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Appli
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                                                                                                         (without alignments)
184.034 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                          September 15, 2003, 17:25:56; Search time 12.6857 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3,
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                                                                                                                                                                                                                                                                                                                                                                                                                                         1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUBCOMB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-922-378-3
                                                                                                                                                                                                                                                            541936 segs, 145912426 residues
                                                                                                                                                                                                                                                                                                                                                                                                                              Published_Applications_AA:*
                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                             protein search, using sw model
                                                                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                 1 ORYGRELRRMSDEFEG 16
                                                                                                                                                                                                                                                                                                                        Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-544-664-28
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Match Length DB
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204
255
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168
168
168
158
215
215
213
282
380
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283
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Perfect score:
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GENERAL INFORMATION:
APPLICANT: Horne, William A.
APPLICANT: Oltersdorf, Tilman
APPLICANT: Oltersdorf, Tilman
TITLE OF INVENTION: HUMBN BAD POLYPEPTIDES, ENCODING NUCLEIC
TITLE OF INVENTION: ACIDS AND METHODS OF USE
FILE REFERENCE: 480140.428D3
CURRENT APPLICATION NUMBER: US/09/922,378
CURRENT APPLICATION NUMBER: US/09/922,378
CURRENT FILING DATE: 2011-08-03
NUMBER OF SEQ ID NGS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                    96.4%; Score 81; DB 9; Length 204;
93.8%; Pred. No. 1.4e-05;
Live 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 3, Application US/10066179; Publication No. US20020115631A1; GENERAL INFORMATION:
                                          Sequence 3, Application US/09922378 Patent No. US20020037869A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 QRYGRELRRMSDEFEG 16
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 93.8
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 2
US-10-066-179-3
RESULT 1
US-09-922-378-3
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Sequence 1, Appli
Sequence 2, Appli
Sequence 147, App
Sequence 145, App
Sequence 18, Appl
Sequence 12, Appl
Sequence 11, Appl
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5 US-10-059-261-258
US-09-922-378-2
US-09-894-657-1
US-09-894-657-1
4 US-10-066-179-2
5 US-10-174-105A-147
5 US-10-156-761-9445
US-09-843-846-18
0 US-09-831-631A-22
5 US-10-156-761-13594
5 US-10-166-087-16
5 US-10-166-087-16
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Gaps

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APPLICANT: Horne, William A. APPLICANT: Oltersdorf, Tilman TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC TITLE OF INVENTION: ACIDS AND METHODS OF USE

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Gaps

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86.9%; Score 73; DB 9; Length 168;
100.0%; Pred. No. 0.00023;
tive 0; Mismatches 0; Indels
                                                             DB 9; Length 168
0.00023;
                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Corley, Neil C.
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
PROLIFERATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
FILING DATE: 28-Jun-2001
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNET/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0421 US
                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 09/410,372 FILING DATE: <Unknown>
                                                                 Score 73;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
                                                                                                                                                                                                                                                                                                Sequence 1, Application US/09894657; Patent No. US20020098569A1; GENERAL INFORMATION:
                                                             86.9%; Scc
100.0%; Pr
tive 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Disket
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CLONE: 358673
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Lal, Preeti
Shah, Purvi
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                                                                                                                                                 1 QRYGRELRRMSDEF 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
                                                             Query Match
Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SECUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Palo Alto
 ; ORGANISM: Homo sapiens US-09-922-378-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMMEDIATE SOURCE:
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US-09-894-657-7
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US-09-894-657-1
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US-10-059-261-258

Sequence 258, Application US/10059261

Publication No. US20030077826A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: CHIMERIC MOLECULES CONTAINING A MODULE ABLE TO TARGET
TITLE OF INVENTION: SPECIFIC CELLS AND A MODULE REGULATING THE APOPTOGENIC
TITLE OF INVENTION: FUNCTION OF THE PERMEABILITY TRANSITION PORE COMPLEX
TITLE OF INVENTION: (PTPC)
TITLE OF INVENTION: (PTPC)
TITLE OF INVENTION: (PTPC)
FILE REFERENCE: 03495.0216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                Query Match 96.4%; Score 81; DB 14; Length 204; Best Local Similarity 93.8%; Pred. No. 1.4e-05; Matches 15; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENCODING NUCLEIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 73; DB 15; Length 25;
Pred. No. 3.1e-05;
0; Mismatches 0; Indels
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Patent No. US20020037869A1
GENERAL INFORMATION:
APPLICANT: Oltersdorf, Tilman
TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENC
TITLE OF INVENTION: ACIDS AND METHODS OF USE
FILE REFERENCE: 480140.428D3
CURRENT FILING DATE: 201-08-03
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
                 CURRENT APPLICATION NUMBER: US/10/066,179 CURRENT FILING DATE: 2002-02-01 NUMBER OF SEQ ID NOS: 15 SOFTWARE: FASTSEQ for Windows Version 4.0 SEQ ID NO 3 EQ ID NO 3 LENGTH: 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/059,261
CURRENT FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: 60/265,594
PRIOR FILING DATE: 2001-02-02
NUMBER OF SEQ ID NOS: 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 86.9%; Sc. Best Local Similarity 100.0%; P. Matches 14; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                              145 QRYGRELRRMTDEFEG 160
                                                                                                                                                                                                                                                                                                                      1 QRYGRELRRMSDEFEG 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 QRYGRELRRMSDEF 19
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FILE REFERENCE: 480140.428C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 258
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Unknown Organism
                                                                                                                                               TYPE: PRT ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 4
US-09-922-378-2
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LENGTH: 168
                                                                                                                                                                                          US-10-066-179-3
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                                                                                                                                                                                                                                    Query Match
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DEPLICANT: CALLAIL INCOMEALING:
APPLICANT: CALLAIL SIGNAL AND HU.
APPLICANT: COMB, Michael J.
APPLICANT: COMB, Michael J.
APPLICANT: COMB, Michael J.
APPLICANT: COMB, Michael J.
APPLICANT: TAN, YI
TITLE OF INVENTION: CONTEXT-INDEPENDENT ANTIBODIES COUPLED WITH DATABASE SEARCHIN
FILE REFERENCE: CST-138 CIP3
CURRENT APPLICATION NUMBER: US/10/174,105A
CURRENT PILING DATE: 1202-004
PRIOR APPLICATION NUMBER: US 09/535,364
PRIOR FILING DATE: 1208-09-04
PRIOR FILING DATE: 1208-03-24
NUMBER OF SEQ ID NOS: 193 -
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 147
LIENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: MOD_RES; LOCATION: (8)...(8); CTHER INFORMATION: PHOSPHORYLATION; serine at position 8 is phosphorylated US-10-174-105A-147
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                                                                                          86.9%; Score 73; DB 14; Length 168; 100.0%; Pred. No. 0.00023; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79.8%; Score 67; DB 15; Length 15; 100.0%; Pred. No. 0.00017; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REPERENCE: 249-262
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-05-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 9145, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                Sequence 147, Application US/10174105A Publication No. US20030068652A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Synthetic Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
                                                                                                                                                                                                                  1 ORYGRELRRMSDEF 14
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Matches 13; Conservative
                                                                                                                                          14; Conservative
    TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                 Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-156-761-9145
                                                                                                                                                                                                                                                                                                      RESULT 8
US-10-174-105A-147
                                                  US-10-066-179-2
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                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
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Sequence 2. Application US/10066179
Publication No. US20020115631A1
GENERAL INFORMATION:
APPLICANT: Horne, William A.
TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC
TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC
TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC
CURRENT APPLICATION NUMBER: US/10/066,179
CURRENT FILING DATE: 2002-02-01
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86.9%; Score 73; DB 9; Length 168; 100.0%; Pred. No. 0.00023; Live 0; Mismatches 0; Indels
                                                                                                                   Shah, Purvi
Shah, Purvi
Corley, Neil C.
TITLE OF INVENTION: PROLIFERATION
                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/894,657
FILING DATE: 28-Jun-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/410,372
                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: PF-0421 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-985-055
TELEPAX: 650-845-4166
INPORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE DESCRIPTION: SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
Sequence 7, Application US/09894657
Patent No. US20020098569A1
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
Yue, Henry
Lal, Preeti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 168 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      108 QRYGRELRRMSDEF 121
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CLONE: 1683637
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Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94304
                                                                                                                                                                                                                                                                                                                                                  STATE: CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-066-179-2
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Indels

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47.6%; Score 40; DB 15; Length 380;
63.6%; Pred. No. 1.2e+02;
ive 3; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                             APPLICANT: Manners, John M.
APPLICANT: Manners, John M.
APPLICANT: Marcus, John Paul
APPLICANT: Grenter, Kenneth C.
APPLICANT: Green, Jodie L.
TITLE CF INVENTION: ANTIMICROBIAL PROTEINS
FILE REFERENCE: CULLN23.001APC
CURRENT APPLICATION NUMBER: US/09/331,631A
CURRENT FILING DATE: 1999-06-21
PRIOR FILING DATE: 1997-12-22
PRIOR APPLICATION NUMBER: AU PO 4275
PRIOR FILING DATE: 1996-12-20
NUMBER CF EQ ID NOS: 40
SOFTWARE: FRASESQ for Windows Version 3.0
SEQ ID NO 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: TKEDA, HARDO
APPLICANT: TKEDA, HARDO
APPLICANT: ISHIKAWA, JUN
APPLICANT: SHIKAWA, JUN
APPLICANT: SAKRAL, HOSHII
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT PAPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-274089
PRIOR FILING DATE: 2001-06-05
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 13594
  Best Local Similarity 43.8%; Pred. No. 21;
Matches 7; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 13594, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
                                                                                                                                                                                                                                               Sequence 22, Application US/09331631A Patent No. US20020168392A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptomyces avermitilis
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                                                                         1 ORYGRELRRMSDEFEG 16
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22 RRFGEELERLLKKYEG 37
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Best Local Similarity 63.6
Matches 7; Conservative
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ORGANISM: Maize
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US-10-156-761-13594
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US-10-156-761-13594
                                                                                                                                                                                                                             US-09-331-631A-22
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APPLICANT: KUNSCH, ARVIND
CHOPRA, ARVIND
CHOPRA, CRAIG A
TITLE OF INVENTION: HUMAN B-CELL TRANSLOCATION GENES-2 AND 3
ANTIBODIES
NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                 ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
CITY: WASHINGTON
                                                                                                                                                                                               Query Match 59.5%; Score 50; DB 15; Length 215; Best Local Similarity 56.2%; Pred. No. 1.6; Matches 9; Conservative 4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 9; Length 213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/843,846
FILING DATE: 30-Apr.-2001
CLASSIFICATION: <UNknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0730005/EKS/PSC
TELEPHONE: (202) 371-2600
TELEPHONE: (202) 371-2540
INFORMATION SEQ TO NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/221,844

FILING DATE: 29-DEC-1998

APPLICATION NUMBER: US 08/718,738

FILING DATE: 18-SEP-1996

APPLICATION NUMBER: US 08/463,382

FILING DATE: 05-JUN-1995

APPLICATION NUMBER: US 08/460,104

FILING DATE: 02-JUN-1995

APPLICATION NUMBER: PCT/US95/03323

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-843-846-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 18, Application US/09843846 Patent No. US2002004236241 GENERAL INFORMATION:
                                                                                                                       ORGANISM: Streptomyces avermitilis US-10-156-761-9145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGIH: 213 amino acids
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108 ERWGGDLRRMRDEADG 123
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PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 9145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
US-09-843-846-18
                                                                           LENGTH: 215
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APPLICANT: Staffa, Alfredo
APPLICANT: Staffa, Alfredo
APPLICANT: Staffa, Alfredo
APPLICANT: Zazopoulos, Emmanuel
TITLE OF INVENTION: Genes and proteins for the biosynthesis of anthramycin
FILE REFERENCE: 3014-205
CURRENT APPLICATION NUMBER: US/10/166,087
CURRENT FILING DATE: 2002-06-11
SUMBER OF SEQ ID NOS: 51
SOFTWARE: Patentin version 3.0
SEQ ID NO 16
LENGTH: 764
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47.6%; Score 40; DB 15; Length 2871; 60.0%; Pred. No. 9.7e+02; tive 1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT; ORGANISM: Streptomyces refuineus subspecies thermotolerans US-10-166-087-16
                                                                                                                                                                                                                                APPLICANT: Scantan, section.
APPLICANT: Gouré, Ivan
APPLICANT: Gure, Ali
APPLICANT: Chen, Yao-Tseng
APPLICANT: Chen, Yao-Tseng
APPLICANT: Old, Lloyd
ITILE OF INVENTION: Breast Cancer Antigens
FILE REFERENCE: L00461/7013(JRV)
CURRENT APPLICATION NUMBER: US/10/146,473
CURRENT FILING DATE: 2002-05-15
CURRENT FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 82
SOFTWARE: Patentin version 3.0
SEQ ID NO 41
LENGTH: 2871
                                                                                                    RESULT 13
US-10-146-473-41
; Sequence 41, Application US/10146473
; Publication No. US20030108888A1
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
US-10-166-087-16
; Sequence 16, Application US/10166087
; Publication No. US20030077767A1
; GENERAL INFORMATION:
; APPLICANT: Ecopia Elosciences Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 15
US-10-092-750-1
; Sequence 1, Application US/10092750
; Publication No. US20030032157A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       220 QRPGREL-TYSNEYEG 234
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Matches 9; Conservative
                                         241 YEKELRRLADE 251
3 YGRELRRMSDE 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-146-473-41
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

September 15, 2003, 17:18:16; Search time 7.2 Seconds (without alignments) 213.708 Million cell updates/sec Run on:

US-09-544-664-28 84 Title: Perfect

1 ORYGRELRRMSDEFEG 16 score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 segs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	Score	M K	Length	DB			Description
	84	100.	204	7	567	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	bad protein - mous
۵.	44	52.4	564	7			glycosyl hydrolase
	43	Ξ.	463	7	303		probable two-compo
	42.5	0	1014	7	503		excinuclease ABC c
	42	0	370	7	318		3-3-de
	42	0	445	7	712		S
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m	39.5	•	\leftarrow	7	H85868		
σ.	<u>.</u>	47.0	\leftarrow	7	A65000		NADH2 dehydrogenas

ALIGNMENTS

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Algorians (strain R1)
C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C;Accession: H75403
R;White, O; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.
M.; Shen, M.; Vamathevan, J.C.; Fraser, C.M.
S; Smith, H.O.; Venter, J.C.; Fraser, C.M.
S; Science 286, 1571, 1999
A; Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A; Reference number: A75250; MUID:20036896; PMID:10567266
A; Status: preliminary
A; Status: preliminary
A; Residues: 1-564 cWHI>
A; Residues: 1-564 cWHI>
A; Experimental source: strain R1
C; Genetics: C; Genetics: CB:AE001983; GB:AE000513; NID:96459123; PIDN:AAF10944.1; PID:96455
                                                                                                                                                                                                                          R:Yang, E.; Zha, J.; Jockel, J.; Boise, L.H.; Thompson, C.B.; Korsmeyer, S.J.
Cell 80, 285-291, 1995
A:Title: Bad, a heterodimeric partner for Bcl-x-L and Bcl-2, displaces Bax and promot
A:Reference number: A55671; MuID:95136361; PMID:7834748
A:Accession: A55671
A;Status: preliminary; not compared with conceptual translation
A;Holecule type: mRNA
A;Residues: 1-204 <MAN>
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                                                                          bad protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 05-Nov-1999
C;Accession: A55671
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:L37296; NID:g639778; PIDN:AAA64465.1; PID:g639779 C;Keywords: heterodimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 52.4%; Score 44; DB 2; Length 564; Best Local Similarity 61.5%; Pred. No. 23; Matches 8; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C, Superfamily: alpha-glucosidase; alpha-amylase core homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                145 QRYGRELRRMSDEFEG 160
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RESULT 1
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Ajzatus: Lrausatorou not shown
Ajzatus: Lrausatorou not shown
Ajzatus: Lrausatorou not shown
AjRosidues: 1-370 cDOI>
Ajcross-references: GB:L20296; NID:g311101; PIDN:AAA65607.1; PID:g311102
Ajcross-references: GB:L20296; NID:g311101; PIDN:AAA65607.1; PID:g311102
R;Aljinovic, G.; Pohl, F.M.; Pohl, T.M.
A;Reference number: S45906
A;Accession: S46126
A;Accession: S46126
A;Accession: S46126
A;Reference number: S45906
A;References: EMBL:236118; NID:g536664; PIDN:CAA85212.1; PID:g536665; MIPS:XBR2
A;Cross-references: EMBL:236118; NID:g53664; PIDN:CAA85212.1; PID:g536665; MIPS:XBR2
R;Aigle, M.; Baclet, M.C.; Barthe, C.; Biteau, N.; Crouzet, M.; Doignon, F.
Submitted to the Protein Sequence Database, August 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable Fe-S oxidoreductase CAC1813 [imported] - Clostridium acetobutylicum C; Species: Clostridium acetobutylicum C; Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001 C; Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001 C; Date: 14-Sep-2001 G; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; I. S; Nolling, J.; Benett, G.N.; Koonin, E.V.; Smith, D.R. J. Bacteriol. 183, 4823-4838, 2001
C;Species: Saccharomyces cerevisiae
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 03-Jun-2002
C;Accession: S38185; S46126; S46130; JN0322; B48651
C;Accession, S38185; S46126; S46130; JN0322; B48651
F;Doignon, F.; Biteau, N.; Aigle, M.; Crouzet, M.
Yeast 9, 1131-1137, 1993
A;Title: The complete sequence of a 6794 bp segment located on the right arm of chrom A;Reference number: S38185; MUID:94078675; PMID:8256522
A;Accession: S38185
A;Status: translation not shown
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C;Function:
A;Description: aldehyde-lyase, carbon-carbon lyase
A;Pathway: aromatic amino acid biosynthesis; shikimate pathway
A;Pathway: aromatic amino acid biosynthesis; shikimate pathway
C;Superfamily: phospho-2-dehydro-3-deoxyheptonate aldolase
C;Keywords: aldehyde-lyase; aromatic amino acid biosynthesis; carbon-carbon lyase; cy
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Pred. No. 32;
4; Mismatches
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Matches 7; Conservative
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G97123
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                                                                                                                                                                                                                                                                                                                C. Species: Pseudomonas aeruginosa
C. Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 14-Sep-2001
C. Accession: R83036
R. Stover, C.K.; Phan, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, Y.; Lory, S.; Olson, M.V.
Nature 406, Bpg-964, 2000
A.Title: Complete genome sequence of Pseudomonas aeruginosa Pa01, an opportunistic pathora, Reference number: A82950; MUTD: 20437337; PMID: 10984043
A. Accession: H83036
A.; Status: preliminary
A.; Molecule type: DNA
A.; Molecule type: DNA
A.; Molecule type: DNA
A.; Molecule type: DNA
A.; Molecule sequence: GB.AE004901; GB.AE004091; NID: 99951147; PIDN: AAG08271.1; GSPDB: GN001
A.; Experimental source: strain PA01
C.; Genetics:
A.; Gene: PA4886
C.; Superfamily: hypothetical protein H11707; sensor histidine kinase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ### Streptomyces coelicolor

N;Contains: excision endonuclease ABC (EC 3.1.-.) chain A
C;Species: Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 02-Feb-2001
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 02-Feb-2001
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 02-Feb-2001
R;Seeger, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
Submitted to the EMBL Data Library, March 1999
A;Reference number: 221581
A;Reference number: 221581
A;Cocssion: T36031
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Gesesion: T36031
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Generics: Tafot 4.5EED
A;Cross-references: EMBL:AL035591; PIDN:CAB38148.1; GSPDB:GN00070; SCOEDB:SCC54.18c
A;Residues: 1-1044 <&SEED
A;Cross-references: EMBL:AL035591; PIDN:CAB38148.1; GSPDB:GN00070; SCOEDB:SCC54.18c
C;Genetics:
A;Genetics:
A;Ge
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2-dehydro-3-deoxy-phosphoheptonate aldolase (EC 4.1.2.15) ARO4 - yeast (Saccharomyces of
N;Alternate names: 3-deoxy-D-arabino-heptulosonate-7-phosphate synthase; DAHP synthase;
                                                                                                                                                                                                                                                                                     probable two-component sensor PA4886 [imported] - Pseudomonas aeruginosa (strain PA01)
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Pred. No. 28;
2; Mismatches
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61.5%;
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GEELRRQAEYFEG 333
                                                                                | ||:||: |||:
YVREMRRVIDEFD 295
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Best Local Similarity
8; Conserve
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Best Local Similarity
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Gaps

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Indels

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Alvariety: strain NRC-1
C; Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 31-Jan-2000
C; Accession: T08234
R; Ng, W.V.; Ciufo, S.A.; Smith, T.M.; Bumgarner, R.E.; Baskin, D.; Faust, J.; Hall, Shy, W.V.; Ciufo, S.A.; Smith, T.M.; Bumgarner, R.E.; Baskin, D.; Faust, J.; Hall, Shyd, W.V.; Ciufo, S.A.; Smith, T.M.; Bumgarner, R.E.; Baskin, D.; Faust, J.; Hall, Shyd, Title: Snapshot of a large dynamic replicon in a halophilic Archaeon: megaplasmid A; Reference number: 216408; MUID:99063795; PMID:9847077
                        A) Residues: 1-113 <HOR>
A) Residues: 1-113 <HOR>
A) Cross-references: EMBL:X55648; NID:943516; PID:943524
A) Experimental source: plasmid pHH1
A) Genetics: PHH
A) Note: the nucleotide sequence was submitted to the EMBL Data Library, September 19: A) Note: the source is designated as Halobacterium halobium
C) Genetics: <NRC>
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A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: F72289
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A,Residues: 1-220 <ARN>
A,Cross-references: GB:AE001772; GB:AE000512; NID:g4981693; PIDN:AAD36230.1; PID:g49
A,Experimental source: strain MSB8
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C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: F72289
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hi
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gas-vesicle operon protein gvpK - Halobacterium sp. (strain NRC-1) plasmid pNRC100 N;Alternate names: hypothetical protein H0228 C;Species: Halobacterium sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-113 <NGW>
A;Cross-references: EMBL:AF016485; NID:g2822278; PID:g2822295; HALOSP:H0228
A;Experimental source: strain NRC-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         oxidoreductase, sol/devB family - Thermotoga maritima (strain MSB8)
  A; Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Length 113;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48.8%; Score 41; DB 46.7%; Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ed. No. 14;
Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 41;
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A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                      48.8%;
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ERLGRQLQALEDELE 64
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Best Local Similarity 46.7
Matches 7; Conservative
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A;Genome: plasmid pNRC100
                                                                                                                                                                                                                                                                    A;Gene: gvpK
A;Genome: plasmid pNRC100
C;Genetics: <PHH>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein Vng2379h [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: F8438
R;NG, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S; Leithauser: B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablo Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li A;Accession: F84388
A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
A;Accession: F84388
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-84 <STO>
A;Cross-references: GB:AE004437; NID:g10581786; PIDN:AAG20474.1; GSPDB:GN00138
C;Genetics:
A;Gene: VNG2379H
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A; Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cld A; Reference number: A96900; MUID:21359325; PMID:21359325
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A;Genetics: NRC
A;Note: the Source is designated as Halobacterium halobium
B;Horne, M.; Englert, C.; Wimmer, C.; Pfeifer, F.
Mol. Microbiol. 5, 1159-1174, 1991
A) Title: A DNA region of 9 kbp contains all genes necessary for gas vesicle synthesis.
A;Reference number: S15183; MUID:92065812; PMID:1956294
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                                                                                                                                          A; Residues: 1-445 < KUR>
A; Cross references: GB:AE001437; PIDN:AAK79778.1; PID:g15024787; GSPDB:GN00168
A; Experimental source: Clostridium acetobutylicum ATCC824
C; Genetics:
A;Gene: CAC1813
C; Superfamily: conserved hypothetical protein b0835
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Pred. No. 10;
1; Mismatches 5; Indels
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A, Molecule type: DNA
A, Residues: 1-113 < JON>
A, Cross-references: GB: M58557; NID: 9150406; PID: 9455299
                                                                                                                                                                                                                                                                                                                                                          DB 2;
39;
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Pred. No.
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R;Jones, J.G.; Young, D.C.; DasSarma, S.
Gene 102, 117-122, 1991
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ORYGKELKELVPEID 99
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8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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Best Local Similarity
'-hoc 7; Conserva
                                                       A, Accession: G97123
A, Status: preliminary
A, Molecule type: DNA
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Righton requilatory protein SNE4 - yeast (Saccharomyces cerevisiae)
NyAlternate names: CAT3 protein: protein G2945; protein IGL115w
C.Species: Saccharomyces cerevisiae
C.Species: A.Species: A.Spec
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R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Doc.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, F. Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weldman, J.F.; McDonald, L. Nature 390, 364-370, 1997
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A, Residues: 1-21 <DOI>
A, Cross references: EMBL:D16506, NID:g391938; PIDN:BAA03958.1; PID:g2160324
A, Cross references: EMBL:D16506, NID:g391938; PIDN:BAA03958.1; PID:g2160324
B, Lauquin, G.
Submitted to the Protein Sequence Database, May 1996
A, Reference number: S64122
A, Accession: S64125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48.8%; Score 41; DB 1; Length 322 61.5%; Pred. No. 41;
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A;Cross-references: SGD:S0003083; MIPS:YGL115w
A;Map position: 7L
C;Function:
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GEALMRRSDDFEG 270
                                                                          YGRELRRMSDEFEG 16
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Matches 8; Conserv
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A; Residues: 1-322 <LAU>
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G59496
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C; Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 17-May-2002
C; Accession: AH1386
C; Buchaud, E.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker C; Domainguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A; Muthors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A; Title: Comparative genomics of Listeria species.
A; Reference number: AB1077; MUID:21537279; PMID:11679669
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A; Status: preliminary
A; Molecule 'type: DNA
A; Residues: 1.271 < GLA>
A; Residues: 1.271 < GLA>
A; Cross-references: GB: NC_003210; PIDN: CAD00574.1; PID: 916411984; GSPDB: GN00177
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Best Local Similarity 57.1%; Pred. No. 34;
Matches 8; Conservative 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18:8%; Score 41; DB 2; Length 271; 1arity 57.1%; Pred. No. 34; Conservative 2; Mismatches 4; Indels
                                                                                                                                 Score 41; DB 2; Length 220;
Pred. No. 27;
5; Mismatches 3; Indels
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                              A;Gene: TM1154
C;Superfamily: yeast SOL3 protein
                                                                                                                                    48.8%;
                                                                                                                                                                                                                                                                                                                               1 ORYGRELRRMSDEFE 15
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66 YLRALNRMNDEIDG 79
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A; Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Woese, C.R.; Venter, J.C.
A; Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaec A; Reference number: A69250; MUID:9804933; PMID:9389475
A; Accession: G69496
A; Attaus: preliminary; nucleic acid sequence not shown; translation not shown A; Molecule type: DNA
A; Residues: 1-398 < KLE>
A; Cross-references: GB: AE000967; GB: AE000782; NID:92689290; PIDN: AAB89280.1; PID:9264856
C; Superfamily: ATP-dependent 265 proteinase; FtsH/SEC18/CDC48-type ATP-binding domain hc C; Reywords: ATP; nucleotide binding; P-loop
F; 155-365/Domain: FtsH/SEC18/CDC48-type ATP-binding domain hc C; Reywords: ATP; nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vicilin-like storage protein Glbl-L, embryo - maize
N;Alternate names: globulin-lL
C;Species: Zea mays (maize)
C;Species: Zea mays (maize)
C;Species: Zea mays (maize)
C;Accession: B5324; $21824
R;Belanger, F.C.; Kriz, A.L.
Genetics 129, 863-872, 1991
A;Title: Molecular basis for allelic polymorphism of the maize Globulin-l gene.
A;Reference number: A53234; MUID:92090707; PMID:1752424
A;Accession: B53234
A;Reference number: A53234; MUID:92090707; PMID:1752424
A;Accession: B53234
A;Reference number: A53234; MUID:92090707; PMID:1752424
A;Accession: B53234
A;Residues: J-582 <BEL>
A;Cross-references: EMBL:X59083; NID:g22283; PIDN:CAA41809.1; PID:g22284
A;Cross-reference extracted from NCBI backbone (NCBIP:71285)
C;Genetics:
A;Chross: 167/1; 225/3; 349/3
C;Superfamily: glycinin
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Pred. No. 51;
2; Mismatches 4; Indels
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533 ERHGREEREKEBEREG 548
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Best Local Similarity 57.1%;
Matches 8; Conservative ;
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Search completed: September 15, 2003, 17:27:01 Job time: 7.2 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

- protein search, using sw model protein September 15, 2003, 17:16:55 ; Search time 3.77143 Seconds
(without alignments)
199.507 Million cell updates/sec Run on:

1 ORYGRELRRMSDEFEG 16 US-09-544-664-28 84 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 seqs, 47026705 residues Searched:

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Q61337 mus musculu	rat	옩	Q9z507 streptomyce							P12904 saccharomyc	Q9p869 kluyveromyc	O28303 archaeoglob	Q01133 calliactis	Q16994 anthopleura	P10419 anthopleura	P22280 rhizomucor	-				Q9pqz2 ureaplasma							7	22	Q9hv01 pseudomonas	57 clos	043521 homo sapien
SUMMARIES	BAD_MOUSE	BAD_RAT	BAD_HUMAN	UVRA_STRCO	BIM_MOUSE	BIM_RAT		- 1	GVK1_HALN1	6PGL_THEMA	SNF4_YEAST	SNF4_KLULA	PSMR_ARCFU	FMRA_CALPA	FMR2_ANTEL	FMR1_ANTEL	RAS3_RHIRA	YAY5_SCHPO	DESP_HUMAN	NUOG_ECOLI	NUOG_SALTY	Y152_UREPA	R37A_HALN1	AP3_ARATH	RA51_SCHPO	SEC3_DROME	UVRA_DEIRA	LML1_CAEEL	SNE1_HUMAN	FRG1_CAEEL	SELA_PSEAE	IF3_CLOPE	BIM_HUMAN
Length DB	1																									889	910	1535 1	797				
& Query Match	- 00	100.0	86	50.6	50.0	50.0	50.0	50.0	48.8	48.8	48.8	48.8	48.8	48.2	48.2	48.2	47.6	47.6	47.6	47.0	47.0	46.4	46.4	46.4	46.4			46.4					
Score	84	84	73	42.5	42	42	42	42	41	41	4.1	41	41	\circ	40.5	\circ	40	40		39.5	Q١	39	39	30	39	39	39	39	39	38.5		38	38
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THIE_PYRAB	AKUG_CANAL STIM_DROME	PERL_HUMAN	GCR3_YEAST	RIR1_CHLMU	RIR1_CHLTR	VGLN_HUMAN	VGLN_CHICK	UBR1_SCHPO	UVRA_MICLU	LEU3_BUCUL
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207	570	712	861	1047	1047	1268	1270	1958	992	126
45.2	45.2	45.2	45.2	45.2	45.2	45.2	45.2	45.2	44.6	44.0
80 C	00 00 11 M	8	202	38	8 3	38	38	38	37.5	37
8. c	36	37	8 M	39	40	47	42	43	44	45

ALIGNMENTS

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Has domain phosphory sinviture remarks coperate to incurrate the properties of the fill-51(2000).

1- FUNCTION: Promotes cell death. Successfully competes for the binding to Bcl.x(L), Bcl.2 and Bcl.w, thereby affecting the level of heterodimerization of these proteins with BAX. Can reverse the death repressor activity of Bcl.x(L), but not that of Bcl.c. Repears to act as a link between growth factor receptor signaling and the apoptotic pathways.

1- SUBUNIT: Forms heterodimers with the anti-apoptotic proteins, Bcl.c. Subunit: Forms heterodimers with the anti-apoptotic proteins, Bcl.c. x(L), Bcl.2 and Bcl.w. Also binds protein S100AlO (By similarity).

2- SUBCELLUIAR LOCATION: Outer mitochondrial membrane. Upon phosphorylation, locates to the cytoplasm.
                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

TISSUB-Brain, and Thymus;

MEDLINE=95186361; PubMed=7834748;

Yang E., Zha J., Jockel J., Boise L.H., Thompson C.B., Korsmeyer S.J.;

"Bad, a heterodimeric partner for Bcl-XL and Bcl-2, displaces Bax and promotes cell death.";

Cell 80:285-291(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN: Intact BH3 domain is required by BIK, BID, BAK, BAD AND BAX for their pro-apoptotic activity and for their interaction with anti-apoptotic members of the Bcl-2 family.

PTM: Phosphorylated on Ser-112 in response to survival stimuli. Subsequent phosphorylation on Ser-136 promotes heterodimerization with 14-3-3 proteins. This interaction then facilitates the phosphorylation at Ser-155, a site within the BH3 domain, leading to the release of Bcl-x(L) and the promotion of cell survival.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              proteins and survival kinases cooperate to inactivate BAD by
                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-98022383; Pubmed-9381178; Del Peso L., Gonzalez-Garcia M., Page C., Herrera R., Nunez G.; Interleukin-3-induced phosphorylation of BAD through the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-20403302; PubMed=10949026;
Datta S.R., Katsov A., Hu L., Petros A., Fesik S.W., Yaffe M.B.,
Greenberg M.E.;
                                       01-NoV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
BCl2-antagonist of cell death (BAD) (Bcl-2 binding component 6) (BCl-xL/BCl-2 associated death promoter).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PHOSPHORYLATION, AND MUTAGENESIS OF SER-112 AND SER-136.
204 AA
  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [3]
MUTAGENESIS OF SERINE RESIDUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Science 278:687-689(1997).
  STANDARD;
                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                     BAD OR BBC
BAD_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        kinase Ak
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CONFLICT
     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce.or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hsu S.Y., Kaipia A., Zhu L., Hsueh A.J.W.; "Interference of BAD (Bcl-xL/Bcl-2-associated death promoter)-induced apoptosis in mammalian cells by 14-3-3 isoforms and Pll."; Mol. Endocrinol, 11:1858-1867(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                O'Agata V., Magro G., Travali S., Musco S., Cavallaro S.; "Cloning and expression of the programmed cell death regulator BAD in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S->A: NO PHOSPHORYLATION.
S->A: NO PHOSPHORYLATION.
S->A: NO PHOSPHORYLATION; INTERACTS WITH
 Ser-136 is the major site of AKT/PKB phosphorylation, Ser-155 the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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PKB).
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035147; 070256; Q9JHX1;
16-0CT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Bcl2-antagonist of cell death (BAD) (Bcl-2 binding component
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 204;
                   major site of protein kinase A (CAPK) phosphorylation. SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain. SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [1]
SEQUENCE FROM N.A., AND MUTAGENESIS OF SER-113 AND SER-137
IISSUE-OVARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                        PHOSPHORYLATION (BY PKA AND PHOSPHORYLATION (BY PKA AND PHOSPHORYLATION (BY PKA AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 84; DB 1; L
100.0%; Pred. No. 1.3e-06;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).

    (Bcl-xL/Bcl-2 associated death promoter).

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BCL-X(L)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Brain;
MEDLINE=98194755; PubMed=9535132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neurosci. Lett. 243:137-140(1998).
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                                                                                                                                                                                                                                                                                                                                 MGD; MGI:1096330; Bad.
InterPro; IPR000712; Bc12_BH.
PROSITE; PS01259; BH3; FALSE_NEG.
Apoptosis; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=98034386; PubMed=9369453;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22080 MW;
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                                                                                                                                                                                                                                                                       EMBL; L37296; AAA64465.1; -.
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Matches 16; Conservative
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                                                                                                                                                                                                                                                                                            PIR; A55671; A55671.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       204 AA;
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MOD_RES
MOD_RES
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MUTAGEN
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TO DETECTION OF THE PROPERTY O
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Hamner S., Arumae U., Yu L.-Y., Sun Y.-F., Saarma M., Lindholm D.;
"Functional characterization of two splice variants of rat BAD and
their interaction with Bcl-w in sympathetic neurons.";
Mol. Cell. Neurosci. 17:97-106(2001).

-!-FUNCTION: Promotes cell death. Successfully competes for the
Dinding to Bcl-x(L), Bcl-2 and Bcl-w, thereby affecting the level
of heterodimerization of these proteins with BAX. Can reverse the
death repressor activity of Bcl-x(L), but not that of Bcl-2 (By
similarity). Appears to act as a link between growth factor
similarity). Appears to act as a link between growth factor
cecptor signaling and the apoptotic pathways.

-!-SUBGNIT: Forms heterodimers with the anti-apoptotic proteins, Bcl-
x(L), Bcl-2 and Bcl-w. Also binds protein S100Al0. The Ser-
113/Ser-137 phosphorylated form binds 14-3-3 proteins.

-!-SUBGELUIAR LOCATION: Outer mitochondrial membrane. Upon
phosphorylation, locates to the cytoplasm (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          brain, liver, spleen and heart. In the brain, restricted to epithelial cells of the choroid plexus. Isoform alpha is the more abundant form.

-!- DOMAIN: Intact BH3 domain is required by BIK, BID, BAK, BAD AND BAX for their pro-apoptotic activity and for their interaction with anti-apoptotic members of the Bcl-2 family.

-!- PTM: Phosphorylated on Ser-113 in response to survival stimuli. Subsequent phosphorylation on Ser-137 promotes heterodimerization with 14-3-3 proteins. This interaction then facilitates the phosphorylation at Ser-156, a site within the BH3 domain, leading to the release of Bcl-x(L) and the promotion of cell survival. Ser-137 is the major site of AKT/PKB phosphorylation, Ser-156 the major site of protein kinase A (CAPK) phosphorylation (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S->A: NO HETERODIMERIZATION WITH 14-3-3
PROTEINS. NO BFFECT ON HETERODIMERIZATION
WITH BCL2 NOR WITH PROTEIN P11.
SDAGGR -> ERRGRK (IN REF. 1).
7AFA/1DAE9CF4A81 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BY SIMILARITY),
LPRPKSAGTATOMROSASWTRIIQSWWDRNLGKGGSTPSQ
-> EELTYSVEFLPVRAIAMEGWPLLWSFQSFPHTLPPTPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /FIId=VSP_000534.
S->A: NO EFFECT ON HETERODIMERIZATION
WITH 14-3-3 PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE SPECIFICITY: Expressed in all tissues tested, including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EVAMFPLRYWTALRRLC (in isoform Beta).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PHOSPHORYLATION (BY PKA AND PKB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BY SIMILARITY).
PHOSPHORYLATION (BY PKA AND PKB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BY SIMILARITY).
PHOSPHORYLATION (BY PKA AND PKB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                similarity).
SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Phosphorylation; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=035147-2; Sequence=VSP_000534;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId=035147-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000712; Bcl2_BH.
PROSITE; PS01259; BH3; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 SD
22228 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF031227; AAC15100.1; -. EMBL; AF279910; AAF91427.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF003523; AAC53374.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF279911; AAF91428.1; -. HSSP; Q92934; 1G5J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  113
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205 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=Alpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=Beta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Apoptosis;
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Query Match
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A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Ribbine Lissol; Fullmed E.A., Grouse L.H., Derge J.G.,

Ribbine R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschal S.F., Jordan H., Moore T., Max S.I., Wang J., Hsheh F.,

Raba S.S., Loquellan K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Roards S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,

Rohitan D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia R.M., Rodriques S., Sanchez A.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriquez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Rodriquez A.C., Grimver M.A., Schein J.E., Jones S.J.M., Marra M.A.,

Roherthan and mouse cDNA sequences ";

I "Generation and initial analysis of more than 15,000 full-length
                                           6
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. Yin D.X., Li Z., Huang B., Chen S., Zhou H.; "A human protein that interacts with Bcl-2 and have homology to mouse
                                                                                                                                                                             BAD_HUMAN STANDARD; PRT; 168 AA.
092934; 014803;
01-NOV-1997 (Rel. 35, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
BCl2-antagonist of cell death (BAD) (BCl-2 binding component 6)
XL/BCl-2 associated death promoter) (BCl2-like 8 protein).
BAD OR BBC6 OR BCL2L8.
                                            Gaps
                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wang Y., Wilson G.,
                                            0;
            Score 84; DB 1; Length 205; Pred. No. 1.3e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND PHOSPHORYLATION BY RAF-1.
MEDLINE=97083574; PubMed=8929532;
Wang H.-G., Rapp U.R., Reed J.C.;
"Bcl-2 targets the protein kinase Raf-1 to mitochondria.";
                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Takayama S., Reed J.C.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[6]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ottilie S., Diaz J.-L., Horne W., Chang J., War Chang S., Weeks S., Fritz L.C., Oltersdorf T.; "Dimerization properties of human BAD."; J. Biol. Chem. 272:30866-30872(1997).
                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND DIMERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Bone marrow;
MFDLINE=98049554; PubMed=9388232;
                                           ,
,
,
               100.0%;
                                                                                        QRYGRELRRMSDEFEG 161
                             100.08;
                                                                          1 ORYGRELRRMSDEFEG 16
            Query Match
Best Local Similarity 100.
Matches 16, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cell 87:629-638(1996
                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                      146
                                                                                                                                                                                                                                                                                                                                                                                                                          BAD."
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                                                                                                                                                                   "Rationale for Bcl-xL/Bad peptide complex formation from structure, mutagenesis, and biophysical studies.";

Protein Sci. 9:2528-2534(2000).
-:- FUNCTION: Promotes cell death. Successfully competes for the binding to Bcl-x(L), Bcl-2 and Bcl-w, thereby affecting the level of heterodimerization of these proteins with BAX. Can reverse the death repressor activity of Bcl-x(L), but not that of Bcl-2 (By similarity). Appears to act as a link between growth factor receptor signaling and the apoptotic pathways.
-:- SUBNIT: Forms heterodimers with the anti-apoptotic proteins, Bcl-x(L), Bcl-2 and Bcl-w. Also binds protein S100AlO (By similarity).

The Ser-75/Ser-99 phosphorylated form binds 14-3-3 proteins (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAUTION: Ref.1 sequence differs from that shown due to frameshifts in position 64 and 91.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        phosphorylation, locates to the cytoplasm.

TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.

DOMAIN: Intact BH3 domain is required by BIK, BID, BAK, BAD AND BAX for their pro-apoptotic activity and for their interaction with anti-apoptotic members of the Bcl-2 family.

PTM: Phosphorylation on Ser-99 promotes heterodimerization with 14-3-3 proteins. This interaction then facilitates the phosphorylation at Ser-118, a site within the BH3 domain, leading to the release of Bcl-x(1) and the promotion of cell survival. Ser-99 is the major site of AKT/PKB phosphorylation, Ser-118 the major site of protein kinase A (CAPK) phosphorylation (by
STRUCTURE BY NAM OF 103-127.
MEDLINE-21073561, PubMed=11206074;
Petros A.M., Nettesheim D.G., Wang Y., Olejniczak E.T., Meadows R.P.,
Mack J., Swift K., Matayoshi E.D., Zhang H., Thompson C.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PHOSPHORYLATION (BY PKA AND PKB) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BY
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SIMILARITY).
A -> S (in dbSNP:3729933).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY).
PHOSPHORYLATION (BY PKA AND PKB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                similarity).
SUBCELLULAR LOCATION: Outer mitochondrial membrane. Upon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain. SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Apoptosis; Phosphorylation; Polymorphism; 3D-structure. DOMAIN 110 124 BH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18392 MW; 69FD8D27DDEE3241 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MIM; buslo;; C:cytoplasm; NAS.
G0; G0:0005737; C:cytoplasm; NAS.
G0; G0:0005515; E:protein binding activity; NAS.
G0; G0:0008632; P:apoptotic program; TAS.
G0; G0:0006917; P:induction of apoptosis; NAS.
Interpro; IPR000712; Bc12_BH.
PROSITE; PS01259; BH3; FALE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FTIG=VAR_015380.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U66879; AAB36516.1; ALT_FRAME.
EMBL; AF021792; AAB72092.1; -.
EMBL; AF031523; AAB88124.1; -.
EMBL; BC001901; AAH01901.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genew; HGNC:936; BAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PDB; 1G5J; 07-FEB-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                168 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118
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                                                                                                               Mack J., Swi
Fesik S.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOD_RES
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86.9%; Score 73; DB 1; Length 168;

us-09-544-664-28.rsp

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HARMAN NA DEN NA DEN NA DESTRETA DE LA PRESENTA DEL PRESENTA DEL PRESENTA DE LA PRESENTA DEL PRESENTA DEL PRESENTA DE LA PRESE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";
Nature 417:141-147(2002).

-!- FUNCTION: The Dynabc repair system catalyzes the recognition and processing of DNA lesions. UVTA is an ATPase and a DNA-binding protein. A damage recognition complex composed of 2 uvrA and 2 uvrB subunits scans DNA for abnormalities. When the presence of a lesion has been verified by uvrB, the uvrA molecules dissociate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pfam; PP00005; ABC_tran; 2.
ProDom; PD000006; ABC_transporter; 1.
TIGRFAMS; TIGR00630; UTT3; 1.
PROSITE; PS00211; ABC_TRANSPORTER_1; 2.
PROSITE; PS0893; ABC_TRANSPORTER_2; 1.
SOS response; Excision nuclease; DNA repair; DNA recombination; DNA excision; ATP-binding; DNA-binding; Repeat; Zinc; Metal-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [1]
STRAIN-A3(2) / M145;
STRAIN-A3(2) / M145;
MEDLINE-21996410; PubMed=12000953;
MEDLINE-21996410; PubMed=12000953;
MEDLINE-21996410; PubMed=12000953;
MEDLINE-21996410; PubMed=12000953;
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Kieser H.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Gronin A., Fraser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Hanng C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares S., Taylor K.,
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                     30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
UNTABC system protein A (UVTA protein) (Excinuclease ABC subunit A).
UVRA OR SC01958 OR SCC54.18C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (By similarity). 
 -!- SUBUNIT: Forms a heterotetramer with uvrB during the search for
                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptomyces coelicolor.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32 39 ATF (PULDMILL).
645 652 ATP (POTENTIAL).
744 770 C4-TYPE.
1014 AA; 110997 MW; 084D6B18692A792D CRC64;
                                     Indels
                           ,0
   Pred. No. 6.7e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                   PRT; 1014 AA.
                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; T36031; T36031.

HAMAP; MF_00205; -; 1.

InterPro; IPR003439; ABC_transporter.

InterPro; IPR004602; Uvra.
                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zinc-finger; Complete proteome.
NP_BIND 32 39 AC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AL035591; CAB38148.1; -.
100.08;
                                                                                                                                                                 108 ORYGRELRRMSDEF 121
                                                                                                1 ORYGRELRRMSDEF 14
                                  14; Conservative
                                                                                                                                                                                                                                                                                                                                      STANDARD;
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hopwood D.A.;
                                                                                                                                                                                                                                                                                                                                   UVRA_STRCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZN_FING
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UP_BIND
                                                                                                                                                                                                                                                                     RESULT 4
UVRA_STRCO
                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE SPECIFICITY: EXPRESSED IN A NUMBER OF B-AND T-LYMPHOID CELL
                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROTEINS INCLUDING MCL-1, BCL-2, BCL-XL, BFL-1, AND BHRF-1, DOES NOT HETERODIMERIZE WITH PROAPOPTOTIC PROTEINS SUCH AS BAD, BOK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BAX OR BAK (BY SIMILARITY).
SUBCELLULAR LOCATION: ASSOCIATED WITH INTRACYTOPLASMIC MEMBRANES.
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      O'COMOOY L., Strasser A., O'Reilly L.A., Hausmann G., Adams J.M., Cory S., Huang D.C.S.;
"Bim: a novel member of the Bcl-2 family that promotes apoptosis.";
EMBO J. 17:384-395(1998).
-!- FUNCTION: INDUCES APOPTOSIS. THE ISOFORMS VARY IN CYTOTOXICITY
WITH ISOFORM BIMS BEING THE MOST POTENT AND ISOFORM BIMEL BEING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus
                                                                                                                                                                                                                                                                                                        BIM_MOUSE STANDARD; PRT; 196 AA. 054918; 054919; 054920; 16-0CT-2001 (Rel. 40, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) BCL2-like protein 11 (BCL2 interacting mediator of cell death). BCL2L11 OR BIM.
                                                            1;
Length 1014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- DOMAIN: THE BH3 DOMAIN IS REQUIRED FOR BCL-2 BINDING AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., FUNCTION, SUBCELLULAR LOCATION, TISSUE SPECIFICITY, AND ALTERNATIVE SPLICING.
MEDLINE-98094360; Pubmed-9430630;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Missing (in isoform BimL).
/FTId=VSP_000536.
Missing (in isoform BimS).
/FTId=VSP_000537.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Event=Alternative splicing; Named isoforms=3;
DB 1;
                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Apoptosis; Alternative splicing; Membrane.

DOMAIN 146 160 BH3.

VARSPLIC 42 97 Missing (in is
                               39,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IsoId=054918-2; Sequence=VSP_000536;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=054918-3; Sequence=VSP_000537;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=BimEL;
IsoId=054918-1; Sequence=Displayed;
Score 42.5;
Pred. No. 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, AF032459; AAC40029.1; -.
EMBL, AF032460; AAC40030.1; -.
EMBL, AF032461; AAC40031.1; -.
MGD, MGD, 11197519; Bcl2111.
Interpro; IPR000712; Bcl2_BH.
PROSITE; PS01259; BH3; FALSE_NEG.
                                                                                                                                                                       368 RYGRE-RRYTTAFEG 381
                                                                                                                           2 RYGRELRRMSDEFEG 16
  Query Match 50.6
Best Local Similarity 66.7
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THE LEAST POTENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOTOXICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=BimL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=BimS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARSPLIC
                                                                                                                                                                                                                                                                                 RESULT 5
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STRAIN-S288c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AROG_YEAST
                                                                                                                                                         Apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
                                                                                                                                                                                                                                                                                                             VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                         INIT MET
                                                                                                                                                                                                                                                                    VARSPLIC
                                                                                                                                                                                                                                                                                                                                                          CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      dUTPase
                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AROG_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
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DDRR
DDDRR
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BRITITITITE BRITING SO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Comment=2 isoforms, BOD-L (shown here) and BOD-S, are produced by alternative initiation at Met-1 and Met-104; TISSUE SPECIFICITY: Widely expressed.

DOMAIN: THE BH3 DOMAIN IS REQUIRED FOR BCL-2 BINDING AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chórdata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM BIML). Chen D., Simon R.P., Chen J.; "Cloning of rat bimEL and bimL, and their differential expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: INDUCES APOPTOSIS.
SUBUNIT: FORMS HETERODIMERS WITH A NUMBER OF ANTIAPOPTOTIC BCL-2
PROTEINS INCLUDING MCL-1, BCL-2, BCL-XL, BFL-1, AND BHRF-1. DOES
NOT HETERODIMERIZE WITH PROAPOPTOTIC PROTEINS SUCH AS BAD, BOK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: ASSOCIATED WITH INTRACYTOPLASMIC MEMBRANES (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hsu S.Y., Lin P., Hsueh A.J.W.;
"BOD (Bcl-2-related ovarian death gene) is an ovarian BH3 domain-containing proapoptotic Bcl-2 protein capable of dimerization with ddiverse antiapoptotic Bcl-2 members.";
Mol. Endocrinol. 12:1432-1440(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId=088498-1; Sequence=Displayed;
Note=Isoform BOD-S is produced by alternative initation at
                                                                                        0;
                                                                                                                                                                                                                                                                                                                                16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
BCL2-like protein 11 (BCL2 interacting mediator of cell death)
(BCl-2 related ovarian death protein).
BCL2L11 OR BIM OR BOD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION, SUBUNIT, AND TISSUE SPECIFICITY
                                         50.0%; Score 42; DB 1; Length 196; 61.5%; Pred. No. 8.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ischemia and normal rat brain.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
531C176E5F1AC9AA CRC64;
                                                                                        .
m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Event=Alternative splicing; Named isoforms=3; Name=BOD-\mathbf{L}_{i}
                                                                                                                                                                                                                                                                                       196 AA.
                                                                                    2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ISoId=088498-3; Sequence=VSP_000539;
Event=Alternative initiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=088498-2; Sequence=VSP_000538;
                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Ovary;
MEDLINE=98400436; PubMed=9731710;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ISOFORMS BOD-L; BOD-M AND BOD-S)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Met-104 of isoform BOD-L;
22066 MW;
                                                                                                                                                         | :||||: |||
RIAQELRRIGDEF 157
                                                                                                                                 2 RYGRELRRMSDEF 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALTERNATIVE PRODUCTS:
                                                                                      Conservative
                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.,
196 AA;
                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BAX OR BAK.
                                                                                                                                                                                                                                                                                                           088498; 088497;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name-BimL;
                                                                                      .
ω
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SEQUENCE
                                           Query Match
                                                                                                                                                                                                                                                                                         BIM_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chen
                                                                                        Matches
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Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: STEREOSPECIFIC CONDENSATION OF PHOSPHOENOLPYRUVATE (PEP)
AND D-ERYTHROSE-4-PHOSPHATE (E4P) GIVING RISE TO 3-DEOXX-D-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SECUENCE FROM N.A.
MEDLINE=92225349; PubMed=1348717;
MEDLINE=92225349; PubMed=1348717;
Mediler M., Paravicini G., Egli C., Irniger S., Braus G.H.;
"Cloning, primary structure and regulation of the ARO4 gene, encoding the tyrosine-inhibited 3-deoxy-D-arabino-heptulosonate-7-phosphate synthase from Saccharomyces cerevisiae.";
Gene 113:67-74(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Doignon F., Biteau N., Aigle M., Crouzet M.; "The complete sequence of a 6794 bp segment located on the right arm of chromosome II of Saccharomyces cerevisiae. Finding of a putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Phospho-2-dehydro-3-deoxyheptonate aldolase, tyrosine-inhibited (EC 4.1.2.15) (Phospho-2-keto-3-deoxyheptonate aldolase) (DAHP synthetase) (3-deoxy-D-arabino-heptulosonate 7-phosphate synthase).
                                                                                                                                                                  Alternative splicing; Membrane; Alternative initiation.
                                                                                                                                                                                      BCL2-LIKE PROTEIN 11, ISOFORM BOD-L. BCL2-LIKE PROTEIN 11, ISOFORM BOD-S. FOR ISOFORM BOD-S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ARABINO-HEPTULOSONATE-7-PHOSPHATE (DAHP).
CATALYIIC ACTIVITY: 2-dehydro-3-deoxy-D-arabino-heptonate 7-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
0
                                                                                                                                                                                                                                                                                                                                                                          /FTId=VSP_000539.

E -> D (IN REF. 1; AAC23594).

B4D2146F9C0B37A0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 196;
8.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Indels
                                                                                                                                                                                                                                                                                                                                                      Missing (in isoform BOD-M).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kuenzler M.; Submitted (NOV-1993) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                  Missing (in isoform BimL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-001-1993 (Rel. 27, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                           000538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  370 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 42;
Pred. No. 8
                                                                                                                                                                                                                                                                                                                         FTIG=VSP_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
EMBL, AF065433, AAC23595.1; -.
EMBL, AF065431, AAC23593.1; -.
EMBL, AF065432, AAC23594.1; -.
INELPIO, AF136927; AAD26594.1; -.
INELPIO, IPR000712; BC12_BH.
PROSITE; PS01259; BH3; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=94078675; PubMed=8256522;
                                                                                                                                                                                                                                                                     BH3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7;
                                                                                                                                                                                                                                                                                                                                                                                                                                   22055 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50.0%;
61.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ARO4 OR YBR249C OR YBR1701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               145 RIAQELRRIGDEF 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 RYGRELRRMSDEF 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              dUTPase in a yeast.";
Yeast 9:1131-1137(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                           196
196
196
160
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REVISIONS TO 205-207
                                                                                                                                                                                                                                                                                                                                                                                                                                   196 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=4932;
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104
146
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GVK1_HALN1
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CONFLICT
SEQUENCE
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          SOURTH AND DRANGE DO DRANG
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                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0003849; F:3-dehydro-3-deoxyphosphoheptonate aldolase . . .; IDA. InterPro; IPR006219; AroFGH. InterPro; IPR006218; DAHP1/KDSA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   013049; Q9NQPB;
01-NOV-1997 (Rel. 35, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Zinc-finger protein HT2A (72 kDa Tat-interacting protein) (Tripartite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SECTION N.A. MEDINE=95297135; PubMed=7778269; Fridell R.A., Harding L.S., Bogerd H.P., Cullen B.R.; Identification of a novel human zinc finger protein that specifically interacts with the activation domain of lentiviral Tat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-22388257; PubMed=12477932; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
phosphate + phosphate = phosphoenolpyruvate + D-erythrose 4-phosphate + H(2)0.
ENZYME REGULATION: INHIBITED BY TYROSINE.
PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIGREAMS; TIGRO0034; arof6H; 1.
Aromatic amino acid biosynthesis; Lyase; Multigene family.
SEQUENCE 370 AA; 39749 MW; 594ED48F24175979 CRC64;
                                                                                                             INDUCTION: By amino acid starvation. SIMILARITY: BELONGS TO CLASS-I DAHP SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50.0%; Score 42; DB 1; Length 370; 43.8%; Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DAHP_Synth_1; 1.
                                                                                                                                                                                                                                                                                                                                                 EMBL; X61107; CAA43419.1; -.
EMBL; L20296; AAA65607.1; -.
EMBL; Z36118; CAA85212.1; -.
PIR; S38185; S38185.
HSSP; P00886; 1QR7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ORYGRELRRMSDEFEG 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Virology 209:347-357(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00793; DAHP_synth_
ProDom; PD005060; AroFGH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGD; S0000453; ARO4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRIM32 OR HT2A
                                                                                           first step
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Skin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HT2A_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 8
HT2A_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sehra
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Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninol P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,
Willalon D.K., Muzny D.M., Sodengren B.J., Lu X., Gibbs R.A.,
Rahes J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butkerfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"""" "Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

-!- FUNCTION: MAY PLAY A SIGNIFICANT ROLE IN MEDIATING THE BIOLOGICAL ACTIVATION PROPER IN VIVO. BINDS SPECIFICALLY TO THE ACTIVATION DOMAIN OF HIV-1 TAT AND CAN ALSO INTERACT WITH THE HY-2 AND EIAV TAT PROTEINS IN VIVO.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- TISSUE SPECIFICITY: SPLEEN, THYMUS, PROSTRATE, TESTIS, OVARY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MLM; 602230; -. 600.0005634; C:nucleus; TAS. 60:00005634; C:nucleus; TAS. 60:00005634; C:nucleus; TAS. 1nterPro; IPR001258; NHL. InterPro; IPR001258; NHL. InterPro; IPR000315; Znf_Bbox. InterPro; IPR001841; Znf_ring. Pfam; PF001436; NHL; S. Pfam; PF000643; Zf_Bbox; I. Pfam; PF000643; Zf_Bbox; I. Pfam; PF000643; Zf_Bbox; I. SMART; SM00336; BBOX; I. SMART; SM00184; RING; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 653;
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F -> I (IN REF. 1).
D83B1595CA8378FD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INTESTINE AND COLON.
-!- SIMILARITY: Contains 1 RING-type zinc finger.
-!- SIMILARITY: Contains 1 B box-type zinc finger.
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Pred. No. 3
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PROSITE; PS00518; ZF_RING_1; 1.
PROSITE; PS50089; ZF_RING_2; 1.
Zinc-finger; Nuclear protein.
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71988 MW;
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EMBL; BC003154; AAH03154.1; -.
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61.5%;
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653 AA;
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MEDLINE-20504483; PubMed=11016950;
My W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
Alam M., Freitas T., Hou S., Daniels C.Y., Dennis P.P., Omer A.D.,
Bebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
"Genome sequence of Halobacterium species NRC-1.",
Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=NRC-1; PLASMID=pNRC100;
MEDLINE=99063795; PubMed=9847077;
NG W.V., Clufo S.A., Smith T.M., Bumgarner R.E., Baskin D., Faust J.,
Hall B., Loretz C., Seto J., Slagel J., Hood L., DasSarma S.;
"Snapshot of a large dynamic replicon in a halophilic archaeon:
megaplasmid or minichromosome?";
Genome Res. 8:1131-1141(1998).
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MEDLINE=91323716; PubMed=1864501;
Jones J.G., Young D.C., Dassarma S.;
"Structure and organization of the gas vesicle gene cluster on the
Halobacterium halobium plasmid pNRC100.";
                                                                                                                                GVPK protein 1. (GVPK12 OR VNG6021G). (GVPK11 OR GVPK OR VNG6021G). (GVPK11 OR GVPK OR VNG5021G) AND (GVPK12 OR VNG6021G), and
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Gas vesicle; Plasmid; Complete proteome.
SEQUENCE 113 AA; 12695 MW; 97A469D2C1643ABF CRC64;
                                                                                                                                                                                                              Halobacterium sp. (strain NRC-1 / ATCC 700922 / JCM 11. Halobacterium sp. (strain NRC-817). Plasmid pNRC100, Plasmid pNRC200, and Plasmid pHH1. Archaea: Euryarchaeota; Halobacteria; Halobacteriales;
P24375; Q9H126; 01-MAR-1992 (Rel. 21, Created) 01-MAR-1992 (Rel. 21, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update)
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MEDLINE-92065812; PubMed-1956294;
Horne M., Englert C., Wimmer C., Pfeifer F.;
                                                                                                                                                                                                                                                                                                                                                               Halobacteriaceae; Halobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF016485; AAC82801.1; -. EMBL; AE005141; AAG20718.1; -.
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PIR; T08234; T08234.
                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=64091, 148370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gene 102:117-122(1991).
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DB 1; Length 113; 7;

Score 41; Pred. No.

48.8%;

Query Match Best Local Similarity

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MEDLINE-99287316; PubMed-10360571;
Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
"Evidence for lateral gene transfer between Archaea and Bacteria from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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-!- PATHWAY: Pentose phosphate pathway; second step.
-!- SIMILARITY: BELONGS TO THE GLUCOSAMINE/GALACTOSAMINE-6-PHOSPHATE ISOMERASE FAMILY. 6-PHOSPHOGLUCONOLACTONASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- CATALYTIC ACTIVITY: 6-phospho-D-glucono-1,5-lactone + H(2)0 = 6-
                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
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                                                                                                                                                                                                                                                                                 30-MAY 2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
6-phosphogluconolactonase (EC 3.1.1.31) (6PGL).
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40.0%; Pred. No. 14;
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(Rel. 12, Last sequence update)
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Nature 399:323-329(1999).
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InterPro; IPR005900; Phosphogluconlac.
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Thermotoga maritima.
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01-0CT-1989
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GO; GO:0005634; C:nucleus; IDA.
GO; GO:000295; F:protein Kinase activator activity; IGI.
GO; GO:0007031; P:peroxisome organization and biogenesis; IMP.
GO; GO:0006357; P:regulation of transcription from Pol II pro. . .; IGI.
InterPro; IPR000644; CBS_domain.
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SIMILARITY: Contains 4 CBS domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SECUENCE FROM N.A.
MEDLINE=90097921; PubMed=2481228;
Celenza J.L., Eng F.J., Carlson M.;
"Molecular analysis of the SNF4 gene of Saccharomyces cerevisiae:
evidence for physical association of the SNF4 protein with the SNF1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIATE=94131988; PubMed=7905477;
Mitchelhill K.I., Stapleton D., Gao G., House C., Michell B.,
Katsis F., Witters L.A., Kemp B.E.;
"Mammalian AMP-activated protein kinase shares structural and
functional homology with the catalytic domain of yeast Snfl protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Biol. Chem. 269:2361-2364(1994).
-!- FUNCTION: THIS PROTEIN CAUSES EXPRESSION OF GLUCOSE-REPRESSIBLE
                                                                                                                                                                                                                                                                                                                       MEDLINE-89006284; PubMed=3049255; Schueller H.-J., Entian K.-D.; Schueller H.-T., Entian K.-D.; "Molecular characterization of yeast regulatory gene CAT3 necessary for glucose derepression and nuclear localization of its product."; Gene 67:247-257(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENES UPON GLUCOSE DEPRIVATION. IT INTERACTS AND HAS FUNCTIONAL
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Carbohydrate metabolism; Transcription regulation; Nuclear protein;
                                                                                                     Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Doi A., Doi K.;
Submitted (JUN-1993) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                   Saccharomycetales; Saccharomycetaceae; Saccharomyces
                              Nuclear protein SNF4 (Regulatory protein CAT3).
SNF4 OR CAT3 OR YGL115W.
16-CCT-2001 (Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tomasini L., Ferrero I., Goffrini P.;
"Molecular characterization of KISNF4 gene.";
Submitted (AFR-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THIS PROTEIN CAUSES EXPRESSION OF GLUCOSE-REPRESSIBLE GENES UPON GLUCOSE DEPRIVATION. IT INTERACTS AND HAS FUNCTIONAL RELATIONSHIP TO THE PROTEIN KINASE SNF1 (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Nuclear (By similarity).
-!- SIMILARITY: BELONGS TO THE 5'-AMP-ACTIVATED PROTEIN KINASE, GAMWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kluyveromyces lactis (Yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
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                                                                                      DB 1; Length 322;
21;
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  246 CBS 3.
318 CBS 4.
36401 MW; 51B387E346EE9561 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                     16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Nuclear protein SNF4.
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Pred. No. 2
                                                                                      Score 41;
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SMART; SM00116; CBS; 4
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Best Local Similarity
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DOMAIN 40
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09P869;
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Calliactis parasitica (Sea anemone).
Eukaryota, Metazoa, Cnidaria, Anthozoa, Soantharia, Actiniaria,
Nynantheae, Hormathiidae, Calliactis.
NCBI_TaxID-6114;
            Antho-RFamide neuropeptides precursor
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            SOLUTION OF THE SET OF
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SIGNINE-98049343; PubMed=9389475;
XMEDLINE-98049343; PubMed=9389475;
XA RIENK H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
XA Katchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
X Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
X Richardson D.L., Merlavage A.R., Lee N.H., Sutton G.G., Gill S.,
X Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
X Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
Peterson S., Reich C.I., McNeill L.K., Badger J.H., Glodek A., Zhou L.,
A Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
Masson T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              between the Swiss Institute of Bloinformatics and the EMBL outstation—
the European Bioinformatics Institute. There are no restrictions on its
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modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Proteasome-activating nucleotidase (Proteasome regulatory subunit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The complete genome sequence of the hyperthermophilic, sulphatereducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
-1- FUNCTION: Required for the ATP- or CTP-dependent degradation proteins, but not small peptides, by the 20S proteasome (By
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-!- SUBUNIT: Homohexamer (Potential).
-!- SUBCELLUIAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: BELONGS TO THE AAA FAMILY OF ATPASES.
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398 AA; 44964 MW; F3293BB7D6A646B4 CRC64;
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InterPro; IPR005937; 26S_p45.
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43 RYEREVRRIRSEVE 56
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                          Darmer D., Schnutzler C., Diekhoff D., Grimmelikhuijzen C.J.P.;
"Primary structure of the precursor for the sea anemone neuropeptide Antho-RFamide (<Glu-Gly-Arg-Phe-NH2).";
Proc. Natl. Acad. Sci. U.S.A. 88:2555-2559(1991).
-!- FUNCTION: NOT KNOWN BUT IT COULD ACT AS A TRANSMITTER AT NEUROMUSCULAR SYNAPSES.
-!- TISSUE SPECIFICITY: NEURONS ASSOCIATED WITH SMOOTH MUSCLE FIBERS.
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SEQUENCE FROM N.A.

MEDLINE=93054550; PubMed=1429603;

Schmutzler C., Darmer D., Diekhoff D., Grimmelikhuijzen C.J.P.;

Schmutzler co., Darmer D., Diekhoff D., Grimmelikhuijzen C.J.P.;

Identification of a novel type of processing sites in the precursor for the sea anemone neuropeptide Antho-RFamide (<Glu-Gly-Arg-Phe-NH2) from Anthopleura elegantissima.";

J. Biol. Chem. 267:22534-22541(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PARTIAL SEQUENCE (ANTHO-RFAMIDE).
MEDLINE-87092339; PubMed=2879288;
Grimmelikhuijzen C.J.P., Graff D.;
"Isolation of pyroGlu-Gly-Arg-Phe-NH2 (Antho-RFamide), a neuropeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AMIDE GROUP).
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16-007-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
Anthor-Remaide neuropeptides type 2 precursor.
Anthopleura elegantissima (Sea anemone).
Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
Nynantheae; Actiniidae; Anthopleura.
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-!- FUNCTION: NOT KNOWN BUT IT COULD ACT AS A TRANSMITTER AT NEUROMUSCULAR SYNAPSES.
-!- SUBCELLULAR LOCATION: Secreted.
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EMBL; M99170; AAA27739.1; -.
Pfam; PF01581; FARP; 14.
Neuropeptide; Amidation; Repeat; Signal.
22 POTENTIAL.
22 ANTHO-RFAMIDE.
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Result

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Sequence:

Title:

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us-09-544-664-28.rspt

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Q8C661 mus musculu
Q8C611 mus musculu
Q8qtn7 oryza sativ
Q8ew78 mycoplasma
Q8qtn2 oryza sativ
Q9xem4 oryza sativ
Q91gr7 oryza sativ
Q91gr6 oryza sativ
Q91gr6 oryza sativ
Q9sw6 oryza sativ
Q8sw6 oryza sativ
Q8sw6 oryza sativ
Q8sw6 oryza sativ
Q8ysh5 oryza sativ
Q8ysh2 oryza sativ
                  Q9p5v2 neurospora
Q94h58 oryza sativ
Q8s6j1 oryza sativ
Q97i40 clostridium
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Q94hul oryza sativ
Q957a7 oryza sativ
Q9vsm1 drosophila
Q9vsm0 drosophila
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Q8f646 leptospira
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MEDLINE-20373792; PubMed=10917738;
Inchara N., Nunez G.;
"Genes with homology to mammalian apoptosis regulators identified in
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Eukaryota: Metazoa; Chordata: Craniata; Vertebrata; Euteleostomi;
Ectinopterygii: Neopterygii; Teleostel; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBL_TAXID=7955;
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cell Death Differ. 7:509-510(2000).
EMBL; AF231017; AAF66962.2; -.
HSSP; Q92934; 1G5J.
ZFIN; ZDB-GENE-000616-1; bad.
SEQUENCE 146 AA; 16546 MW; 28A5650BB5107ECB CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
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Q9SSW6
Q8RYW0
Q8R315
Q8LSS
Q9VSM2
Q94HU1
Q9STA7
Q9VSM1
Q9VSM1
                  Q995V2
Q94H58
Q856J1
Q97I40
Q8LM44
Q8F646
Q8C6N1
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Q8EW78
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Q8xxs6 ralstonia s
Q9fv20 oryza sativ
Q8qtn3 oryza sativ
Q98974 rhizobium l
Q8kgy8 rhizobium l
Q8es55 oceanobacil
Q9ruk9 deinococcus
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Q9hus7 pseudomonas
Q93y86 oryza sativ
Q9ngnl leishmania
Q9kgw3 pseudomonas
Q8ei34 shewanella
Q8ztil pyrobaculum
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237.680 Million cell updates/sec
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Q8ZTI1
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Gapop 10.0 , Gapext 0.5
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sp_unclassified:*
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A Allahult A., Furmed-1102030, Mangenot S., Arlat M., Genin S., Artiquenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L., Canadler M., Claudel-Renard C., Cunnac S., Demange N., Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Siquier P., Tabbault P., Whalen M., Wincker P., Levy M., Meissenbach J., Boucher C.A.;

"Genome sequence of the plant pathogen Ralstonia solanacearum.";

"The Common sequence of the plant pathogen Ralstonia solanacearum.";

"RENEL, ALG46067; CAD15739.1;

"RENEL, ALG46067; CAD15739.1;

"TherPro; IPR003593; AAA_ATPase.

InterPro; IPR003593; AAA_ATPase.

Refam; PF00005; ABC_transporter.

Refam; PF00005; ABC_transporter;

RENDOM; DEND000066; ABC_transporter;

RENDOM; SMART; SM00382; AAA; 1.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-cv. Zhaiyeqing 8; TRANSPOSON-unspecified; TISSUE-Shoot; Yu F., Zhang A., Zhang F., Chen S.; Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AF259976; AAG15480.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 45; DB 16; Length 230;
Pred. No. 20;
1; Mismatches 4; Indels
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Pred. No. 52;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                            230 AA; 25231 MW; 7C3FDA1E7A19A2A4 CRC64;
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SEQUENCE 567 AA; 64419 MW; BD4F47AB33A685BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
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                                 STRAIN=GMI1000;
MEDLINE=21681879; PubMed=11823852;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002156; RNaseH.
InterPro; IPR000477; RVTse.
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168 QEIGRTLRRLVDEF 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | :|:|: |:|||
547 YRQEVRKLEDKFEG 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ORYGRELRRMSDEF 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 YGRELRRMSDEFEG 16
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des 9; Conservative
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            SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                     Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=39946;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polyprotein.
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-21996410, PubMed-12000953;
MEDLINE-21996410, PubMed-12000953;
MEDLINE-21996410, PubMed-12000953;
MEDLINE-21996410, PubMed-12000953;
MEDLINE-21996410, PubMed-12000953;
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford R., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";
Nature 417:141-147(2002).
EMBL, A1939129: CABB9025-1; -
InterPro; IPR003265; B006_3c.
Pfam; PF00730; HHH-GPD; 1.
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Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Ralstoniaceae; Ralstonia.
                                                                                                             Streptomyces coelicolor.

Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56.0%; Score 47; DB 16; Length 216; 50.0%; Pred. No. 8.7;
                                                                                                                                                                                                                                                                                                                                                                             Thomson N.R., Parkhill J., Barrell B.G., Rajandream M.A., Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                   Saunders D.C., Harris D.;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complete proteome.
8810 MW; DDD7C717D60F7AA7 CRC64;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein SC06964.
SC06964 OR SC6F7.17C.
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Probable ATP-binding ABC transporter protein.
RSC2037 OR RS03602.
                                                                                                                                                  Streptomycineae; Streptomycetaceae; Streptomyces. NCBI_TaxID=1902;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Mismatches
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216 AA; 23810 MW;
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109 ERWGGDLRRLRDEADG 124
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nes 8; Conservative
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SEQUENCE FROM N.A.
STRAIN=HTE831 / DSM 14371 / JCM 11309;
MEDLINE=22220767; PubMed=12235376;
Takami H., Takaki Y., Uchiyama I.;
"Genome sequence of Oceanobacillus iheyensis isolated from the Iheya
                                                                                                                                                                                                                                                                                               Sullivan J.T., Trzebiatowski J.R., Cruickshank R.W., Gouzy J.,
Brown S.D., Elliot R.M., Fleetwood D.J., McCallum N.G., Rossbach U.,
Stuart G.S., Weaver J.E., Webby R.J., de Bruijn F.J., Ronson C.W.;
"Comparative sequence analysis of the symbiosis island of
Mesorhizobium loti strain R7A.";
J. Bacteriol. 184:3086-3095(2002).
EMBL; ALG72112; CAD31464.1;
InterPro; IPR03563; SUWC_protease.
PROSITE; PS50600; ULP_PROTEASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53.6%; Score 45; DB 2; Length 1798; 69.2%; Pred. No. 1.8e+02; Live 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52.4%; Score 44; DB 16; Length 157; 50.0%; Pred. No. 19;
                                                                                                                                                      Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Phyllobacteriaceae; Mesorhizobium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein.
SEGUENCE 1798 AA; 196214 WW; A750A49B8C0D581B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AP004595; BAC12744.1; -. Hypothetical protein; Complete proteome. SEQUENCE 157 AA; 17809 MW; 128229251596C18C CRC64;
01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Mypothetical protein.
MST059.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-WAR-2003 (TrEMBLrel. 23, Last sequence update) 01-WAR-2003 (TrEMBLrel. 23, Last annotation update) Hypothetical conserved protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oceanobacillus iheyensis.
Bacteria: Firmicutes; Bacillales; Oceanobacillus.
NCBI_TaxID=182710;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           564 A.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic Acids Res. 30:3927-3935(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2003 (TrEMBLrel. 23, Created)
                                                                                                                               Rhizobium loti (Mesorhizobium loti).
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                                                                                                                                                                                                                                                            STRAIN=R7A;
MEDLINE=21999272; PubMed=12003951;
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126 FSRELKRIGEEFSG 139
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Matches 9; Conservative
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                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                              NCBI_TaxID=381;
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Q8ES55
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MEDLINE-21082930; PubMed-11214968;
Raneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; "Complete genome structure of the nitrogen-fixing symbiotic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                   STRAIN-EV. Nipponbare;
Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.,
Overton II L.L., Tsittin T., Kim M.M., Bera J.J., Jin S.S.,
Fadrosh D.W., Tallon L.J., Koo H., Zismann V., Hsiao J., Blunt S.,
Vanaken S.S., Riedmuller S.B., Vlterback T.T., Feldblyum T.V.,
Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.,
White O., Salzberg S.L., Fraser C.M.;
Oryza sativa chromosome 10 BAC OSJNBa0041L14 genomic sequence.";
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
BNBL; AC099042; AAN08247.1; -
SEQUENCE 1696 AA; 190501 MW; 516B35CFDFA2F068 CRC64;
                       Oryza sativa (japonica cultivar-group).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1696;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Phyllobacteriaceae; Mesorhizobium.
NCBI_TaxID=381;
                                                                                                                                                                                                                                                                                                                                                                                                                      53.6%; Score 45; DB 10; Length 16
50.0%; Pred. No. 1.7e+02;
Live 5; Mismatches 2; Indels
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01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein mlr6316.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 1748 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein, Complete proteome. SEQUENCE 1748 AA; 190454 MW; 2A9CE71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mesorhizobium loti.";
DNA Res. 7:331-338(2000).
EMBL; AP003008. BAB52630.1;
InterPro: IPR001653; SUMO_protease.
Pfam; PF02902; Peptidase_C48; 1.
PROSITE; PS50600; ULP_PROTEASE; 1.
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1341 YRQEVRKLEDKFEG 1354
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 50.00,
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Best Local Similarity 69.2
Matches 9; Conservative
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                                                                                                           NCBI_TaxID=39947
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Q8KGY8

RESULT 7 Q8KGY8

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321 GEELRRQAEYFEG 333
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Matches 8; Conserve
                                                                                         Phosphopantetheine.
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                                                                                                              SEQUENCE
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MEDLINE-22056096; PubMed=12060743;

MEDLINE-22056096; PubMed=12060743;

MEDLINE-22056096; PubMed=12060743;

Moss S.J., Leistner E., Floss H.G.;

"The biosynthetic gene cluster of the maytansinoid antitumor agent
ansamitodin from Actinosynnema pretiosum.";

Proc. Natl. Acad. Sci. U.S.A. 99:7968-7973(2002).

BMBL, AFK53501; AAM54077.1; -

InterPro; IPR000794; Ketoacyl-synt.

InterPro; IPR0006163; Ppantne_attach.

InterPro; IPR006163; Pp_bnine_attach.

InterPro; IPR006163; Pp_bnine_attach.

R Fiam; PF00109; ketoacyl-synt; 1.

Pfam; PF00109; ketoacyl-synt; 1.

Pfam; PF00109; ketoacyl-synt; 1.
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MEDLINE-20036896; PubMed=10567266;
Miblian D. Bisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D., Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Pseudonocardineae; Actinosynnemataceae; Actinosynnema.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.\,{}^{\mu},
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 44; DB 16; Length 564;
Pred. No. 76;
3; Mismatches 2; Indels
                                                                                                                        Deinococcus radiodurans.

Bacteria; Deinococcus Thermus; Deinococcales; Deinococcaceae; Deinococcaceae; Deinococcaceae; NCBI_TaxID=1299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TLOK; DRLJ),
TLOK; DRLJ),
TLOK; DRO06047; Alpha_amyl_cat.
InterPro; IPR006589; Alp_amyl_cat_sub.
Pfam; PF00128; alpha-amylase; 1.
SMART; SM00642; Aamy; 1.
Hydrolase; Complete proteome.
SEQUENCE 564 AA; 63667 MW; B8F50B9B0DFC8D51 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Glycosyl hydrolase, family 13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 1589 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science 286:1571-1577(1999).
EMBL; AE001983; AAF10944.1; -.
HSSP; P21332; 1UOK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52.4%;
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283 YVREMRRVIDEFD 295
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Q8KUF5
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STRAIN=ATCC 15692 / PAO1;
MEDLINE-20437337; PubMed=10984043;
MEDLINE-20437337; PubMed=10984043;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                        Gaps
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Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
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                                                                                                                                                                                                                51.8%; Score 43.5; DB 2; Length 1589; 56.2%; Pred. No. 2.7e+02; Live 3; Mismatches 3; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 406:959-964(2000).
-!- SIMILARITY: TO PROKARYOTE SENSORY TRANSDUCTION PROTEINS.
EMBL; AE004901; AAG08271.1; -.
HSSP; P02933; 1BXD.
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PROSITE; PS50109; HIS_KIN; 1.
PROSITE; PS00041; HTH_ARAC_FAMILY_1; 1.
Kinase; Phosphorylation; Sensory transduction; Transferase;
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                                                                                                                                                          1589 AA; 164712 MW; 5067CF9A772A525F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  463 AA.
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Pfam; PF00550; pp-binding; 1.
PROSITE; PS50075; ACP_DOMAIN; 1.
PROSITE; PS00606; B_KETOACYL_SYNTHASE; 1.
PROSITE; PS00012; PHOSPHOPANTETHEINE; 1.
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InterPro: IPR0043594; Bact_sens_Pr_C.
InterPro: IPR0043595; Bact_sens_Pr_C.
InterPro: IPR003660; HAMP.
InterPro: IPR003661; His_kina.
InterPro: IPR005467; His_kinase.
InterPro: IPR006290; Mctal_his_kin.
Pfam; PF00672; HAMP; 1.
Pfam; PF00512; HisRa; 1.
Prim: PF00512; HisRa; 1.
PRINTS; PR00344; BCTRISENSOR.
SWART; SW00304; HAMP; 1.
SWART; SW00387; HAMP; 1.
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Matches 9; Conservative
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SMART; SM00382; AAA; 4.
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SEQUENCE FROM N.A.
STRAIN=MR-1;
                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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Q8EI34;
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Q8EI34
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STRAIN-cv. Nipponbare;
Buell C.R., Yuan Q., Ouyang S., Moffat K.S., Hill J.N., Gansberger K.,
Buell C.R., Yuan Q., Ouyang S., Moffat K.S., Hill J.N., Gansberger K.,
Brenner M., Burgess S., Hance M., Shvartsbeyn M., Tsitrin T.,
Riggs F., Hsiao J., Zismann V., Blunt S., Pai G., Vanaken S.E.,
Utterback T.R., Feldblyum T.V., Quackenbush J., Salzberg S.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dynein heavy chain, cytosolic.
13302.02.
Leishmania major.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
                                                                  01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2002 (TrEMBLrel. 22, Last annotation update)
Putative gag-pol.
Oryza sativa (Rice).
Bukaryota: Viridiplantae, Streptophyta: Embryophyta: Tracheophyta;
Spermatophyta: Magnoliophyta: Liliopsida: Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                  "Oryza sativa chromosome 3 BAC OSJNBa0026A15 genomic sequence."; Submitted (MAY 2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AC084404; AAK50597.1; ... Gramene; Q93X86; ...
                                                                                                                                                                                                                                                                                                                                                                                                                     6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Friedlin;
Hilbert H., Wedler H., Wedler E., Duesterhoeft A., Ivens A.C.
Quail M., Rajandream M.A., Barrell B.G.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M., Smith D.F.;
"A physical map of the Leishmania major Friedlin genome.":
Genome Res. 8:135-145(1998).
EMBL; AL359781; CAB95305.1; -.
InterPro; IPR004273; Dynein.heavy.
InterPro; IPR004169; SHprot_acsite.
Pfam; PF03028; Dynein_heavy: 1.
                                                                                                                                                                                                                                                                                                                                                                                           51.2%; Score 43; DB 10; Length 674; 50.0%; Pred. No. 1.3e+02; cive 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                   Outerpro; 1PR002156; RNaseH.
Interpro; 1PR0021584; Rve.
Pfam; PF00075; rnaseH; 1.
Pfam; PF00665; rve; 1.
SEQUENCE 674 AA; 75473 MW; 9FA929B1426E725E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 5635 AA.
                                               674 AA.
                                               PRT;
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MEDLINE=98146435; PubMed=9477341;
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258 EAYVREVRRMERNFDG 273
                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ORYGRELRRMSDEFEG 16
                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 50.0%,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                               PRELIMINARY;
                                                                                                                                                                                                                                                               White O., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                   NCBI_TaxID=4530;
                                                           Q93Y86;
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                                               Q93Y86
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                       RESULT 12
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Characterization of NADH dehydrogenases of Pseudomonas fluorescens
"Characterization of NADH dehydrogenases of Pseudomonas fluorescens
WCS365 and their role in competitive root colonisation.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF281148; AAF97803.1;
InterPro; IPR000283; Complex1_75K.
InterPro; IPR00010141; Ferredoxin.
InterPro; IPR006565; Molybdopterin.
InterPro; IPR006565; Molybdopterin.
PFam; PF00111; fer2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas.
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                                                                                                              Score 43; DB 5; Length 5635;
Pred. No. 1.3e+03;
2; Mismatches 1; Indels
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PROSITE; PS00639; THIOL_PROTEASE_HIS; 1.
ATP-binding.
SEQUENCE 5635 AA; 620050 MW; 64A9EB81A9B14641 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Iron; Iron-sulfur.
SEQUENCE 904 AA; 98157 MW; C25E86C6D4DFA457 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
NADH dehydrogenase I, G subunit.
NUOG OR SO1016.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-001-2000 (TrEMBLrel. 15, Created)
01-001-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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241 ERYG-ELRRIENRFNG 255
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                                                                                                              Query Match 51.2%;
Best Local Similarity 72.7%;
Matches 8; Conservative 3
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|1535 QRFGRDLRRWS 1545
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                                                                                                                                                                                                                                     1 QRYGRELRRMS 11
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RX MEDLINE=22297686; PubMed=12368813;
RA Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,
RA Meder T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A.,
Ra Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Hatt D.H., Rolonay J.F.,
RA Madupu R., Peterson J.D., Umrayam L.A., White O., Wolf A.M.,
RA Wanathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C.,
RA Wueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A.,
RA Peldbyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.;
RY "Genome Sequence of the dissimilatory metal ion-reducing bacterium
RI "Shewanella oneidensis.";
RY "Shewanella oneidensis.";
RY Shewanella oneidensis.";
RY Shewanella oneidensis.";
RY Shewanella oneidensis.";
RY Complete proteome
SQ SEQUENCE 909 AA; 100079 MW; F71859F385BDCAC8 CRC64;
Complete proteome
SQ SEQUENCE 909 AA; Mismatches 3; Indels 1; Gaps 1;
Matches 9; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

QY IQRY ERRERRENEFIG 16

241 ERYG-ELRRIENRFHG 255
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Search completed: September 15, 2003, 17:25:48 Job time : 19.3714 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

using sw model - protein search, OM protein

September 15, 2003, 17:16:01 ; Search time 22.6286 Seconds Run on:

(without alignments) 112.231 Million cell updates/sec

US-09-544-664-29

1 ORYGRELRRMSDEFVD 16 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1107863 seqs, 158726573 residues Searched:

1107863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_19Jun03:*

1: /SIDS1/gcgdata/geneseq/geneseqp.embl/AA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseqp.embl/AA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseqp.embl/AA1981.DAT:*
4: /SIDS1/gcgdata/geneseq/geneseqp.embl/AA1983.DAT:*
5:IDS1/gcgdata/geneseq/geneseqp.embl/AA1983.DAT:*
6: /SIDS1/gcgdata/geneseq/geneseqp.embl/AA1985.DAT:*
7: /SIDS1/gcgdata/geneseq/geneseqp.embl/AA1986.DAT:*
8: /SIDS1/gcgdata/geneseq/geneseqp.embl/AA1989.DAT:*
9: /SIDS1/gcgdata/geneseq/geneseqp.embl/AA1989.DAT:*
10: /SIDS1/gcgdata/geneseq/geneseqp.embl/AA1989.DAT:*
11: /SIDS1/gcgdata/geneseq/geneseqp.embl/AA1989.DAT:*
12: /SIDS1/gcgdata/geneseq/geneseqp.embl/AA1999.DAT:* /SIDS1/gogdata/geneseq/geneseqp-embl/AA1992.DAT:
/SIDS1/gogdata/geneseq/geneseqp-embl/AA1993.DAT:
/SIDS1/gogdata/geneseq/geneseqp-embl/AA1994.DAT:
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/SIDS1/gogdata/geneseq/geneseqp-embl/AA1996.DAT:
/SIDS1/gogdata/geneseq/geneseqp-embl/AA1996.DAT:
/SIDS1/gogdata/geneseq/geneseqp-embl/AA1996.DAT: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1998.DAT:*/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*/SIDS1/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*/SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*/SIDS1/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*/SIDS1/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT:*

SUMMARIES

	ň	Description	Human BAD BH3 doma	Bcl2 polypeptide B	Mutant Bc12 compet	Human Bad peptide	Mutant Bcl2 compet	Human Bad peptide	Human Bad peptide	Human Bad peptide	Human Bcl2 fluores
		QI	AAY05421		. 4		•		AAU78629	•	
		jth DB	16 20	16 21			21 23		22 23	23 23	24 23
сЮ	Query	Match Length DB	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
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WPI; 1999-255058/21.

$\Omega_{1} \Omega_{2} \sigma$	BC12 f1	t Bcl2	it Bcl2	t Bcl2	it Bel	it Bcl2	t Bcl	t Bcl2	Bcl2	E Bcl2	CJ	ad	ال ا	adr	ad pepti	rd			ad pept	pepti	Bad pepti	ad pepti	Bad pepti	d pepti	Bad peptid	Mammalian Bad Bcl-	nse	otein for	Bcl-xL/Bcl	l prolif	Human BAD mutant a
23 AAU78605 23 AAU78627 23 ARP56161	ABG7848 ABG7848	3 ABG7848	3 ABG7848	3 ABG7848	3 ABG7848	3 ABG7849	3 AAU7860	3 AAU7861	3 AAU7861	3 AAU7861	3 AAU7861	3 AAU7861	3 AAU7861	3 AAU7861	3 AAU7861	3 AAU7861	3 AAU7861	3 AAU7862	3 AAU7862	3 AAU7862	1 AAY9632	2 AAB7037	8 AAW3247	9 AAW5577	1 AAB1351	2 AAB7036					
224 24	2	2 2 2	25	25 25	7 7 2	25	25	25	25	25	25	25	25	25	25	25	25	25	25	25	25	25	25	25	25	26	26	ω	Q	168	Q
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ALIGNMENTS

BH3 domain; cell death agonist; bcl homology domain; BCL-2 family; apoptosis promoter; cancer cell; virus infected cell; inflammation; autoantibody producing cell; cancer; lymphoproliferative condition; arthritis; autoimmune disease; therapy. AAY05421 standard; peptide; 16 AA 97US-0946039. 97US-0060133. 98WO-US19765 (first entry) (UNIW) UNIV WASHINGTON Human BAD BH3 domain. Homo sapiens W09916787-A1 07-OCT-1997; 26-SEP-1997; 22-SEP-1998; 02-JUL-1999 08-APR-1999 Korsmeyer AAY05421; RESULT 1 AAY05421

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Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a peptide conjugate having the formula: (R-X)n-peptide where n=1-10; X=C=0, when the R-X group is attached to the N-terminus of the peptide, or a side chain of the peptide where the functional group of the side chain is NH2 or OH; or X=O or NH, when the R-X group is attached to the C-terminus of the peptide, or a side chain of the peptide, where the side chain functional group is COH=1000 or COH=1000 and R=1000 alkyl or alkoxy, L=1000 and L=1000 or two double bonds, cyclobutyl, cyclobentyl, cyclohexyl optionally
                                                             This sequence represents the BH3 domain of human BAD.

The invention relates to a bcl homology domain 3 (BH3 domain),
derived from a prospoptotic member of the BCL-2 family. The
BH3 polypeptide can be used in a method for promoting apoptosis in a
target cell, especially where the cell is a cancer cell a virus infected
cell or an autoantibody producing cell. The BH3 polypeptide can be used
in therapeutic compositions for treating disease including cancer, other
lymphoproliferative conditions, arthritis, inflammation, and autoimmune
diseases, which may result from the down regulation of cell death
                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       മ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective; cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad; apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate; colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma; melanoma; lymphocytic_leukemia; neurodegenerative disorder; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    eptide conjugates for modulating apoptosis or for inhibiting lymphoma/leukemia 2 (Bcl-2) function, especially useful for
                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                 Length 16;
                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                Score 83; DB 20;
Pred. No. 1.3e-07;
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                                                                                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bcl2 polypeptide BH3 domain peptide #29.
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Bcl homology domain 3 polypeptide
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                                   Example 1; Fig 4; 104pp; English.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB37029 standard; peptide; 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 stroke, myocardial infarction.
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ilarity 100.0%;
Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0128202.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                           Local Similarity
es 16; Conserv
                                                                                                                                                                                                                                                16 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  peptide
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                                                                                                                                                                                                                 regulation.
                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Huang Z,
                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 2
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monosubstituted with a 1-5C straight or branched chain alkyl group,

phenyl optionally monosubstituted with a 1-5C straight or branched chain

alkyl group, or benzyl. The peptides AAB37001-B37058 represent examples

of the peptide portion of the conjugate. The peptides represent analogues

of a Bc1-2 superfamily polypeptide corresponding to amino acids 72-97 of

to a Bc1-2 superfamily polypeptide corresponding to amino acids 72-97 of

of a Bc1-2 superfamily polypeptide corresponding to amino acids 72-97 of

cuseful for modulating apoptosis in the cells of a subject, or for

reversing B cell lymphoma/leukemia 2 (Bc1-2)-mediated blockage of

apoptosis in cancer cells. It is also useful for inhibiting Bc1-2

cunction. In particular, the peptide conjugate is useful for treating a

subject afflicted with a cancer characterized by cancer cells that

express Bc1-2. The cancer includes prostate, colorectal, gastric,

non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or

acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide

conjugate is also useful for treating disorders characterized by

increased apoptosis, e.g. neurodegenerative disorders, acquired

immunodeficlency syndrome (AIDS), stroke or myocardial infarction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention relates to a novel mutant protein which is derived from a wild type human Bcl-2 protein. The mutant is created by replacing a sequence of amino acid residues comprising a flexible loop from the wild type Bcl-2 protein with an amino acid sequence comprising at least two acidic amino acids. The mutant Bcl-2 protein comprises a 166 residue shown in the specification. The invention also comprises an assay for identifying substances that bind to the Bcl-2 protein. The protein sequences of the invention are useful in biological assays to identify substances that block the ability of Bcl-2 to inhibit programmed cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New mutant Bcl-2 proteins derived from a wild type human Bcl-2 protein, useful in biological assays to identify substances that block the ability of Bcl-2 to inhibit programmed cell death or apoptosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mutant Bcl2 competitive binding assay peptide #16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 1.3e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 83; DB 21;
100.0%; Pred. No. 1.3e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yoon H, Nettesheim DG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2; Page 17; 36pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABG78499 standard; Peptide; 20 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-490141/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ABBO ) ABBOTT LAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200240530-A2.
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This invention relates to a novel mutant protein which is derived from a wild type human Bcl-2 protein. The mutant is created by replacing a sequence of amino acid residues comprising a flexible loop from the wild type Bcl-2 protein with an amino acid sequence comprising at least two acidic amino acids. The mutant Bcl-2 protein comprises a 166 residue shown in the specification. The invention also comprises an assay for identifying substances that bind to the Bcl-2 protein. The protein sequences of the invention are useful in biological assays to identify substances that block the ability of Bcl-2 to inhibit programmed cell death, or apoptosis. The present sequence represents a human Bcl2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New mutant Bcl-2 proteins derived from a wild type human Bcl-2 protein, useful in biological assays to identify substances that block the ability of Bcl-2 to inhibit programmed cell death or apoptosis
                                                                                                                                                                             Human; Bcl2; BclXl; programmed cell death; apoptosis; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; Bad; Bcl-2; apoptosis; cancer; inducer; degenerative disease;
ischemic injury; suppressor; BH3 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human Bad peptide #30 which binds to a member of the Bcl-2 family.
                                                                                                                                              Mutant Bcl2 competitive binding assay peptide #17
                                                 ABG78500 standard; Peptide; 21 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2; Page 17; 36pp; English.
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                                                                                                               (first entry)
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Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                         Petros AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-490141/52.
                                                                                                                                                                                                                                                                                                                                                                                         (ABBO ) ABBOTT LAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 AA;
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                                                                                                             15-NOV-2002
                                                                                                                                                                                                                                                                                           23-MAY-2002
                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                        SW,
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                                                                                ABG78500;
                                                                                                                                                                                                                                                                                                                                                                                                                        Fesik
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                               ABG78500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New derivatives of Bad peptide, useful for identifying compounds that
bind to Bcl-2 proteins, potential agents for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                      Human; Bad; Bcl-2; apoptosis; cancer; inducer; degenerative disease;
                                                                                                                                                                                                                                                                                                                                                        Human Bad peptide #26 which binds to a member of the Bcl-2 family.
apoptosis. The present sequence represents a human Bcl2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 83; DB 23; Length 20; 100.0%; Pred. No. 1.7e-07; ive 0; Mismatches 0; Indels
                                                                             Length 20;
                                                                                                             Indels
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                                                                                                            0
                                                                             Score 83; DB 23;
Pred. No. 1.7e-07;
                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                      ischemic injury; suppressor; BH3 domain.
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                                                                                                                                                                                                                                                         AAU78626 standard; Peptide; 20 AA.
                                                                                                            0;
                                                                             100.0%;
100.0%;
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              peptide of the invention.
                                                                                                            16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             degenerative disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-292254/33.
                                                                                             Similarity
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                                               20 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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                                                                                                                                                                                                                                                                                          AAU78626;
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                                                                                Query Match
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S 22 X S
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Nettesheim DG;

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Yoon

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Gaps

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Length 21; Indels

100.0%; Score 83; DB 23; 100.0%; Pred. No. 1.8e-07;

Mismatches

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14-MAR-2002.

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The present invention relates to new peptides that are derived from a wild-type human Bad peptide and are able to bind to a member of the Bcl-2 protein family. The peptides are useful, when labelled, in competitive/displacement assays for identifying substances that bind to members of the Bcl-2 family and may induce or suppress apoptosis so are potentially useful for treating cancer (inducers) or degenerative diseases or ischemic injury (suppressors). The peptides of the invention have high helix propensity, maintain the contacts of the wild-type Bad peptide and, compared with the Bad peptide, may have better physical properties, particularly solubility. The present sequence represents of a collection of Bad peptides (AAU78601-AAU78631) that were derived from the BH3 domain of the human wild-type Bad peptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 es of Bad peptide, useful for identifying compounds that proteins, potential agents for treating cancer and
                                                           peptide, useful for identifying compounds that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; Bad; Bcl-2; apoptosis; cancer; inducer; degenerative disease; ischemic injury; suppressor; BH3 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human Bad peptide #28 which binds to a member of the Bcl-2 family.
                                                                                  proteins, potential agents for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 83; DB 23;
Pred. No. 1.9e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fesik SW, Meadows RP, Joseph MK, Olejniczak
Nettesheim DG, Swift KW, Matayoshi E, Zhang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU78628 standard; Peptide; 23 AA.
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                                                                                                                                           Claim 15; Page 18; 31pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New derivatives of Bad peptide,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 16; Conservative
                                                           New derivatives of Bad
                                                                                bind to Bcl-2 protein
degenerative disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  degenerative disease
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                   WPI; 2002-292254/33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          22 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200220568-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bind to Bcl-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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AAU78628
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to new peptides that are derived from a wild-type human Bad peptide and are able to bind to a member of the Bcl-2 protein family. The peptides are useful, when labelled, in members of the Bcl-2 family and may induce or suppress apoptosis so are potentially useful for treating cancer (inducers) or degenerative diseases or ischemic injury (suppressors). The peptides of the invention have high helix propensity, maintain the contacts of the wild-type Bad peptide and, compared with the Bad peptide, may have better physical properties, particularly solubility. The present sequence represents of a collection of Bad peptides (AAU78601-AAU78631) that were derived from the BH3 domain of the human wild-type Bad peptide.
                                                                                                                                                                                                                                                                                                                              New derivatives of Bad peptide, useful for identifying compounds that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bad; Bcl-2; apoptosis; cancer; inducer; degenerative disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human Bad peptide #29 which binds to a member of the Bcl-2 family.
                                                                                                                                                                                                                                                                                                                                      Ding to Bcl-2 proteins, potential agents for treating cancer and degenerative disease
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                                                                                                                                                                                                                              Petros AM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                            ET,
H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fesik SW, Meadows RP, Joseph MK, Olejniczak ET, Nettesheim DG, Swift KM, Matayoshi E, Zhang H;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 83; DB 23;
Pred. No. 1.8e-07;
                                                                                                                                                                                                                            Fesik SW, Meadows RP, Joseph MK, Clejniczak
Nettesheim DG, Swift KM, Matayoshi E, Zhang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA.
                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 15; Page 18; 31pp; English.
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100.0%;
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                                                                                                  04-SEP-2001; 2001WO-US27410.
                                                                                                                                         06-SEP-2000; 2000US-0656399
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es 16; Conserv
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                                                                                                                                                                                     (ABBO ) ABBOTT LAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 AA;
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               WO200220568-A2
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Query Match Best Local Si Matches 16;

Seguence

Petros AM;

ET, H;

18-JUN-2002

AAU78629;

RESULT 7

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14-MAR-2002

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Gaps

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Indels Length

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ORYGRELRRMSDEFVD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24 AA;
                                                                                                                                                                                                                                                                                                                         Key
Misc-difference
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Best Local S
Matches 16
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                                                                                                                                              AAU78605;
                                                                                 RESULT 10
                                                                                                 AAU78605
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                                            have high helix propensity, maintain the contacts of the wild-type Bad peptide and, compared with the Bad peptide, may have better physical properties, particularly solubility. The present sequence represents one of a collection of Bad peptides (AAU78601-AAU78631) that were derived from the BH3 domain of the human wild-type Bad peptide.
members of the Bcl-2 family and may induce or suppress apoptosis so are potentially useful for treating cancer (inducers) or degenerative diseases or ischemic injury (suppressors). The peptides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New mutant Bcl-2 proteins derived from a wild type human Bcl-2 protein, useful in biological assays to identify substances that block the ability of Bcl-2 to inhibit programmed cell death or apoptosis -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; Bcl2; BclX1; programmed cell death; apoptosis; mutant; mutein.
                                                                                                                                                                                                               Gaps
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                                                                                                                                                                             Length 23;
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0;
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Pred. No. 1.9e-07;
Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                          A.
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                                                                                                                                                                                                                                                                                                                                                       ABG78482 standard; Peptide; 24
                                                                                                                                                                             100.0%;
                                                                                                                                                                                            100.0%;
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Matches 16; Conservative
                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Petros AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-490141/52.
                                                                                                                                                                             Query Match
Best Local Similarity
Matches 16; Conserv
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                                                                                                                                               23 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                 Seguence
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                                                                                                                                                                                                                                                                         9
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The present invention relates to new peptides that are derived from a wild-type human Bad peptide and are able to bind to a member of the Bcl-2 protein family. The peptides are useful, when labelled, in competitive/displacement assays for identifying substances that bind to members of the Bcl-2 family and may induce or suppress apoptosis so are potentially useful for treating cancer (inducers) or degenerative diseases or ischemic injury (suppressors). The peptides of the invention have high helix propensity, maintain the contacts of the wild-type Bad peptide and, compared with the Bad peptide, may have better physical properties, particularly solubility. The present sequence represents one of a collection of Bad peptides (AAU78601-AAU78631) that were derived from the BH3 domain of the human wild-type Bad peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 useful for identifying compounds that
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; Bad; Bcl-2; apoptosis; cancer; inducer; degenerative disease; ischemic injury; suppressor; BH3 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bind to Bcl-2 proteins, potential agents for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                        Human Bad peptide #5 which binds to a member of the Bcl-2 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ő
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Joseph MK, Olejniczak ET,
1, Matayoshi E, Zhang H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU78627 standard; Peptide; 24 AA.
                                                                                                                                                                                                                              AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New derivatives of Bad peptide,
                                                                                                                                                                                                                              AAU78605 standard; Peptide; 24
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16
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Nettesheim DG, Swift KM,
                                    6 ORYGRELRRMSDEFVD
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les 16; Conservative
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AAU78627
ID AAU78
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15-NOV-2001; 2001WO-US45693.
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                            WO200261105-A2.
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Synthetic.
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                                                             08-AUG-2002
Synthetic.
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ABG78481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mitochondrial membrane permeabilisation; mitochondrion; PTPC; permeability transition pore complex; virucide; neuroprotective; vasotropic; cytostatic; infection; cell death regulation; apoptosis; mitochondrial permeability transition pore complex modulator; cancer; apoptogenic; ischaemia; neurodegenerative disease; fulminant hepatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                 New derivatives of Bad peptide, useful for identifying compounds that bind to Bcl-2 proteins, potential agents for treating cancer and degenerative disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                         Human; Bad; Bcl-2; apoptosis; cancer; inducer; degenerative disease; ischemic injury; suppressor; BH3 domain.
                                                                             Human Bad peptide #27 which binds to a member of the Bcl-2 family.
                                                                                                                                                                                                                                                                                                                                                           Petros AM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 83; DB 23; Length 24; 100.0%; Pred. No. 2e-07;
                                                                                                                                                                                                                                                                                                                                                        ET,
H;
                                                                                                                                                                                                                                                                                                                                                       ows RP, Joseph MK, Olejniczak
Swift KM, Matayoshi E, Zhang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 15; Page 18; 31pp; English.
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                                                                                                                                                                                                                                                                                         2000US-0656399.
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nes 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 AA;
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                                                                                                                                                                                         WO200220568-A2.
                                                                                                                                                             Homo sapiens.
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                                              18-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
            AAU78627;
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comprising at least a first functional molecule covalently linked to a second functional molecule, which is able to modulate the activity of the permeability transition pore complex (PPC) of the mitochondria.

(I) has the function of specifically targeting and entering a tissue cell population. The second functional molecule has the function of specifically targeting, and inducing or preventing the death of the cells by apoptosis by regulating the opening or the closing of the PTPC of the mitochondria or its fragment. (I) has vinculed, neuroprotective, vasotropic and cytostatic activities, and can be used as a mitochondrial permeability transition pore complex (PTPC) modulator. (I) is useful for treating or preventing a pathological infection or disease. (I) is also useful for regulating call death regulatory molecules, specifically the apoptogenic function of the PTPC, for treating e.g. cancer, ischaemia, neurodegenerative diseases, fulminant hepatitis or viral infections.

The present sequence represents a PTPC, interacting TOX peptide which is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes a chimeric bifunctional molecule (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                            New chimeric bifunctional molecules that target specific cells and regulate the apoptosis function of the permeability transition pore complex of the mitochondria, useful for treating or preventing e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 83; DB 23;
ilarity 100.0%; Pred. No. 2.1e-07;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human Bcl2 fluorescein labelled peptide #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABG78481 standard; Peptide; 25 AA.
                                                                                                                                                                                                                                                                                    Briand J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 9; Page 11; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QRYGRELRRMSDEFVD 16
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                                                                               02-FEB-2001; 2001US-265594P
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                                                                                                                                                                                                 (CNRS ) CENT NAT RECH SCI.
                                                                                                                                                                                                                                                                                    Edelman L, Jacotot E,
                                                                                                                                                               PASTEUR
                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-619260/66.
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Les 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer or ischemia
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25 AA;
                                                                                                                                                                           25 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                15-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mutant Bcl2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-MAY-2002
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                                                                                                                                                                           Seguence
                                                                                                                                                                                                                                                                                                                                                                                                   ABG78485;
                                                                                                                                                                                                                                                                                                                                           RESULT 15
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ID ABG7
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                                                                                                                                                                                                                This invention relates to a novel mutant protein which is derived from a wild type human Bcl-2 protein. The mutant is created by replacing a sequence of amino acid residues comprising a flexible loop from the wild type Bcl-2 protein with an amino acid sequence comprising at least two acidic amino acids. The mutant Bcl-2 protein comprises a 166 residue shown in the specification. The invention also comprises an assay for identifying substances that bind to the Bcl-2 protein. The protein sequences of the invention are useful in biological assays to identify substances that block the ability of Bcl-2 to inhibit programmed cell death or apoptosis. The present sequence represents a human Bcl2 peptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New mutant Bcl-2 proteins derived from a wild type human Bcl-2 protein, useful in biological assays to identify substances that block the ability of Bcl-2 to inhibit programmed cell death or apoptosis -
                                                                                                                            New mutant Bcl-2 proteins derived from a wild type human Bcl-2 protein, useful in biological assays to identify substances that block the ability of Bcl-2 to inhibit programmed cell death or apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; Bcl2; BclXl; programmed cell death; apoptosis; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      competitive binding assay peptide #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 83; DB 23; 100.0%; Pred. No. 2.1e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nettesheim DG;
                                                                      Nettesheim DG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABG78484 standard; Peptide; 25 AA
                                                                                                                                                                                        Example 2; Page 15; 36pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2; Page 17; 36pp; English
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                                                                      Yoon H,
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           20-NOV-2000; 2000US-0716395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Petros AM,
                                                                      Petros AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-490141/52.
                                                                                                WPI; 2002-490141/52
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                                         (ABBO ) ABBOTT LAB.
                                                                                                                                                                                                                                                                                                                                                                                                   25 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                      Fesik SW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABG78484;
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fesik
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This invention relates to a novel mutant protein which is derived from a wild type human Bc1-2 protein. The mutant is created by replacing a sequence of amino acid residues comprising a flexible loop from the wild type Bc1-2 protein with an amino acid sequence comprising at least two acidic amino acids. The mutant Bc1-2 protein comprises a 166 residue shown in the specification. The invention also comprises an assay for identifying substances that bind to the Bc1-2 protein. The protein sequences of the invention are useful in biological assays to identify substances that block the ability of Bc1-2 to inhibit programmed cell death, or apoptosis. The present sequence represents a human Bc12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention relates to a novel mutant protein which is derived from a wild type human Bcl-2 protein. The mutant is created by replacing a sequence of amino acid residues comprising a flexible loop from the wild type Bcl-2 protein with an amino acid sequence comprising at least two acids: The mutant Bcl-2 protein comprises a 166 residue shown in the specification. The invention also comprises an assay for identifying substances that bind to the Bcl-2 protein. The protein sequences of the invention are useful in biological assays to identify substances that block the ability of Bcl-2 to inhibit programmed cell death, or apoptosis. The present sequence represents a human Bcl2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New mutant Bcl-2 proteins derived from a wild type human Bcl-2 protein, useful in biological assays to identify substances that block the ability of Bcl-2 to inhibit programmed cell death or apoptosis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; Bcl2; BclXl; programmed cell death; apoptosis; mutant; mutein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 83; DB 23;
Pred. No. 2.1e-07;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           competitive binding assay peptide #2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 83;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
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Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                      peptide of the invention.
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      Best Local Similarity 100.0%; Pred. No. 2.1e-07;

      Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
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                        GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-410-372-1

US-09-375-257-2

US-08-333-565-10

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US-08-733-505A-55

US-08-733-505A-55

US-08-733-505A-56

US-08-733-505A-56

US-08-733-505A-11

US-08-733-505A-11

US-08-733-505A-12

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                                                                                                                                                                                September 15, 2003, 17:22:21
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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83
1 QRYGRELRRMSDEFVD 16
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Perfect score:
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Sequence 2, Appli
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Sequence 10, April
Sequence 10, April
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Sequence 2, Appli
Sequence 2, Appli
Sequence 5559, Ap
Sequence 5559, Ap
Sequence 7710, Ap
Sequence 28443, A
Sequence 27256, A
Sequence 2, Appli
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Sequence 1, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
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Patent No. 5663316
GENERAL INFORMATION:
APPLICANT: Xudong, Yin
TITLE OF INVENTION: Gene and Protein for Regulation of Cell Death
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ó
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC Compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,617
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: 31,794
REFERENCE/DOCKET NUMBER: 31,794
REFERENCE/DOCKET NUMBER: 31,794
REFERENCE/SOCKET NUMBER: 31,794
REFERE
                         US-08-996-621-2
US-09-134-0010-3032
US-09-328-352-6559
US-09-328-352-7710
US-09-252-991A-31592
US-09-252-991A-28443
US-09-252-991A-26443
US-09-252-991A-26270
US-09-272-991A-26270
US-09-272-991A-26270
US-09-472-971-1
US-08-913-805A-10
US-08-913-805A-10
US-09-442-629-2
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US-09-391-104-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Saliwanchik & Saliwanchik STREET: 2421 N.W. 41st Street, Suite A-1 CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 106 QRYGRELRRMSDEFVD 121
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Best Local Similarity 100.
Matches 16; Conservative
       single
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// MOLECULE TYPE: protein
US-08-665-617-2
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: USA
          STRANDEDNESS:
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us-09-544-664-29.rai

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TOPOLOGY: line
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CLONE: 358673
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Matches
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       Sequence 2, Application US/08717123
Sequence 2, Application US/08717123
Patent No. 5965703
GENERAL INFORMATION:
APPLICANT: Horne, William A.
APPLICANT: Oltersdorf, Tilman
TITLE OF INVENTION: Acids and Methods of Use
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 83; DB 2; Length 168; Pred. No. 2.2e-07;
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APPLICANT: Lal, Preeti
APPLICANT: Shah, Purvi
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: PROIFFINS ASSOCIATED WITH CELL
TITLE OF INVENTION: PROLIFFRATION
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEB: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
                                                                                                                                                                                                                                                           CINIT. SAU DIEGO
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/717,123
FILING DATE: 20-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATICN:
NAME: Campbell, Cathryn A.
REGISTAATION NUMBER: 31,815
                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
STREET San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE DOCKET NUMBER: P-ID 1929
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
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Best Local Similarity 100.0%;
Matches 16; Conservative 0
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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MOLECULE TYPE: protein
US-08-717-123-2
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STATE: CA
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ZIP: 94304
US-08-717-123-2
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Gaps
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APPLICANT: Lal, Preeti
APPLICANT: Shah, Purvi
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: PROLIFERATION
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSBE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 100.0%; Score 83; DB 3; 1 Local Similarity 100.0%; Pred. No. 2.2e-07; hes 16; Conservative 0: Mismatheria
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                        NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0421 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFRAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: PF-0421 US TELECOMMUNICATION INFORMATION: TELEPHONE: 650-855-0555 TELEFAX: 650-845-4166 INFORMATION FOR SEQ ID NO: 7:
                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,335
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
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FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                108 ORYGRELRRMSDEFVD 123
                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 168 amino acids TYPE: amino acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ORYGRELRRMSDEFVD 16
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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STATE: CA
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Sequence 7, Application US/09410372
Patent No. 6281334
                                                                                                                                                           APPLICANT: Hillman, Jennifer L. APPLICANT: Yue, Henry
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TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
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INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS: LENGTH: 168 amino acids TYPE: amino acid
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IBM Compatible
                                                                                                                                                                              APPLICANT: Yue, Henry
APPLICANT: Lal, Preeti
APPLICANT: Shah, Purvi
APPLICANT: COILey, Neil C.
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Best Local Similarity 100.
Matches 16; Conservative
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MEDIUM TYPE: Diskett
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                                                                                                                                             GENERAL INFORMATION:
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CLONE: 1683637
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                                                                        RESULT 6
US-09-410-372-7
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                                                                                                                                                                             100.0%; Score 83; DB 3; Length 168; 100.0%; Pred. No. 2.2e-07; Live 0; Mismatches 0; Indels
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Patent No. 6281334

GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: I.e., Henry
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
TITLE OF INVENTION: PROLIFERATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 83; DB 3; I Best Local Similarity 100.0%; Pred. No. 2.2e-07; Matches 16; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/410,372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PF-0421 US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                           TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 QRYGRELRRMSDEFVD 16
                                                                                                                                                                                                                                                       1 QRYGRELRRMSDEFVD 16
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 168 amino acids TYPE: amino acid
              LENGTH: 168 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                               Best Local Similarity 100. Matches 16; Conservative
 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; LIBRARY: SYNORAB01
; CLONE: 358673
US-09-410-372-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                        TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1683637
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IMMEDIATE SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
STREET: 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: CA
                                                                                                                                             US-08-985-335-7
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US-09-410-372-1
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APPLICANT: Oltersdorf, Tilman
TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC
TITLE OF INVENTION: ACIDS AND METHODS OF USE
FILE REFERENCE: 480140.428D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 83; DB 3; Length 168; 100.0%; Pred. No. 2.2e-07; tive 0; Mismatches 0; Indels
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL IIILE OF INVENTION: PROLIFERATION NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/410,372
                                                                                                                ADDRESSEE: Incyte Pharmaceuticals, Inc
STREET: 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 480140.428D1
CURRENT APPLICATION NUMBER: US/09/375,257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PE-0421 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/985,335
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REPERENCE/DOCKET NUMBER: PF-0421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/09375257; Patent No. 6504022; GENERAL INFORMATION:
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CLASSIFICATION: 530
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                                                                                                                                                                            100.0%; Score 83; DB 4; Length 168; 100.0%; Pred. No. |2.2e-07;
                                                                                                                                                                                                                                                                                                                                                                 US-08-333-565-10;
Sequence 10, Application US/08333565;
Patent No. 5622852;
GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: REGULATOR
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88.0%; Score 73; DB 1; Length 23; 100.0%; Pred. No. 1.5e-06; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                    0; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: ELM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/33,565
FILING DATE: 31-07-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726A-000700
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQUENCE: (415) 326-2422
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
                                                                                                                                                                                                                  0; Mismatches
CURRENT FILING DATE: 1999-08-16
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 168
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; Sequence 10, Application US/08661479
; Patent No. 5834209
                                                                                                                                                                                                                                                                                 108 ORYGRELRRMSDEFVD 123
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                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Palo Alto
STATE: California
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
                                                                                                                                                                                                Best Local Similarity
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ZIP: 94301
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                                                                                                                                                                                                                    16;
                                                                                                                                      US-09-375-257-2
                                                                                                                                                                                Query Match
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US-08-733-505A-55
Squence 55, Application US/08733505A
Squence 56, Application US/08733505A
Sevence 57, Patent No. 5856445
Trice of invention: Serine Substituted Mutants of Title of Invention: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
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APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
TITLE OF INVENTION: REGULATOR
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                     COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/661,479
FILING DATE: 11-JUN-1995
CLASSIFICATION AATA
APPLICATION NUMBER: US 08/33,565
FRING APPLICATION DATA:
APPLICATION NUMBER: US 08/33,565
FILING DATE: 31-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: SMITH, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726A-000700
                                                                                                                      Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 7733 FORSYTH BLVD., SUITE 1400 CITY: ST. LOUIS STATE: MISSOURI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HOWELL & HAFERKAMP, L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                      ADDRESSEE: Townsend ....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 QRYGRELRRMSDEF 14
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Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-661-479-10
                                                                                                                                                             CITY: Palo Alto
STATE: California
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 63105
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                                                                                                                                                                                                                                     94301
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us-09-544-664-29.rai

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Sequence 57, Application US/08733505A;
Patent No. 5856445;
GENERAL INFORMATION:
APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR;
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 58, Application US/08733505A
Patent No. 585645
GENERAL INFORMATION:
APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/733,505A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SISTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.2e-06;
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100.0%; Pred. No. 4.2e-0
live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REFERENCE/POCKET NUMBER: 35,197
REFERENCE/POCKET NUMBER: 965458
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (314) 727-50-5188 TELEFAX: (314) 727-6092 INFORMATION FOR SEQ ID NO: 57: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46 QRYGRELRRMSDEF 59
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Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 59 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: peptide US-08-733-505A-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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ZIP: 63105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63105
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                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: ST.
STATE: MJ
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 56, Application US/08733505A; Sequence 56, Application US/08733505A; Sequence 56, Application US/08733505A; Sequence 56, Application US/08733505A; GENERAL INFORMATION:
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR: NUMBER OF SEQUENCES: 60; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88.0%; Score 73; DB 2; Length 59; 100.0%; Pred. No. 4.2e-06;
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COMPUTER READABLE FORM:
MADDITER TIEM PC COMPATIBLE
COMPUTER: TLOPPY disk
COMPUTER: TEM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REFERENCE/DOCKET NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 36,197
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REFERENCE/DOCKET NUMBER: 35,197
REFERENCE/D
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                                                                                              965458
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100.0%; Pre
                                                                                   REFERENCE/DOCKET NUMBER: 9654
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 59 amino acids
TYPE: amino acids
                                                               35,197
ATTORNEY/AGENT INFORMATION:
                              NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46 QRYGRELRRMSDEF 59
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Best Local Similarity 100.
Matches 14; Conservative
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; MOLECULE TYPE: peptide
US-08-733-505A-56
                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: peptide
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Matches 14; Conserv
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Length 59;

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88.0%; Score 73; DB 2; Length 204; 100.0%; Pred. No. 1.6e-05; tive 0; Mismatches 0; Indels
                                            Query Match 88.0%; Score 73; DB 1; Length 204; Best Local Similarity 100.0%; Pred. No. 1.6e-05; Matches 14; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08661479
; Patent No. 5834209
; GENERAL INFORMATION:
    APPLICANT: KORGMEYER, Stanley J.
    TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
    TITLE OF INVENTION: REGULATOR
    NUMBER OF SEQUENCES: 59
    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/661,479
FILING DATE: 11-JUN-1995
CLASSIFICATION DATA:
APPLICATION ATA:
APPLICATION ATA:
APPLICATION NUMBER: US 08/33,565
FILING DATE: 31-0CT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 30,223
TELEROMUNICATION INFORMATION:
TELEROMUNICATION INFORMATION:
TELEROMUNICATION INFORMATION:
TELEROMUNICATION INFORMATION:
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TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
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Best Local Similarity 100.
Matches 14; Conservative
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) LOCATION: 1..204
) OTHER INFORMATION: /;
) US-08-661-479-2
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STRANDEDNESS: si
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US-08-661-479-2
    US-08-333-565-2
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Fatent No. 5622852
GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: Bel-x/Bel-2 ASSOCIATED CELL DEATH
TITLE OF INVENTION: REGULATOR
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 59;
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ZIP: 94201

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IEBM PC compatible
OPERATING SYSTEM: PC-DoS/MS-DoS
SOFTWARR: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/333,565
FILING DATE: 31-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 15726A-000700
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 73; DB 2; L
Pred, No. 4.2e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 88.0%; Score 73; Db Best Local Similarity 100.0%; Pred. No. 4.2 Matches 14; Conservative 0; Mismatches
                    APPLICATION NUMBER: US/08/733,505A FILING DATE:
                                                                                                                                                                        965458
                                                   FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOKET NUMBER: 9654:
TELECOMMUNICATION INFORMATION:
TELEFONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 59 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ORYGRELRRMSDEF 14
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CURRENT APPLICATION DATA:
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; MOLECULE TYPE: peptide
US-08-733-505A-58
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                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid STRANDEDNESS:
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US-08-333-565-2
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Sequence 258, App Sequence 2, Appli Sequence 1, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 147, App Sequence 117, App Sequence 1303, A Sequence 5312, Ap Sequence 5312, Ap Sequence 7650, Ap
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2: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
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4: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
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10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
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18: /cgn2_6/ptodata/1/pubpaa/US10A_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd
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9 US-09-922-378-2

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9 US-09-894-657-7

14 US-10-066-179-2

9 US-09-922-378-3

15 US-10-166-179-3

15 US-10-166-761-9145

15 US-10-156-761-9735

15 US-10-156-761-9735

16 US-10-156-761-9735

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18 US-10-156-761-9735

19 US-09-815-242-12033

19 US-09-815-242-1303

10 US-10-156-761-9735

11 US-10-156-761-9735

12 US-09-815-242-1303

13 US-10-156-761-7630
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       541936 seqs, 145912426 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                        OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length DB
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Sequence:
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Sequence 64, Appl
Sequence 62, Appl
Sequence 452, Appl
Sequence 452, Appl
Sequence 458, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 36, Appl
Sequence 137, Appl
Sequence 1237, Appl
Sequence 162, Appl
Sequence 162, Appl
Sequence 162, Appl
Sequence 1633, Appl
Sequence 162, Appl
Sequence 234, Appl
Sequence 3426, Appl
Sequence 344, Appl
Sequence 22, Appl
                    Sequence 46, Appl
Sequence 40, Appl
Sequence 10330, A
Sequence 1, Appli
                                                                                                                                                                                                Sequence 14659, A
Sequence 12, Appl
           5 US-10-156-761-13594
5 US-10-166-087-46
5 US-10-166-087-46
5 US-10-156-761-10330
6 US-09-971-980-64
6 US-09-971-980-64
7 US-09-971-980-62
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7 US-09-971-980-62
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7 US-09-971-98-626-4522
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7 US-09-9819-128-10
7 US-09-9819-128-10
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7 US-09-9819-128-10
7 US-09-9819-128-10
7 US-09-738-626-4453
7 US-09-738-626-4456
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7 US-09-738-626-4426
7 US-09-738-626-4426
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US-09-712-363-205
US-10-156-761-14659
US-09-950-510-12
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GENERAL INFORMATION:
GENERAL INFORMATION:
FAPLICANT: BELMAN, LENA
APPLICANT: BELMAN, LENA
APPLICANT: BRIAND, JEAN-PAUL
TITLE OF INVENTION: CHIMERIC MOLECULES CONTAINING A MODULE ABLE TO TARGET
TITLE OF INVENTION: CHIMERIC MOLECULES CONTAINING A MODULE REGULATING THE APOPTOGENIC
TITLE OF INVENTION: PUNCTION OF THE PERMEABILITY TRANSITION PORE COMPLEX
TITLE OF INVENTION: (PTPC)
FILE REFERENCE: 03495.0216
CURRENT APPLICATION NUMBER: 60/265,594
PRIOR APPLICATION NUMBER: 60/265,594
PRIOR APPLICATION NUMBER: 60/265,594
PRIOR FILING DATE: 2001-02-02
NUMBER OF SEQ ID NOS: 325
SOFTWARE: PALENTIN Ver. 2.1
SEQ ID NO 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Description of Unknown Organism: TOX peptide
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03-10-059-261-258
; Sequence 258, Application US/10059261
; Publication No. US20030077826A1
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Best Local Similarity
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US-09-922-378-2

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us-09-544-664-29.rapb

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Gaps

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Indels

Length 168;

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COTIEY, Neil C. TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/894,657
FILING DATE: 28-Jun-2001
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 83; DB 9; L
100.0%; Pred. No. 3.9e-06;
tive 0; Mismatches 0;
                                                                                                 100.0%; Score 83; DB 9; I
100.0%; Pred. No. 3.9e-06;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lacy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0421 US
TELECOMMUNICATION INFORMATION:
CLONE: 358673

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-894-657-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 09/410,372
FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; SEQUENCE DESCRIPTION: SEQ ID NO: 7: US-09-894-657-7
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                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/09894657; Patent No. US20020098569Al; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                          108 ORYGRELRRMSDEFVD 123
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Lal, Preeti
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shah, Purvi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIBRARY: GenBank
CLONE: 1683637
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Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                          Conservative
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STATE: CA
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                                                                                                 Query Match
Best Local Similarity
Matches 16; Conserva
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                                                                   APPLICANT: Horne, William A.
APPLICANT: Borne, William A.
APPLICANT: Oltersdorf, Tilman
TITLE OF INVENTION: HUMAN BAD POLIPEPTIDES, ENCODING NUCLEIC
TITLE OF INVENTION: ACIDS AND METHODS OF USE
TITLE OF INVENTION: ACIDS AND METHODS OF USE
CURRENT APPLICATION NUMBER: US/09/922,378
CURRENT FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Corley, Neil C.
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COPERATING SYSTEM: DOS
SOFTWARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/894,657
FILING DATE: 28-Jun-2001
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 09/410,372
FILING DATE: <Unknown>
APPLICATION THEOREMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Dr. CITY: Palo Alto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/09894657
Patent No. US20020098569A1
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
Tue, Henry
Lal, Preeti
Shah, Purvi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
         Sequence 2, Application US/09923378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 650-845-4166
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                               Patent No. US20020037869A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
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                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                         LENGTH: 168
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US-09-894-657-1
                                                                                                                                                                                                                                                                                                               TYPE: PRT
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Length 168; Indels

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SOFTWARE: Patentin version 3.1
SEQ ID NO 147
LENGTH: 15
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ISHIKAWA, JUN
HORIKAWA, HIROSHI
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                                                                                                                                 Conservative
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Matches 11; Conservative
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         TYPE: PRT ORGANISM: Mus musculus
                                                                                       Query Match
Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: MOD_RES
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                                                US-10-066-179-3
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APPLICANT:
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APPLICANT:
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US-10-066-179-2; Sequence 2, Application US/10066179; Sequence 2, Application No. US20020115631A1; GENERAL INFORMATION:
; APPLICANT: Horne, William A.; APPLICANT: Oltersdorf, Tilman; TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC; TILE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC; TILE REFERENCE: 480140.428C1; CURRENT APPLICATION NUMBER: US/10/066,179; CURRENT FILING DATE: 2002-02-01; NUMBER OF SEQ ID NOS: 15; SOFTWARE: FastSEQ for Windows Version 4.0; SEQ ID NO 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/10066179

Publication No. US20020115631A1

GENERAL INFORMATION:

APPLICANT: Horne, William A.

APPLICANT: Oltersdorfy Tilman

TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC

TITLE OF INVENTION: ACIDS AND METHODS OF USE

FILE REPRENCE: 480140.428C1

CURRENT APPLICATION NUMBER: US/10/066,179

CURRENT PILICA DATE: 2002-02-01

NUMBER OF SEQ ID NOS: 15

SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 83; DB 14; Length 168; Best Local Similarity 100.0%; Pred. No. 3.9e-06; Matches 16; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/09922378
Patent No. US20020037869A1
Patent No. US20020037869A1
APPLICANT: HORID: William A.
APPLICANT: OltersObrf, Tilman
TITLE OF INVENTION: ACIDS AND METHODS OF USE
FILE REFERENCE: 480140.428D3
CURRENT APPLICATION UNMER: US/09/922,378
CURRENT FILING DATE: 2001-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 70; DB 9; Length 204;
Pred. No. 0.00064;
1; Mismatches 0; Indels
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    108 QRYGRELRRMSDEFVD 123
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92.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 84.3
Best Local Similarity 92.9
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Mus musculus US-09-922-378-3
                                                                                                                                                                                                                                                                                            LENGIH: 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 6
US-09-922-378-3
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LENGTH: 204
                                                                                                                                                                                                                                                                                                                                                      US-10-066-179-2
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TITLE OF INVENTION: POSITIVE IDENTIFICATION OF PHOSPHO-PROTEINS USING MOTIF-SPECI
TITLE OF INVENTION: CONTEXT-INDEPENDENT ANTIBODIES COUPLED WITH DATABASE SEARCHI
FILE REFERENCE: CST-138 CIP3
CURRENT APPLICATION NUMBER: US/10/174,105A
CURRENT FILING DATE: 2002-06-18
PRIOR FILING DATE: 1998-09-04
PRIOR FILING DATE: 1998-09-04
PRIOR FILING DATE: 2000-03-24
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CTHER INFORMATION: PHOSPHORYLATION; serine at position 8 is phosphorylated US-10-174-105A-147
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Score 70; DB 14; Length 204;
Pred. No. 0.00064;
1: Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67.5%; Score 56; DB 15; Length 15; 100.0%; Pred. No. 0.0084; Live 0; Mismatches 0; Indels
                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                             Sequence 147, Application US/10174105A Publication No. US20030068652A1 GENERAL INFORMATION:
APPLICANT: Cell Signaling Technology, Inc. APPLICANT: ZHANG, Hui APPLICANT: TANG, Hui APPLICANT: TAN, Yi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/156,761 CURRENT FILING DATE: 2002-05-29 PRIOR APPLICATION NUMBER: JP 2001-204089 PRIOR FILING DATE: 2001-05-30 PRIOR APPLICATION NUMBER: JP 2001-272697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 9145, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:
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APPLICANT: Carr, Grant J.

APPLICANT: Yamamoto, Robert T.

APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes in

TITLE OF INVENTION: Prokaryotes

FILE REFERENCE: ELITRA.011A

CURRENT APPLICATION NUMBER: 05/29/815,242

CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/245,578

PRIOR PLILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR APPLICATION NUMBER: 60/255,931

PRIOR APPLICATION NUMBER: 60/255,931

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR APPLICATION NUMBER: 60/257,931
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Pred. No. 1.1e+02;
3; Mismatches 2; Indels
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61.5%; Pred. No. 1.1e+02;
tive 3; Mismatches 2; Indels
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/259,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12636
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13003
LENGTH: 876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 13003, Application US/09815242; Patent No. US20020061569A1; GENERAL INFORMATION: APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
Carr, Grant J.
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61.5%;
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185 GRELPILADEYVD 197
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Best Local Similarity 61.50
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Best Local Similarity 61.5
Matches 8; Conservative
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                       Score 44; DB 15; Length 215; Pred. No. 12; 3; Mismatches 2; Indels
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APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Tammorto, Robert T.
APPLICANT: Tammorto, Robert T.
APPLICANT: Proward
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
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APPLICANT: IKEDA, HAROO
APPLICANT: ISHIKAWA, JUN
APPLICANT: ISHIKAWA, JUN
APPLICANT: SHIBA, TADANOSHI
APPLICANT: SAKRAKI, YOSHIYUKI
APPLICANT: SAKRAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
ITILE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT FAPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR PILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 9735
LENGTH: 647
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 9735, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/191,078 PRIOR FILING DATE: 2000-03-21
                                                                                                      TYPE: PRT
CRGANISM: Streptomyces avermitilis
US-10-156-761-9145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Streptomyces avermitilis US-10-156-761-9735
                                                                                                                                                                                                         Query Match 53.0%;
Best Local Similarity 61.5%;
Matches 8; Conservative
  PRIOR FILING DATE: 2001-09-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 9145
LENGTH: 215
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Best Local Similarity
8; Conserve
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US-10-156-761-9735
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us-09-544-664-29.rapb

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RESULT 15
US-10-156-761-7867
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                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Xu, H. Howard
HITLE OF INVENTION: Identification of Essential Genes in
HILE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-27
PRIOR PRILING DATE: 2000-11-27
PRIOR PLILING DATE: 2000-11-27
PRIOR PLILING DATE: 2000-11-27
PRIOR PLILING DATE: 2000-11-27
PRIOR PLILING DATE: 2000-12-22
PRIOR PLILING DATE: 2001-12-27
PRIOR PLILING DATE: 2001-12-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FASLSEQ for Windows Version 4.0
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APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
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CTHER INFORMATION: Xaa = Any Amino Acid
US-09-815-242-5312
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                                                                                                                                                                 Sequence 5312, Application US/09815242 Patent No. US20020061569A1
                                                                                                                                                                                                                                             APPLICANT: Ohlsen, Kodert
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Staphylococcus aureus
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61.5%;
                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Baselbeck, Robert
APPLICANT: Ohlsen, Kari I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ||||| ::||:||
255 GRELPILADEYVD 267
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251 GRELPILADEYVD 263
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4 GRELRRMSDEFVD 16
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Best Local Similarity 61.5
Matches 8; Conservative
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US-10-156-761-7630
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                                                                                                                                                                                                                                                                         Score 41; DB 15; Length 312; Pred. No. 57;
                                                                                                                                                                                                                                                                                                                           5; Indels
                                                                                                                                                                                                                                                                                                                         3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: IKEDA, HARUO
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAZAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
ITILE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: UP 2001-274089
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 7867
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CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 7630
LENGTH: 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7867, Application US/10156761; Publication No. US20030119018A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Streptomyces avermitilis US-10-156-761-7867
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Best Local Similarity 50.0%
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GenCore version 5.1.6
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sw model - protein search, using protein ΜO

September 15, 2003, 17:16:55 ; Search time 3.77143 Seconds
(without alignments)
199.507 Million cell updates/sec Run on:

1 QRYGRELRRMSDEFVD 16 US-09-544-664-29 83 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 seqs, 47026705 residues Searched:

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Q92934 homo sapien	mus m	035147 rattus norv	O54918 mus musculu								-						Q8xfc4 salmonella		Q8tpf7 methanosarc					Q9hv01 pseudomonas		,	homo sa	kvb9	7514	5392	8fka7	P22257 escherichia
O.	BAD_HUMAN	BAD_MOUSE	BAD_RAT	BIM_MOUSE	BIM_RAT	HGD_RHILO	HT2A_HUMAN	AROG_CANAL	GCR3_YEAST	YGFG_ECOLI	PHLC_TRYCR	MTA1_ACEPA	RPSD_BORBU	- 1	RA51_SCHPO	VSI2_REOVD	VSI2_REOVL	TIG_SALTY	MTBR_BPRH1	SYFB_METAC	SYFB_METMA	SYV_BACST	- 1	DEFL_RHIME	SELA_PSEAE	Y152_UREPA	RRF_THEMA	BIM_HUMAN	KDKA_VIBCH	ODP2_MYCGE	O	- 1	TIG_ECOLI
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38	38	38	38	38	38	37	37	37	37	37	37
34	35	36	37	38	39	40	47	42	43	44	45

ALIGNMENTS

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Klausherg R.L., Feligold E.A., Grouse L.H., Derge J.G.,
Klausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A poptins R.F., Jordan H., Moore T., Max S.L., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Ganzia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
                                                                                                                                                                                                                                                                                        [1] SEQUENCE FROM N.A. Yin D.X., Li Z., Ruang B., Chen S., Zhou H.; Yin D.X., Li Z., Ruang B., Chen S., Zhou H.; "A human protein that interacts with Bcl-2 and have homology to mouse "A human protein that
                                    BAD_HUMAN STANDARD, PRT; 168 AA.
092934; O14803;
01-NOV-1997 (Rel. 35, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
BCl2-antagonist of cell death (BAD) (BCl-2 binding component 6)
XL/BCl-2 associated death promoter) (BCL2-like 8 protein).
BAD OR BEC6 OR BCL2L8.
                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-98049534; PubMed=9388232; Ottile S., Diaz J.-L., Horne W., Chang J., Wang Y., Wilson G., Chang S., Weeks S., Fritz L.C., Oltersdorf T.; Dimerization properties of human BAD."; J. Biol. Chem. 272:30866-30872(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                [2]
SEQUENCE FROM N.A., AND PHOSPHORYLATION BY RAF-1.
MEDLINE=97083574; Pubmed=8929532;
Wang H.-G., Rapp U.R., Reed J.C.;
"Boll-2 targets the protein kinase Raf-1 to mitochondria.";
cell 87:629-638(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Takayama S., Reed J.C.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                           Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [4] SEQUENCE FROM N.A., AND DIMERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Lung;
MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                       Homo sapiens (Human)
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SEQUENCE FROM N.A.
RESULT 1
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WEDLINE=21073561; PubMed=11206074;

WEDLINE=21073561; PubMed=11206074;

WEDLINE=21073561; PubMed=11206074;

Retros A.M., Nettesheim D.G., Wang Y., Olejniczak E.T., Meadows R.P.,

Mack J., Swift K., Matayoshi E.D., Zhang H., Thompson C.B.,

Resik S.W.;

Rationale for Bcl-xL/Bad peptide complex formation from structure,

mutagenesis, and biophysical studies.";

R. Protein Sci. 9:2528-2534(2000).

-- FUNCTION: Promotes cell death. Successfully competes for the

Dinding to Bcl-x(L), Bcl-2 and Bcl-w, thereby affecting the level

of heterodimerization of these proteins with BAX. Can reverse the

death repressor activity of Bcl-x(L), but not that of Bcl-2 (By

similarity). Appears to act as a link between growth factor

receptor signaling and the apoptotic pathways.

C. receptor signaling and the apoptotic pathways.

C. SUBUNIT: Forms heterodimers with the anti-apoptotic proteins, Bcl-

x(L), Bcl-2 and Bcl-w. Also binds protein S100Al0 (By similarity).

The Ser-75/Ser-99 phosphorylated form binds 14-3-3 proteins (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             phosphorylation, locates to the cytoplasm.

-!-SUBCELLUAR LOCATION: Outer mitochondrial membrane. Upon phosphorylation, locates to the cytoplasm.
-!-TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.
-!-DOMAIN: Intact BH3 domain is required by BIK, BID, BAK, BAD AND BAX for their pro-apoptotic activity and for their interaction with anti-apoptotic members of the BCl-2 family.
-!-PTM: Phosphorylated on Ser-75 in response to survival stimuli. Subsequent phosphorylation on Ser-99 promotes heterodimerization with 14-33 proteins. This interaction then facilitates the phosphorylation at Ser-118, a site within the BH3 domain, leading to the release of Bcl-x(L) and the promotion of cell survival. Ser-99 is the major site of AKT/PKB phosphorylation, Ser-118 the major site of protein kinase A (CAPK) phosphorylation (by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CAUTION: Ref.1 sequence differs from that shown due to frameshifts in position 64 and 91.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PHOSPHORYLATION (BY PKA AND PKB) (BY
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Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PKB)
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GO:0005741; C:mitochondrial outer membrane; NAS.
GO:0005515; F:protein binding activity; NAS.
GO:0008632; P:apoptotic program; TAS.
GO:0006917; P:induction of apoptosis; NAS.
                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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PHOSPHORYLATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U66879; AAB36516.1; ALT_FRAME.
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PROSITE; PS01259; BH3; FALSE_NEG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, AF021792, AAB72092.1; -.
EMBL, AF031523; AAB88124.1; -.
EMBL; BC001901; AAH01901.1; -.
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Mol. Cell 6:41-51(2000).

-!-FUNCTION: Promotes cell death. Successfully competes for the binding to Bcl-x(1, Bcl-2 and Bcl-w, thereby affecting the level of heterodimerization of these proteins with Bax. Can reverse the death repressor activity of Bcl-x(L), but not that of Bcl-2. Appears to act as a link between growth factor receptor signaling and the apoptotic pathways.

-!- Appears to act as a link between growth factor receptor signaling and the apoptotic pathways.

-!- SUBGNIM: Forms heterodimers with the anti-apoptotic proteins, Bcl-x(L), Bcl-2 and Bcl-w. Also binds protein $100A10 (By similarity).

The Ser-112/ser-136 phosphorylated form binds 14·3-3 proteins.

-!- SUBCELLUAR LOCATION: Outer mitochondrial membrane. Upon phosphorylation, locates to the cytoplasm.

-!- DOMAIN: Intact BH3 domain is required by BIK, BID, BAK, BAD AND BAX for their pro-apoptotic activity and for their interaction with anti-apoptotic members of the Bcl-2 family.

-!- PTM: Phosphorylated on Ser-112 in response to survival stimuli.

-!- TH: Also appropriated on Ser-112 in response to survival stimuli.

-!- TH: Also appropriated on Ser-112 in response to survival stimuli.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Brain, and Thymus;
MEDLINE=95136361; PubMed=7834748;
MEDLINE=95136361; DubMed=7834748;
Mang E., Zha J., Jockel J., Bolse L.H., Thompson C.B., Korsmeyer S.J.;
"Bad, a neterodimeric partner for Bcl-XL and Bcl-2, displaces Bax and promotes cell death.";
Cell 80:285-291(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   with 14-3-3 proteins. This interaction then facilitates the phosphorylation at Ser-155, a site within the BH3 domain, leading to the release of Bcl-x(L) and the promotion of cell survival. Ser-136 is the major site of AKT/PKB phosphorylation, Ser-155 the major site of protein kinase A (CAPK) phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "14-3-3 proteins and survival kinases cooperate to inactivate BAD by
                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [2]
PHOSPHORYLATION, AND MUTAGENESIS OF SER-112 AND SER-136.
MEDLINE=98022383; PubMed~9381178;
Del Peso L., Gonzalez-Garcia M., Page C., Herrera R., Nunez G.;
"Interleukin-3-induced phosphorylation of BAD through the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa, Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Datta S.R., Katsov A., Hu L., Petros A., Fesik S.W., Yaffe M.B.,
Greenberg M.E.;
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01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Bcl2-antagonist of cell death (BAD) (Bcl-2 binding component
                                                                                                                           Length 168;
                                                                                                                                                                   0; Indels
SIMILARITY).
A -> S (in dbSNP:3729933).
                                                              121
18392 MW; 69FD8D27DDEE3241 CRC64;
                                                                                                                           Score 83; DB 1; 1
Pred. No. 1.8e-06;
                                         /FTIG=VAR_015380.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       6) (Bcl-xL/Bcl-2 associated death promoter). BAD OR BBC6.
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MEDLINE=20403302; PubMed=10949026;
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                                                                                                                                                                                                                                  108 QRYGRELRRMSDEFVD 123
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Mol. Cell 6:41-51(2000).
                                                                                                                           100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Science 278:687-689(1997).
                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
                                                                                   168 AA;
                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                      107
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                                                                                                                                                                                                                                                                                                                                                    BAD_MOUSE
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP;
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                                                                                                                                                                                                                                                                                                                                                                           PHOSPHORYLATION (BY PKA AND PKB).
PHOSPHORYLATION (BY PKA AND PKB).
PHOSPHORYLATION (BY PKA AND PKB).
S->A: NO PHOSPHORYLATION.
S->A: NO PHOSPHORYLATION.
S->A: NO PHOSPHORYLATION.
BCL-X(L).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hsu S.Y., Kaipia A., Zhu L., Hsueh A.J.W.;
"Interference of BAD (Bcl-xL/Bcl-2-associated death promoter)-induced
apoptosis in mammalian cells by 14-3-3 isoforms and Pll.";
Mol. Endocrinol. 11:1858-1867(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ı.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D'Agata V., Magro G., Travali S., Musco S., Cavallaro S.; "Cloning and expression of the programmed cell death regulator BAD the rat brain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIINE=21100372; PubMed=11161472; Hamner S., Arumae U., Yu L.-Y., Sun Y.-F., Saarma M., Lindholm D.; "Functional characterization of two splice variants of rat BAD and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001 [Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Bcl2-antagonist of cell death (BAD) (Bcl-2 binding component 6) (Bcl-xL/Bcl-2 associated death promoter).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 73; DB 1; Length 204; Pred. No. 9e-05; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND MUTAGENESIS OF SER-113 AND SER-137
SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain. SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6C2BA910205053F7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            205 AA.
                                                                                                                                                                                                                                    PIR; A55671; A55671.

HSSP; Q92934; 1G5J.

MGD; MGI:1096330; Bad.

InterPro; IPR000712; Bcl2_BH.

PROSITE; PS01259; BH3; FALSE_NEG.

APOPTOSIS; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=98194755; PubMed=9535132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=98034386; PubMed=9369453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neurosci. Lett. 243:137-140(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    204 AA; 22080 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
                                                                                                                                                                                                                 EMBL; L37296; AAA64465.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ORYGRELRRMSDEF 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BAD_RAT STANDARD 035147; 070256; 09JHX1;
                                                                                                                                                                                                                                                                                                                                                         161
112
1136
1136
1136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SECUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                             RES
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              Mol. Cell. Neurosci. 17:97-106(2001).

Mol. Cell. Neurosci. 17:97-106(2001).

-!-FUNCTION: Promotes cell death. Successfully competes for the binding to Bcl-x(L), Bcl-2 and Bcl-w, thereby affecting the level of heterodimerization of these proteins with BAX. Can reverse the death repressor activity of Bcl-x(L), but not that of Bcl-2 (By similarity). Appears to act as a link between growth factor receptor signaling and the apoptotic pathways.

-!- SUBGNIT: Forms heterodimers with the anti-apoptotic proteins, Bcl-x(L), Bcl-2 and Bcl-w. Also binds protein $100A10. The Ser-1137 phosphorylated form binds l4-3-3 proteins.

-!- SUBCELLULAR LOCATION: Outer mitochondrial membrane. Upon phosphorylation, locates to the cytoplasm (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolde035147-2; Sequence=VSP_000534;
Isolde035147-2; Sequence=VSP_000534;

Lisource SPECIFICITY: Expressed in all tissues tested, including brain, liver, spleen and heart. In the brain, restricted to epithelial cells of the choroid plexus. Isoform alpha is the more abundant form.

-!- DOMAIN: Intact BH3 domain is required by BIK, BID, BAK, BAD AND BAX for their pro-apoptotic activity and for their interaction with anti-apoptotic members of the Bcl-2 family.

-!- PTM: Phosphorylated on Ser-133 in response to survival stimuli. Subsequent phosphorylation on Ser-137 promotes heterodimerization with 14.3-3 proteins. This interaction then facilitates the phosphorylation at Ser-156, a site within the BH3 domain, leading to the release of Bcl-x(L) and the promotion of cell survival. Ser-137 is the major site of AKT/PKB phosphorylation, Ser-156 the major site of protein kinase A (CAPK) phosphorylation (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LPRPKSAGTATQMRQSASWTRIIQSWWDRNLGKGGSTPSQ
-> EELTYSVEFLPVRAIAMEGWPLLWSFQSFPHTLPPTPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EVAMEPLRYWTALRRIC (in isoform Beta). /FTId=VSP_000534. S->A: NO EFFECT ON HETERODIMERIZATION WITH 14-3-3 PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BY SIMILARITY).
PHOSPHORYLATION (BY PKA AND PKB)
(BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     !- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
interaction with Bcl-w in sympathetic neurons.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : IPR000712; Bcl2_BH.
PS01259; BH3; FALSE_NBG.
s; Phosphorylation; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IsoId=035147-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF003523; AAC53374.1; -.
EMBL; AF031227; AAC15100.1; -.
EMBL; AF279910; AAF91427.1; -.
EMBL; AF279911; AAF91428.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           \frac{162}{113}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=Alpha
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S->A: NO HETERODIMERIZATION WITH 14-3-3
PROTEINS. NO EFFECT ON HETERODIMERIZATION
WITH BCLZ NOR WITH PROTEIN P11.
TABA71DAE9GF4A81 CRC64;

DB 1; Length 205,

Score 73;

34 SI 22228 MW; 88.0%; SG

29 205 AA;

137

137

Q7 DB

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Query Match
Best Local Similarity
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%
                                                                                                                                                                                    BIM_RAT
                                Matches
                                                                                                                                                RESULT 5
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                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ISOIG=054918-3; Sequence=VSP_000537;
TISSUE SPECIFICITY: EXPRESSED IN A NUMBER OF B-AND T-LYMPHOID CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: FORMS HETERODIMERS WITH A NUMBER OF ANTIADOPTOTIC BCL-2 PROTEINS INCLUDING MCL-1, BCL-2, BCL-XL, BFL-1, AND BHRF-1. DOES NOT HETERODIMERIZE WITH PROAPOPTOTIC PROTEINS SUCH AS BAD, BOX,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BAX OR BAK (BY SIMILARITY).
SUBCELLULAR LOCATION: ASSOCIATED WITH INTRACYTOPLASMIC MEMBRANES.
ALTERNATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms=3;
                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                               O'CONDOT L., Strasser A., O'Reilly L.A., Hausmann G., Adams J.M., CCTY S., Huang D.C.S.;
"Bim: a novel member of the Bcl-2 family that promotes apoptosis.";
EMBO J. 17:384-395(1998).

- : FUNCTION: INDUCES APOPTOSIS. THE ISOFORMS VARY IN CYTOTOXICITY
WITH ISOFORM BIMS BEING THE MOST POTENT AND ISOFORM BIMEL BEING
                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                       054918; 054919; 054920;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
BCL2-like protein 11 (BCL2 interacting mediator of cell death).
                  ·;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN: THE BH3 DOMAIN IS REQUIRED FOR BCL-2 BINDING AND
                                                                                                                                                                                                                                                                                                                                                               SECTENCE FROM N.A., FUNCTION, SUBCELLULAR LOCATION, TISSUE SPECIFICITY, AND ALTERNATIVE SPLICING.
MEDLINE-98094360; PubMed-9430630;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOTOXICITY. SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BH3.
Missing (in isoform BimL).
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Missing (in isoform BimS).
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531C176E5F1AC9AA CRC64;
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0
Pred. No. 9e-05;
                                                                                                                                                                 196 AA
                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS01259; BH3; FALSE_NEG.
Apoptosis; Alternative splicing; Membrane.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=054918-1; Sequence=Displayed;
                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF032459; AAC40029.1; -.
EMBL; AF032460; AAC40030.1; -.
EMBL; AF032461; AAC40031.1; -.
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InterPro; IPR000712; Bcl2_BH.
 100.0%;
                                                                     1 QRYGRELRRMSDEF 14
                  14; Conservative
                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    THE LEAST POTENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       196 AA;
 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=BimEL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=BimL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=BimS;
                                                                                                                                                                 BIM_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARSPLIC
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                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                         ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBDUIT: FORMS HETEROLIMERS WITH A NUMBER OF ANTIAPOPTOTIC BCL-2 PROTEINS INCLUDING MCL-1, BCL-2, BCL-XL, BFL-1, AND BHRF-1. DOES NOT HETERODIMERIZE WITH PROAPOPTOTIC PROTEINS SUCH AS BAD, BOK,
                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chen D., Simon R.P., Chen J.;
"Cloning of rat bimEL and bimL, and their differential expression in ischemia and normal rat brain.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: INDUCES APOPTOSIS.
-!- FUNCTION: INDUCES APOPTOSIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Comment=2 isoforms, BOD-L (shown here) and BOD-S, are produced by alternative initiation at Met-1 and Met-104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: ASSOCIATED WITH INTRACYTOPLASMIC MEMBRANES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hsu S.Y., Lin P., Hsueh A.J.W.;
"BOD (Bcl-2-related ovarian death gene) is an ovarian BH3 domain-
containing proapoptotic Bcl-2 protein capable of dimerization with
diverse antiapoptotic Bcl-2 members.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Note-Isoform BOD-S is produced by alternative initation at Met-104 of isoform BOD-L;
                                                                         ·;
                                                                                                                                                                                                                                                                                                                                                                                                                         088498; 088497; Q9WUI8; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) BCL2-like protein 11 (BCL2 interacting mediator of cell death) (Bcl-2 related ovarian death protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., FUNCTION, SUBUNIT, AND TISSUE SPECIFICITY (ISOFORMS BOD-L; BOD-M AND BOD-S).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISĞUE SPECIFICITY: Widely expressed.
DOMAIN: THE BH3 DOMAIN IS REQUIRED FOR BCL-2 BINDING AND
Score 42; DB 1; Length 196; Pred. No. 8.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Event=Alternative splicing; Named isoforms=3;
                                                                         .,
m
                                                                                                                                                                                                                                                                                                                                                                                         196 AA
                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IsoId=088498-3; Sequence=VSP_000539;
Event=Alternative initiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId=088498-2; Sequence=VSP_000538;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=BOD-L;
IsoId=088498-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mol. Endocrinol. 12:1432-1440(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM BIML).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=98400436; PubMed=9731710;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF065433; AAC23595.1; -.
      50.6%;
61.5%;
                                                                                                                                                                                   | :||||: |||
145 RIAQELRRIGDEF 157
                                                                                                                                            2 RYGRELRRMSDEF 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BY SIMILARITY).
                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                         STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOTOXICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                      088497;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=BOD-M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BAX OR BAK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=BimL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Ovary;
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us-09-544-664-29.rsp

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TISSUE=Skin;
                      METAL
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                          proteins.
                                                           Query Match
            METAL
                                                                                                                                                                             HT2A_HUMAN
                                                                               Matches
                                                                                                                                                                RESULT
                                                                                                                                                                                          FT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   between the Swiss Institute of Bioinformatics and the EMBL cutstation-
the European Bioinformatics Institute. There are no restrictions on its
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modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S., "Complete genome structure of the nitrogen-fixing symbiotic bacterium Mesorhizobium loti."
                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -:- CATALYTIC ACTIVITY: Homogentisate + O(2) = 4-maleylacetoacetate.
-:- COFACTOR: Iron (By similarity).
-:- PATHWAY: Catabolism of tyrosine; third step.
-:- PATHWAY: Catabolism of phenylalanine; fourth step.
-:- SIMILARITY: Belongs to the homogentisate dioxygenase family.
                                                         Apoptosis: Alternative splicing; Membrane; Alternative initiation. CHAIN 196 BCL2-LIKE PROTEIN 11, ISOFORM BOD-L. CHAIN 104 196 BCL2-LIKE PROTEIN 11, ISOFORM BOD-S.
                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                    28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Homogentisate 1,2-dioxygenase (EC 1.13.11.5) (Homogentisicase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TIGREAMS; TICRO1015; hmgA; 1.
Oxidoreductase; Dioxygenase; Phenylalanine catabolism;
Tyrosine catabolism; Metal-binding; Iron; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                             Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                                               -> D (IN REF. 1; AAC23594).
B4D2146F9C0B37A0 CRC64;
                                                                                                                                                                                                   Score 42; DB 1; Length 196;
                                                                                                                                                                                                                           3; Indels
                                                                                                                                        Missing (in isoform BOD-M). /FIId=VSP_000539.
                                                                                                                   Missing (in isoform BimL). /FTIG=VSP_000538.
                                                                                             FOR ISOFORM BOD-S.
                                                                                                                                                                                                                                                                                                                               457 AA.
                                                                                                                                                                                                                           2; Mismatches
                                                                                                                                                                                                                Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21082930; PubMed=11214968;
                                             PS01259; BH3; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AP003013; BAB53887.1; -.
         EMBL; AF065432; AAC23594.1; -.
EMBL; AF136927; AAD26594.1; -.
InterPro; IPR000712; Bc12_BH.
                                                                                                                                                                             22055 MW;
                                                                                                                                                                                                   50.6%;
                                                                                                                                                                                                               61.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      _00334; -; 1.
IPR005708; HmgA.
                                                                                                                                                                                                                                                                        145 RIAQELRRIGDEF 157
                                                                                                                                                                                                                                                 2 RYGRELRRMSDEF 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Res. 7:331-338(2000).
                                                                                                                                                                                                                          8; Conservative
                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                     196
196
104
160
97
                                                                                                                                        127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF04209; HgmA;
                                                                                                                                                                          196 AA;
                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=MAFF303099;
                                                                               104
104
146
42
                                                                                                                                                                                                                                                                                                                                                                                                                   HMGA OR MLR8303.
                                                                                                                                        42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=381;
                                                                                                                                                                                                                                                                                                                                 HGD_RHILO
                                                                                           INIT_MET
DOMAIN
VARSPLIC
                                              PROSITE;
                                                                                                                                                                             SEQUENCE
                                                                                                                                         VARSPLIC
                                                                                                                                                                                                    Query Match
                                                                                                                                                                CONFLICT
                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA
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Altsounder 12477932;

A trausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A trausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A ltschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,

B Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Hopkins R.F., Jordan H.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

R A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

R Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

R Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

R Richards S., Worley K.C., Shevchenko Y., Bouffard G.G.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

R Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

R Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

R Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HT2A_HUMAN STANDARD; PRT; 653 AA. Q13049; Q9NQPB; 01-NOV-1997 (Rel. 35, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) Zinc-finger protein HT2A (72 kDa Tat-interacting protein) (Tripartite motif-containing protein 32).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
FUNCTION: MAY PLAY A SIGNIFICANT ROLE IN MEDIATING THE BIOLOGICAL ACTIVITY OF THE HIV-1 TAT PROTEIN IN VIVO. BINDS SPECIFICALLY TO THE ACTIVATION DOMAIN OF HIV-1 TAT AND CAN ALSO INTERACT WITH THE
                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE-95297135; Pubmed=7778269; Fridell R.A., Warding L.S., Bogerd H.P., Cullen B.R.; Inferition of a novel human zinc finger protein that specifically interacts with the activation domain of lentiviral Tat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HIV-2 AND EIAV TAT PROTEINS IN VIVO.
SUBCELLULAR LOCATION: Nuclear.
TISSUE SPECIFICITY: SPLEEN, THYMUS, PROSTRATE, TESTIS, OVARY, INTESTINE AND COLON.
                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                           1; Length 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
IRON (BY SIMILARITY).
IRON (BY SIMILARITY).
IRON (BY SIMILARITY).
6A20B69E9A2B2BD1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: Contains 1 RING-type zinc finger.
                                                                                                                                                                           DB
                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                           Score 42;
                                                                                                                                                                                                          Préd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human and mouse cDNA sequences.";
                                                                                                                                                                                                                                         2;
                                                                                                          51046 MW;
                                                                                                                                                                        50.6%;
                                                                                                                                                                                                                                                                                                                                                                             425 RYGAELETRODNYID 439
                                                                                                                                                                                                                                                                                                              2 RYGRELRRMSDEFVD 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Virology 209:347-357(1995).
                                                                                                                                                                                                                                                Conservative
   351
357
387
351
357
387
457 AA;
                                                                                                                                                                                                          Local Similarity
les 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRIM32 OR HT2A
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9

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HSSE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCR3_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 9
  δŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             qq
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MEDLINE=96207468, PubMed=8625423;
Pereira S.A., Livi G.P.;
"Aromatic amino-acid blosynthesis in Candida albicans: identification of the ARO4 gene encoding a second DAHP synthase.";
Curr. Genet. 29:441-445(L996).
-!- FUNCTION: STEREOSPECIFIC CONDENSATION OF PHOSPHOENOLPYRUVATE (PEP)
AND D-ERYTHROSE-4-PHOSPHATE (E4P) GIVING RISE TO 3-DEOXY-D-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
03-FBB-2003 (Rel. 41, Last annotation update)
Phospho-2-dehydro-3-deoxyheptonate aldolase, tyrosine-inhibited
(EC 4.1.2.15) (Phospho-2-Reto-3-deoxyheptonate aldolase) (DAHP
synthetase) (3-deoxy-D-arabino-heptulosonate 7-phosphate synthase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes, Saccharomycetales, mitosporic Saccharomycetales, Candida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
0
                                                                                                                                                                                                                                                                                                                                                                                         co-activator activity; TAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 653;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=ATCC 11651 / B792;
Sousa S., Pereira S.A., Livi G.P.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RING-TYPE.
B BOX-TYPE.
F -> I (IN REF. 1).
; D83B1595CA8378FD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 42; DB 1
Pred. No. 30;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  370 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POLY-ALA
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                                                                                                                                                                                                                                                                                                                                             MIM; 602290; -.

GO; 602005634; C:nucleus; TAS.
GO; GO:000713; F:transcription co-
InterPro; IPR001258; NHL.
InterPro; IPR00135; Znf_Bbox.
InterPro; IPR00135; Znf_Bbox.
InterPro; IPR001841; Znf_ring.
Pfam; PF00643; Zf_Bbox; 1.
Pfam; PF000643; Zf_Bbox; 1.
SMART; SM00136; BBOX; 1.
SWART; SM00136; BBOX; 1.
PROSITE; PS50119; ZF_BBOX; 1.
PROSITE; PS50119; ZF_RING_1; 1.
PROSITE; PS50089; ZF_RING_2; 1.
Zinc_finger; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65 RI
133 B
27 F
71988 MW;
                                                                                                                                                                                                                                         EMBL; AL133284; CAB92723.1; -. EMBL; BC003154; AAH03154.1; -. HSSP; P29590; 1BOR.
                                                                                                                                                                                                                  EMBL; U18543; AAA86474.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50.6%;
61.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           186 QEYGHEERRVQDE 198
                                                                                                                                                                                                                                                                                                             HGNC:16380; TRIM32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ORYGRELRRMSDE 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Candida albicans (Yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           653 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=5476;
                                                                                                                                                                                                                                                                                                               Genew; HGNC:
MIM; 602290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AROG_CANAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T., Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S., Jagels K., Lye G., Moule S., Odell C., Pearson D., Rajandream M.A., Rice P., Skelton J., Walsh S., Whitehead S., Barrell B.G.; "The nucleotide sequence of Saccharomyces cerevisiae chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           οţο
                                                                                    ENZYME REGULATION: INHIBITED BY TYROSINE (BY SIMILARITY).
PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-92380925; PubMed=1512188; UGmura H., Jigami Y.; UGmura H., Jigami Y.; "GCR3 encodes an acidic protein that is required for expression 91ycolytic genes in Saccharomyces cerevisiae."; J. Bacteriol. 174:5526-5532(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                       CATALYTIC ACTIVITY: 2-dehydro-3-deoxy-D-arabino-heptonate
                                           phosphate + phosphate = phosphoenolpyruvate + D-erythrose phosphate + H(2)0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1994 (Rel. 28, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
GCR3 protein (ST01 protein) (SUT1 protein)
GCR3 OR ST01 OR SUT1 OR YMR125W OR YM8564.07 OR YM9553.01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00793; DAHP, synth_1, 1.
ProDon; PD005060; AroFGH; 1.
TIGRFAMS; TIGR00034; aroFGH; 1.
Aromatic amino acid biosynthesis; Lyase; Multigene family.
SEQUENCE 370 AA; 40291 MW; 11E5E324C8D786DB CRC64;
                                                                                                                                    first step.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pandit S., Sternglanz R.;
Submitted (DEC-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Guo Z., Russo P., Sherman F.;
Submitted (XXX-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomycetales; Saccharomycetaceae; Saccharomyces
ARABINO-HEPTULOSONATE-7-PHOSPHATE (DAHP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           861 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR006218; DAHP1/KDSA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 49.4%;
Best Local Similarity 42.9%;
                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U53216; AAB48240.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR006219; AroFGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ||: |:::|| | 77 YGKRLKKLADELKD 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 YGRELRRMSDEFVD 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
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STRAIN-S288c / AB972;
Pubmed-9169872;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                        P00886;
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P34160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
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Pfam; PF00388; PI-PLC-X; 1.
                                                                                                                                                                                                                                                                                                                                                              PHLC_TRYCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota;
                                                                                                                                                                                                                                                                                                                                                   PHLC_TRYCR
                                                                                                                                                                                                                                                        Matches
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                                                                                                  This SMISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                 SHOWN FROM POSITION 708
                                                                                                                                                                                                                                                                                                                                                                          NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SECUENCE FROM N.A.
STRAIN=KI2 / MG1655,
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
-!- SIMILARITY: BELONGS TO THE ENOYL-COA HYDRATASE/ISOMERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.
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0
       Nature 387:90-93(1997).

-!- FUNCTION: REQUIRED FOR EXPRESSION OF GLYCOLYTIC GENES. F CERTAIN CHARACTERISTICS OF A TRANSCRIPTIONAL ACTIVATOR.
-!- SUBCELLULAR LOCATION: NUCLEAR (Probable).
-!- SIMILARIY: SOME, TO HUMAN CEP80.
-!- CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN FROM POSONWARD AND IS SHORTER (725 AA) DUE TO A FRAMESHIFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 861;
58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                         164 D -> V (IN REF. 3).
633 R -> I (IN REF. 3).
704 A -> R (IN REF. 3).
100017 MM; EDD04907BDC9207D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                      ASP/GLU-RICH (ACIDIC). ARG/LYS-RICH (BASIC).
                                                                                                                                                                                                                                                                            GO, GO:0000243; C:commitment complex; IPI. GO; GO:0005846; C:snRNA cap binding complex; IDA. GO; GO:0003729; F:mRNA binding activity; IPI. GO; GO:0006371; P:mRNA splicing; IPI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P52045; P76643; Ol-OCT-1996 (Rel. 34, Created) Ol-OCT-1996 (Rel. 34, Last sequence update) I5-SEP-2003 (Rel. 42, Last annotation update) Hypotherical protein ygfG. PGC OR B2919.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 41;
Pred. No.
                                                                                                                                                                                            EMBL; D10224; BAA01076.1; ALT_SEO.
EMBL; L07650; NOT_ANNOTATED_CDS.
EMBL; L27744; -; NOT_ANNOTATED_CDS.
EMBL; 249273; CAA88274.1; -.
EMBL; 248622; CAA88550.1; -.
                                                                                                                                                                                                                                                                                                                                                            protein.
                                                                                                                                                                                                                                                                                                                           InterPro; IPR003890; IF_eIF4G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :|| | | ::|:|
821 RRYSHEYRELADKFI 835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                   Pfam, PF02854; MIF4G; 1
SMART; SM00543; MIF4G; 1
DNA-binding; Nuclear prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                  801
825
164
633
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633 6
704 7
861 AA;
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SGD; S0004732; STOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
es 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=562;
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                                                                                                                                                                                                                                                                                                                                                                                                          CONFLICT
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Matches
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                                                                                                                                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.lsb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Redpath M., Carnall N., Webb H., Courel M., Amorim A.,
Cardosodealmeida M.L., Carrington M.;
Submitted (JUL-1997) to the EMEL/GenBank/DDBJ databases.
-!- FUNCTION: BY HYDROIYSIS OF THE ATTACHED GIYCOLIPID, RELEASES
SOLUBLE VARIANT SURFACE GLYCOPROTEIN CONTAINING PHOSPHOINOSITOL
FROM THE CELL WALL OF T.BRUCEI AFTER CELL LYSIS. IT ALSO CLEAVES
SIMILAR MEMBRANE ANCHORS ON SOME MAMMALIAN PROTEINS. VSG LIPASE
MAY PLAY A ROLE IN PROCESSES SUCH AS PARASITE DIFFERENTIATION OR
ANTIGENIC ACTIVITY: Variant-surface-glycoprotein 1,2-didecanoyl-
sn-phosphatidylinositol + H(2)0 = 1,2-didecanoyldycerol + soluble
variant-surface-glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT: Monomer (By similarity).
SUBCELLULAR LOCATION: Membrane-associated.
SIMILARITY: DOMAIN X IS CONSERVED IN DIFFERENT FORMS OF PLC AND IS
ESSENTIAL FOR CATALYTIC ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         015886;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Variant-surface-glycoprotein phospholipase C (EC 3.1.4.47) (VSC lipase) (Glycosylphosphatidylinositol-specific phospholipase C) (GPI-PLC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
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InterPro; IPR001753; EnCoA_hydrtse.
Phfam; PF00378; ECH; 1.
PROSITE; PS00166; ENOYI_COA_HYDRATASE; 1.
Hypothetical protein; Lyase; Complete proteome; 3D-structure.
SEQUENCE 261 AA, 29172 MW; B6A8A13EC2C2EBE0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48.2%; Score 40; DB 1; Length 261; 50.0%; Pred. No. 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Interpro; IPR000909; PI_PLC_Xdom.
Interpro; IPR003633; Varsurfglyc_PPLC.
                                                                                                                                                                                                                                                                                                                           EMBL; U28377; AAC9086.1; ALT_INIT.
EMBL; AE000375; AAC75956.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 YGRELRRMSDEFVD 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                 PDB; 1EF8; 24-MAY-00
PDB; 1EF9; 24-MAY-00
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us-09-544-664-29.rsp

129 GRDLARLVREFVD 141

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RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European conformations institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SEQUENCE FROM N.A.

SEQUENCE 12875;

MEDLINE-99077292; PubMed=9862476;

MEDLINE-90077292; PubMed=9862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Acetobacter pasteurianus (Acetobacter turbidans).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
Acetobacteraceae; Acetobacter.
                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Modification methylase ApaLI (EC 2.1.1.73) (Cytosine-specific methyltransferase ApaLI) (M.ApaLI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48.2%; Score 40; DB 1; Length 429;
                                                                                                                                                                                                                 Length 380;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Indels
                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E011C7D15B33F5F3 CRC64;
                                                                                                                                    DOMAIN X.
273CD402B52068C5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; racology, cantase_1; FalsE_NEG.
PROSITE; PS00094; C5_MTASE_1; FALSE_NEG.
Transferase; Methyltransferase; Restriction system.
81 BY SIMILARITY.
                                                                                                                                                                                                            Score 40; DB 1;
Pred. No. 36;
1; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         429 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 41;
Pfam; PF03490; Varsurf_PPLC; 1.
ProDom; PD041675; Varsurfglyc_PPLC; 1.
SMART; SM00148; PLCXc; 1.
PROSITE; PS50007; PIPLC_X_DOMAIN; 1.
Hydrolase; Membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REBASE; 3281; M.ApalI.
InterPro; IPR001525; C5_DNA_meth.
Pfam; PF00145; DNA_methylase; 1.
PRINTS; PR00105; C5METTRFRASE.
                                                                                                                                                                                                                                                                       4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF044847; AAC97180.1; -.
                                                                                                                                                             SEQUENCE 380 AA; 42736 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          429 AA; 46547 MW;
                                                                                                                                                                                                                   48.2%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61.5%;
                                                                                                                                                                                                                                                                                                                                                        : ||| |:|| |:
165 KFFRELDRLSDRFI 178
                                                                                                                                                                                                                                                                                                                        2 RYGRELRRMSDEFV 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8; Conservative
                                                                                                                                                                                                                   Query Match
Best Local Similarity 50.0°
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                       205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MTA1_ACEPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
MTA1_ACEPA
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4 GRELRRASDEFVD 16

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-ATCC 35210 / B31;
MEDLINE-98065943; PubMed=9403685;
Frascr C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
Lathigra R., White C., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
Dougherty B., Tomb J.F., Fleachmann R.D., Richardson D.,
Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
van Vugt R., Palmer N., Adams M.D., Gooayne J.D., Weidman J.,
Utterback T., Watthey L., McDonald L., Artiach P., Bowman C.,
Garland S., Fulii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
Smith H.O., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pan M. Yeh J., Tsai C.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THE SIGMA FACTOR IS AN INITIATION FACTOR THAT PROMOTES
ATTACHMENT OF THE RNA POLYMERASE TO SPECIFIC INITIATION SITES AND
THEN IS RELEASED. THIS IS THE PRIMARY SIGMA-FACTOR OF THIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pranscription regulation; Sigma factor; DNA-directed RNA polymerase;
                                                                                                                                                                                                                                                              Borrelia burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           132 POLYMERASE CORE BINDING (POTENTIAL).
508 H-T-H MOTIF (BY SIMILARITY).
73642 MW; BD565AB7D8F44796 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Smith H.O., Venter J.C.; "Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: Belongs to the sigma-70 factor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thesis (1994), National Taiwan University, Taiwan.
                                                                                        01-0CT-1996 (Rel. 34, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                          RNA polymerase sigma factor rpoD (Sigma-70). RPOD OR BB0712.
                                 631 AA.
                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PP03979; sigma70_r1_; 1.
Pfam; PF00140; sigma70_r1_2; 1.
Pfam; PF04542; sigma70_r2; 1.
Pfam; PF04539; sigma70_r3; 1.
Pfam; PF04545; sigma70_r4; 1.
PROSITE; PS00715; SIGMA70_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA-binding; Complete proteome.
DOMAIN 419 432 PO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000943; Sigma_70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 165-614 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U17591; AAC44104.1; -. EMBL; AE01171; AAC67061.1; -EMBL; U68006; AAC45100.1; -. PIR; G70188; G70188.
                                                                                                                                                                                                                                                                                                                                                             [1]
SEQUENCE OF 89-631 FROM N.A.
STRAIN-ATCC 35210 / B31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 390:580-586(1997).
                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P00579; 1SIG.
TIGR; BB0712; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               631 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=139;
                              RPSD_BORBU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA_BIND
SEQUENCE
RPSD_BORBU
                                                                SO THE WAR BRANCH BRANC
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STRAIN=972;
DDT TO THE SET OF SET O
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   between the Swiss Institute of Bloinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
"Evidence for lateral gene transfer between Archaea and Bacteria from
genome sequence of Thermotoga maritima.";
Nature 399:323-329(1999).
-!- FUNCTION: HYDROLYSIS OF 6-PHOSPHOGLUCONOLACTONE TO 6-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         phospho-D-gluconate.
-!- PATHWAY: Pentose phosphate pathway; second step.
-!- SIMILARITY: BELONGS TO THE GLUCOSAMINE/GALACTOSAMINE-6-PHOSPHATE ISOMERASE FAMILY. 6-PHOSPHOGLUCONOLACTONASE SUSFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- CATALYTIC ACTIVITY: 6-phospho-D-glucono-1,5-lactone + H(2)0 = 6-
                                                                                                                                                                                                                                                                                                                                                                                                    Thermotoga maritima.
Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47.0%; Score 39; DB 1; Length 220;
               DB 1; Length 631;
61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Indels
                                                             4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hydrolase; Complete proteome.
SEQUENCE 220 AA; 25325 MW; 9B0FD07EE01E60C3 CRC64;
                                                                                                                                                                                                                                                                                            30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
6-phosphogluconolactonase (EC 3.1.1.31) (6PGL).
PGL OR DEVB OR TM1154.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    365 AA.
                   Score 40; DB 1
Pred. No. 61;
3; Mismatches
                                                                                                                                                                                                                                                      220 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 30;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interpro; IPR006148; Gluc_gal_isom.
Interpro; IPR005900; Phosphogluconlac.
                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF01182; Glucosamine_iso; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-MSB8 / DSM 3109;
MEDLINE-99287316; PubMed=10360571;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE001772; AAD36230.1; -.
PIR; F72289; F72289.
                 48.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGRFAMS; TIGR01198; pgl; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ::| ||:| :|:|
EKYEREIRSAIDOF 126
                                                                                                                                  279 YOEELRIFSDDYID 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 QRYGRELRRMSDEF 14
                                                                                                      3 YGRELRRMSDEFVD 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 42.9
les 6; Conservative
                                       Best Local Similarity 50.0 Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PHOSPHOGLUCONATE
                                                                                                                                                                                                                                                                                          30-MAY-2000 (Rel.
30-MAY-2000 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=2336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIGR; TM1154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RA51_SCHPO
                                                                                                                                                                                                                                                    6PGL_THEMA
09X0N8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
RA51_SCHPO
ID RA51_SO
                                                                                                                                                                                                             RESULT 14
6PGL_THEMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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AECHINE=21848401; PubMed=11859360;

WEDLINE=21848401; PubMed=11859360;

Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,

Rad Sqource J., Peat N., Bayles J., Baker S., Basham D., Bowman S.,

Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

Collins M., Connor R., Cronin A., Harris D., Hidalgo J., Hodgson G.,

Rad Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,

A James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,

RAD Monorey P., Moule S., Murghyl L., Niblett D., Odell C.,

RAD Monorey P., Moule S., Murghyl M., Niblett D., Odell C.,

RAD R., Connor S., Ruther S., Saunders S., Stevens K.,

RAD R., Colles M., Squares S., Stevens K.,

RAD R., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,

RAD R., Modwart G., Aert R., Robben J., Grymonprez B.,

RAD R., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,

RAD R., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,

REGT P., Zimmermann W., Wedler H., Wambutt R., Purrelle B.,

Goffeau A., Cadieu E., Drean S., Choux S., Lelaure V., Mottier S.,

Golfeau A., Cadieu E., Drean S., Choux S., Lelaure V., Mottier S.,

A Borzym K., Langer I., Jumenez J., Sanchez M., del Rey F., Benito J.,

RAD Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,

Baga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,

Bondinguez A., Revuella J.L., Moreno S., Armstrong J., Forsburg S.L.,

RAD Baga R.R., Revuella J.L., Moreno S., Armstrong J., Forsburg S.L.,

RAD Baga R.R., Praves P., Barrell B.G., Nurse P.,

RAD Radeones sequence of Schizosaccharomyces pombe.",

R., Revuella B., Revuella
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.lsb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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MEDLINE-93364417; PubMed=8358431;
Shinohara A., Ogawa H., Matsuda Y., Ushio N., Ikeo K., Ogawa T.;
"Cloning of human, mouse and fission yeast recombination genes homologous to RAD51 and recA.";
Nat. Genet. 4:239-243(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Cloning the RAD51 homologue of Schizosaccharomyces pombe."; Nucleic Acids Res. 21:4586-4591(1993).
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-!- SIMILARITY: BELONGS TO THE RECA FAMILY. RAD51 SUBFAMILY.
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                                                                                                              update)
01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
28-FB2-2003 (Rel. 41, Last annotation update)
AMA repair protein rho51 (RAD51 homolog).
RHP51 OR RAD51 OR SPAC644.14C.
                                                                                                                                                                                                                                                                         Schizosaccharomyces pombe (Fission yeast).
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SEQUENCE FROM N.A.
MEDLINE=94252568; PubMed=8194753;
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MEDLINE=94051565; PubMed=8233794;
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NCBL_TaxID=4896;
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Matches 7; Conservative 4; Mismatches 2; Indels
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Search completed: September 15, 2003, 17:23:01 Job time : 4.77143 secs

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28puzl methanosarc

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064492 arabidopsis

29i0h8 pseudomonas

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            09v7y6 drosophila 0960b3 drosophila
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MEDLINE=20373792; PubMed=10917738;
Inchara N., Nunez G.;
"Genes with homology to mammalian apoptosis regulators identified in zebrafish.";
Cell Death Differ. 7:509-510(2000).

EMBL, AF731017; AAF66962.2; -.

HSSP; Q92934; 1G5J.
ZFIN; ZDB-GENE-000616-1; bad.
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Brachydanio rerio (Zebrafish) (Danio rerio).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;

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Q8ew78 mycoplasma
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Nature 414:450-453(2001).

EMBL: AL590446; CAD2552911; -.

Hypothetical protein.

SEQUENCE 458 AA; 51914 MW; 24111BF78D4A534D CRC64;
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                                                                                                       Encephalitozoon cuniculi.
Eukaryota; Fungi; Microsporidia; Unikaryonidae; Encephalitozoon.
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Bature 414.450-4453(2001).
EMBL; AL590446; CAD25364.1; --
Hypothetical protein.
SEQUENCE 477 AA; 54.039 MW; B5DCF6299724CC96 CRC64;
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                                                                                                                                                                                                                                                       Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein ECU06_0040.
 01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein ECU06_1680.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       477 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21576510; PubMed=11719806;
                                                                                                                                                                                                                                                                                                                   STRAIN=GB-M1;
MEDLINE=21576510; PubMed=11719806;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 RYGRELRRMSDEFVD 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 RYGRDVMRMLDDMIE 27
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Best Local Similarity 46.7
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Encephalitozoon cuniculi.
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                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                               NCBI_TaxID=6035;
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01-JUN-2002 (
01-JUN-2002 (
01-OCT-2002 (
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                                                                                                                                                                                                                                     Genoscope;
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Gaps
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EMBL, AL590450; CAD25913.1; -.

Hypothetical protein.

SEQUENCE 641 AA; 72408 MW, A87E6EBE49732FC2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N. Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Fichault P., Whalen M., Wincker P., Levy M., Weissenbach J., Boucher C.A.;
Weissenbach J., Boucher C.A.;
Nature 415:497-502(2002).

EMBL; AL646067; CAD15739.1; -.
InterPro; IPR003593; AAA_ATPase.
                                                                                                                                                                                                                                                                                                   Bukaryota; Fungi; Microsporidia; Unikaryonidae; Encephalitozoon.
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Ralstoniaceae; Ralstonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55.4%; Score 46; DB 5; Length 641; 46.7%; Pred. No. 34; Live 5; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                  01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypotherical protein ECU11_0030.
ECU11_0030.
Encephalitozon cuniculi.
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Probable ATP-binding ABC transporter protein.
RSC2037 OR RS03602.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ralstonia solanacearum (Pseudomonas solanacearum)
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641 AA
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us-09-544-664-29.rspt

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Streptomycineae; Streptomycetaceae; Streptomyces.
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InterPro; IPR001647; HTH_TETR.
InterPro; IPR004111; TetR_C.
Pfam; PF004401; tetR_C.
Pfam; PF02909; tetR_C; 1.
                                                                                                                                                                                                                                                                                                                                                                      DNA-binding, Transcription, TraseQUENCE 247 AA;
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241 RVGVVYRRLSDEFLD 255
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50.0%;
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01-MAR-2001 (TTEMBLEEL 16,
01-MAR-2003 (TTEMBLEEL 23,
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 50.0%,
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186 YGKEVGRTADEFLE 199
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Best Local Similarity
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SEQUENCE FROM N.A.
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                            NCBI_TaxID=1961;
                                                                                                                                                                                                             REGULATORS.
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01-MAR-2003
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Q8G3Z1;
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MEDLINE-20036896; PubMed=10567266;

White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,

Bodson R.J., Eaft D.H., Gwinn M.L., Melson W.C., Richardson D.L.,

Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,

Wamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,

Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,

Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,

Fraser C.M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptomyces virginiae.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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                                                                                                                                             Length 230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Deinococcus radiodurans.

Bacteria; Deinococcus-Thermus; Deinococca; Deinococcacea; Deinococcaceae; Deinococcaceae; Deinococcus.

NCBI_TAXID=1299;
                                                                                                                                                                                        4; Indels
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SMART; SM00642; Aamy; 1.
Hydrolase; Complete proteome.
SEQUENCE 564 AA: 63667 MW; BBF50B9B0DFC8D51 CRC64;
                                                                                                      230 AA; 25231 MW; 7C3FDA1E7A19A2A4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Glycosyl hydrolase, family 13.
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Last annotation update)
                                                                                                                                            Score 45; DB 16;
Pred. No. 17;
1; Mismatches 4;
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64.3%; Pred. No. 44;
tive 2; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                      564 AA.
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InterPro; IPR006589; Alp_amyl_cat_sub.
       Pfan, PF00005, ABC_transporter. Pr000005, ABC_trans, 1.
Pr0000006, ABC_transporter; 1.
SWART; SW00382, AAA; 1.
Complete proteome.
SEQUENCE 230 AA; 25231 MW: 767871
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01-JUN-2001 (TrEMBLRE1. 17, Last sequ
01-OCT-2002 (TrEMBLRE1. 22, Last anno
InterPro; IPR003439; ABC_transporter.
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EMBL; AE011983; AAF10944.1; -.
HSSP; P21332; 1UOK.
                                                                                                                                             54.2%;
64.3%;
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283 YVREMRRVIDEFDD 296
                                                                                                                                                                                                                                                    1 QRYGRELRRMSDEF 14
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                                                                                                                                      Query Match 54.27
Best Local Similarity 64.35
Matches 9; Conservative
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     δλ
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The grown sequence of Bifidobacterium longum reflects its adaptation to the human gastrointestinal tract.";
Proc. Natl. Acad. Sci. U.S.A. 99:14427-14427(2002).
EMBL; AE014794; AAN25398.1;
Hypothetical protein; Complete proteome.
SEQUENCE 726 AA, 81866 NW; 6BEB86B6IFCBC586 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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SEQUENCE FROM N.A.
MEDLINE-21125565; PubMed=11222601;
Namwat W., Lee C.K., Kinoshita H., Yamada Y., Nihira T.;
"Identification of the varR gene as a transcriptional regulator of virginiamycin S resistance in Streptomyces virginiae.";
                                                                                                                                           J. Bacteriol. 183:2025-2031(2001).
-!- SIMILARITY: BELONGS TO THE TETR/ACRR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 247;
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MEDLINE-22294977; PubMed=12381787;
Schell M.A., Karmirantzou M., Snel B., Vilanova D., Berr
Pessi G., Zwahlen M.-C., Desiere F., Bork P., Delley M.
Pridmore R.D., Arigoni F.;
                                                                                                                                                                                                                                                                                                                                                                                                                      Transcription regulation.
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Last sequence update)
Last annotation update)
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01-MAR-2003 (TrEWBLrel. 23, Last sequence update)
01-MAR-2003 (TrEWBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 44; DB 2
Pred. No. 27;
5; Mismatches
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Query Match
Best Local Similarity
'-hos 8; Conserve
                                                                                                                                                                                                                                                                            NCBI_TaxID=28227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                       Q8EW78
Q8EW78;
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Q8EW78
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Southwick A., Nguyen M., Tripp M., Palm'C.J., Jones T., Wu T.,

Carninci P., Chen H., Cheuk R., Chan M.M., Chang C.H., Dale J.M.,

Deng J.M., Hayashizaki Y., Hsuan V.W., Lee J.M., Ishida J., Kamiya A.,

Kawai J., Kim C.J., Narusaka M., Quach H.L., Sakurai T., Satou M.,

Seki M., Shinn P., Tang C.C., Toroumi M., Wallender E.K., Wong C.,

Wu H.C., Yamada K., Yu G., Yuan S., Shinozaki K., Ecker J.,

Theologis A., Davis R.W.;

Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                               STRAIN=ATCC 15692 / PAO1;
STRAIN=ATCC 15692 / PAO1;
SEQUENCE FROM N.A.
STRAIN=ATCC 15692 / PAO1;
STRAIN=20437337; PubMed=10984043;
Stover C.K., Pham X.-Q.IT., Erwin A.L., Mizoguchi S.D., Warrener P., Stover C.K., Goltry L., Tolentino E., Westbrock-Wadink D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Westbrock-Wadinan S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Relzer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;
"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana (Mouse-ear cress).

Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TAXID=3702;
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Kawai J.,
                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                 Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas.
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                                                                                                                                                                                                                                                                                                                                                                  Length 1248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-cv. Columbia;
Seki M., Iida K., Satou M., Sakurai T., Akiyama K., Ishida Seki M., Iida K., Kamiya A., Narusaka M., Carninci P., Hayashizaki Y., Shinozaki K., "Arabidopsis thaliana full-length cDNA.";
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY136474; AAM97139.1;
EMBL; AKI18269; BAC42887.1;
                                                                                                                                                                                                                                                                                                                                                    1248 AA; 138499 MW; C3D3DBFEE6736C7A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .1 protein.
205 AA; 22583 MW; 1BD8D1358ECFFF81 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-0CT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               205 AA.
                                                                                                                                                                                                                                 opportunistic pathogen.";
Nature 406.959-964(2000).
EMBL; AE004720; AAG66332.1; -.
InterPro; IPR003672; CobN/Mg_chltase.
InterPro; IPR000408; Reg_chr_condens.
Pfam; PF02514; cobN-Mg_chl, 1.
PROSITE; PS00626; RCC1_2; 1.
         Cobalamin biosynthetic protein CobN. COBN OR PA2944.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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615 ESYGPLRDLERLADEFYD 632
                                                                                                                                                                                                                                                                                                                                                                                                                     1 ORYG--RELREMSDEFVD 16
                                                                                                                                                                                                                                                                                                                                                                                             9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                    Pseudomonas aeruqinosa.
                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                             Complete proteome SEQUENCE 1248 A
                                                                           NCBI_TaxID=287;
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SEQUENCE 20
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"The complete genomic sequence of Mycoplasma penetrans, an intracellular bacterial pathogen in humans.";

Nucleic Acids Res. 30:5293-5300(2002).

EMBL; AP004171; BAC44118.1; -.

Complete proteome.

SEQUENCE 804 AA; 88008 MW; 69C71AA628FEF7A3 CRC64;
                                                   Gaps
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NCBI_TaxID=5664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bāctēria; Fīrmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
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Quail M., Rajandream M.A., Barrell B.G.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=Friedlin;
MEDLINE=98146435; PubMed=9477341;
Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M., Smith D.F.;
"A physical map of the Leishmania major Friedlin genome.";
Genome Res. 8:135-145(1998).
EMBL; AL359781; CAB95305-1; -.
InterPro; IPR003593; AAA_ATPase.
InterPro; IPR004273; Dynein_heavy.
InterPro; IPR00169; SHprot_acsite.
DB 10; Length 205; 32;
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                                                   3; Indels
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                                                                                                                                                                                                                                                                                                                                    01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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66.7%; Pred. No. 1.4e+02;
live 2; Mismatches 2;
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                                                                                                                                                                                                                                                                                        804 AA
                                                   Mismatches
  Score 43;
Pred. No.
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                                                                                                                                                                                                                                                                                        PRT;
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MEDLINE=22354719; PubMed=12466555;
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51.8%;
61.5%;
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428 GSELREMSDEYL 439
                                                                                                      4 GRELRRMSDEFVD 16
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Matches 8; Conservative
                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycoplasma penetrans.
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[1]
SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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  ARTI OR TIE0512,
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STRAIN-C2A / ATCC 35395 / DSM 2834;

STRAIN-C2A / ATCC 35395 / DSM 2834;

KEDLINE=21929760; PubMed=11932238;

MEDLINE=21929760; PubMed=11932238;

Allen J.E., Nusbaun C., FOY A., Endrizzi M.G., Macdonald P.,

Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R.,

Linton L., McEwan P., McMernan K., Talamas J., Tirrell A., Ye W.,

Linton L., McEwan P., McMernan K., Talamas J., Tirrell A., Ye W.,

A Leigh J.A., Ingram-Smith C., Kuettner H.C., Krzycki J.A.,

Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,

Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,

Rerry J.G., Jarrell R.F., Jing H., Macario A.J.L., Paulsen I.,

Metcalf W.W., Birren B.;

The genome of Methanosarcin a acetivorans reveals extensive metabolic
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01-000. (TrEMBLrel. 21, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
ABC-type amino acid transport system, periplasmic component.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 17; Length 213;
                                                                                                                            51.8%; Score 43; DB 5; Length 5635; 72.7%; Pred. No. 1.1e+03; Ative 2; Mismatches 1; Indels
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                                                        ATP-binding.
SEQUENCE 5635 AA; 620050 MW; 64A9EB81A9B14641 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Methanosarcina acetivorans.
Archaea; Euryarchaecta; Methanococci; Methanosarcinales;
Methanosarcinaceae; Methanosarcina.
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ATP-binding; Complete proteome.

23676 MW; B548F93D94D109C9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MR-2003 (TrEMBLrel. 23, Last annotation update)
ABC transporter, ATP-binding protein.
MA3957.
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1; Mismatches
                SMART; SM00382; ÅAA; 4.
PROSITE; PS00639; THIOL_PROTEASE_HIS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and physiological diversity.",
Genome Res. 12:532-542(2002).
EMBL; AE011107; AAM07308.1; -.
InterPro; IPR003593; AAA_ATPase.
InterPro; IPR003439; ABC_transporter.
Pfam; PF00005; ABC_tran; 1.
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E; PSO0211; ABC_TRANSPORTER; 1.
                                                                                                                                                                                                                                                                                                                                                                          PRT;
Pfam; PF03028; Dynein_heavy; 1.
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                                                                                                                                                                                                                                                                1535 QRFGRDLRRWS 1545
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Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                          8; Conservative
                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                     1 QRYGRELRRMS 11
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GRDLHRMSDE 68
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                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=2214;
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Q8RCC4
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Q8TJ31
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CSTRAINWE-21992816; PubMed=11997336;

MEDLINE-21992816; PubMed=11997336;

MEDLINE-21992816; PubMed=11997336;

MEDLINE-21992816; PubMed=11997336;

MEDLINE-21992816; PubMed=11997336;

MEDLINE-21992816; PubMed=11997336;

MEDLINE-21992816; Marg J., Yu J., Yang H.;

Margin H., Chen R., Wang J., Yu J., Yang H.;

Margin H., Chen R., Wang J., Yu J., Yang H.;

Margin H., Chen R., Wang J., Yu J., Yang H.;

Margin H., Chen R., Wang J., Yu J., Yang H.;

Margin H., Archarate Sequence of T. tengcongensis genome.";

Menchania Menchania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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CG30456 OR CG15612 OR CG15613.
Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera: Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
NCBI_TAXID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 16; Length 260;
61;
Thermoanaerobacter tengcongensis.
Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
Thermoanaerobacteriaceae; Thermoanaerobacter.
NCBI_TaxID=119072;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         260 AA; 28849 MW; F3D87ED16B18DCBC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-2002 (TrEMBLrel, 22, Created)
01-0CT-2002 (TrEMBLrel, 22, Last sequence update)
01-MAR-2003 (TrEMBLrel, 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ۲;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 42; DB 1
Pred. No. 61;
4; Mismatches
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Matches 8; Conservative
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Best Local Similarity :
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Search completed: September 15, 2003, 17:25:49 Job time: 18.3714 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                   using sw model
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OM protein

September 15, 2003, 17:18:16; Search time 7.2 Seconds (without alignments) 213.708 Million cell updates/sec Run on:

1 QRYGRELRRMSDEFVD 16 US-09-544-664-29 83 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 segs, 96168682 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 00% Maximum Match 100% Listing first 45 summaries

PIR_76:* Database

pirl:* pir2:* pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

GCR3 protein - yea hypothetical prote conserved hypothet conserved hypothet hypothetical prote probable enzyme [i probable enzyme [i transcription regusite-specific DNA-probable Fe-S oxid transcription init hypothetical prote oxidoreductase, so transporter homolo hypothetical profe gibberellin 2beta-hypothetical prote conserved hypothet hypothetical prote hypothetical prote hypothetical prote hypothetical cytos hypothetical prote bad protein - mous glycosyl hydrolase cobalamin biosynth valine-tRNA ligase membrane transport Description SUMMARIES A85948 F65076 F87644 JC4986 G97123 F72289 C69808 A55671 H75403 G83278 E89949 AD3414 F85356 T40297 A44919 F84388 A75088 E91102 G70188 B96695 E87441 B84275 B95043 D97913 T52577 AC3365 B83311 Query Match Length DB 48.2 48.2 47.6 47.6 Score

DNA repair protein	protein F12K11.20	RAD51 protein homo	hypothetical prote	hypothetical prote	sigma 2 protein -	siqma 2 protein -	trigger factor [im	site-specific DNA-	acylaminoacyl-pept	hypothetical profe	valine-tRNA ligase	probable kinesin -	two-component hybr	similar to late em	hypothetical prote
E90121	D86200	S42107	T32163	T31738	FOXRL2	FOXR3D	AB0558	CIBPRH	F90299	T29772	SYBSVS	B71405	AE2452	T02712	S64604
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331	360	365	380	383	418	418	432	503	536	689	880	959	965	1805	1967
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0	31	32	33	34	5	98	3.7	88	39	01	디	12	13	4	5

ALIGNMENTS

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Dad protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 05-Nov-1999
C;Accession: A55671
B;Yang, B:, 20a, 01; Jockel, J.; Boise, L.H.; Thompson, C.B.; Korsmeyer, S.J.
Cell 80, 285-291, 1995
A;Title: Bad, a heterodimeric partner for Bcl-x-L and Bcl-2, displaces Bax and promot A;Reference number: A55671; MUID:95136361; PMID:7834748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: H75403
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-564 < MHI>
A; Cross references: GB: AE001983; GB: AE000513; NID: g6459123; PIDN: AAF10944.1; PID: g645
A; Experimental source: strain R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HJOSOYI hydrolase, family 13 - Deinococcus radiodurans (strain R1)
C.Species: Deinococcus radiodurans
C.Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C.Accession: H75403
R.White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.;
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
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                                                                                                                                                                                                                                                                                                                             A)Status: preliminary, not compared with conceptual translation
A)Molecule type: mRNA
A)Residues: 1-204 <YAN>
A)Cross-references: GB:L37296; NID:g639778; PIDN:AAA64465.1; PID:g639779
C)Keywords: heterodimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QRYGRELRRMSDEF 14
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H75403
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Score 45, DB 2; Length 564; Pred. No. 14; 2; Mismatches 3; Indels A;Map position: 1 C;Superfamily: alpha-glucosidase; alpha-amylase core homology Query Match 54.2%; Best Local Similarity 64.3%; Matches 9; Conservative

C; Genetics

0;

Gaps

0;

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Gaps

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C;Accession: F85356
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sp Nature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thallana. A;Reference number: A85001; MUID:20083488; PMID:10617198
C;Accession: AD3414
R;DelVecchio, V.G.; Kapatral, V.; RedKar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanov , Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Let Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melit A;Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  H.; Moestl, D.; Duest
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A;Cross-references: EMBL:AL023589; PIDN:CAA19050.1; GSPDB:GN00067; SPDB:SPBC36.02c
A;Experimental source: strain 972h-; cosmid c36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references: GB: NC_001268; NID: 97269950; PIDN: CAB79767.1; GSPDB: GN00140
                                                                                                                                                                                                                                                                             PIDN:AAL52479.1; PID:g17983287; GSPDB:GN00190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        membrane transporter - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 18-Feb-2000
C;Accession: T40297
R;Lyne, M.; Wood, V.; Rajandream, M.A.; Barrell, B.G.; Hilbert, H.: Woestl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein AT4930490 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Peb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          submitted to the EMBL Data Library, May 1998
A; Reference number: 221919
A; Accession: 140297
A; Accession: 140297
A; Accession: 140297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 447;
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C; Superfamily: benomyl/methotrexate resistance protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 41; DB 2
Pred. No. 52;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 18;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 41.5;
                                                                                                                                                                                                                                                            A;Cross-references: GB:AE008917; I
A;Experimental source: strain 16M
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49.4%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 33.3%;
Matches 11; Conservative
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84 RELQRLYDELVD 95
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Matches 8; Conserv
                                                                                                                                                                                         A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-191 <KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-447 <STO>
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A;Map position: 4
                                                                                                                                                                                                                                                                                                                                                        A; Gene: BMEI1298
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                                                                                                                                                                                                                                                                                                                                 M.J.; Br
K.; Lim,
                                                                                                                                                                                                                                                                                                                                                                                                                               Argute: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathor, A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: G83278
A;Accession: G83278
A;Accession: G8278
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1248 (STO>
A;Cross_references: GB:AE004720; GB:AE004091; NID:g9949032; PIDN:AAG06332.1; GSPDB:GN001
A;Experimental source: strain PAO1
C;Genetios:
A;Gene: cobN; PA2944
C;Superfamily: Rhodobacter capsulatus magnesium-protoporphyrin O-methyltransferase
                                                                                                                                                                                                                    cobalamin biosynthetic protein CobN PA2944 [imported] - Pseudomonas aeruginosa (strain C;Species: Pseudomonas aeruginosa C;Species: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 02-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AD3414
hypotherical cytosolic protein BMEI1298 [imported] - Brucella melitensis (strain 16M)
C; Species: Brucella melitensis
C; Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: B89949
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.;
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
                                                                                                                                                                                                                                                                                                                               Hickey, h
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A;Experimental source: strain N315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A;Reference number: A89758; MUID:21311952; PMID:11418146 A;Accession: E89949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               valine-tRNA ligase [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
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R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, .: Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
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Best Local Similarity 50.0%;
Matches 9; Conservative
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Best Local Similarity 61.5%,
'has 8; Conservative
                                                                     | ||:||: ||| |
283 YVREMRRYIDEFOD 296
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251 GRELPILADEYVD 263
                                     3 YGRELRRMSDEFVD 16
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A; Molecule type: DNA
A; Residues: 1-876 <KUR>
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on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Read, T.D.; Peterson, S.; I nson, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapp. Science 293, 498-506, 2001
A; Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morris A; Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae. A; Reference number: A95000; MUID:21357209; PMID:11463916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                conserved hypothetical protein spr0332 [imported] - Streptococcus pneumoniae (strain C; Species: Streptococcus pneumoniae C; Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 22-Oct-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:AE005672; FIDN:AAK74539.1; PID:g14971841; GSPDB:CN00164; TIGR A;Experimental source: strain TIGR4
                                                                                                                                                                                                                                                                                                                               conserved hypothetical protein SP0372 [imported] - Streptococcus pneumoniae (strain C;Species: Streptococcus pneumoniae C;Species: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Accession: D97913
R; Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B. e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, Y. P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A; Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, A; Reference number: A97872; MUID:21429245; PMID:11544234
A; Accession: D97913
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C;Genetics:
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18;
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14;
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Pred. No. 1
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Pred. No. 1
                                                         Score 40;
Pred. No.
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18 QEFGREVRGYNKVEVDEFLD 37
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45.0%;
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                                                                               Similarity 66.7
8; Conservative
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Best Local Similarity
9; Conserve
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A;Molecule type: DNA
A;Residues: 1-109 <KUR>
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A; Residues: 1-113 <KUR>
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         A; Gene: VNG2379H
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                                                         Query Match
Best Local S
Matches 8
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N;Alternate names: protein YM8564.07; protein YM9553.01; protein YMR125w
C;Species: Saccharomyces cerevisiae
C;Decies: Saccharomyces cerevisiae
C;Decies: Saccharomyces cerevisiae
C;Decies: Saccharomyces cerevisiae
C;Decies: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 29-Oct-1999
C;Decession: A44919; S53055; S54494
R;Gemura, H.; Jigami, Y.
J. Bacteriol. 174, 5526-5532, 1992
A;Title: GCRS encodes an acidic protein that is required for expression of glycolytic ge
A;Recession: A44919
A;Recession: A44919
A;Rocession: A44919
A;Recession: GB:D10224; NID:q464221; PIDN:BAA01076.1; PID:d1001545; PID:q464222
A;Note: sequence extracted from NCBI backbone (NCBIN:112104, NCBIP:112106)
R;Badcock, K.; Churcher, C.
Submitted to the EMBL Data Library, March 1995
A;Reference number: S53055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Release the number: $33035
A; Molecule type: DNA
A; Residues: $339-858 <BAD>
A; Residues: $33-858 <BAD>
A; Cross-references: EMBL: Z48622; NID: g728663; PIDN: CAA88550.1; PID: g728664; MIPS: YMR125N
A; Cross-reference number: $54014
A; Reference number: $54014
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 'MFNRKRG', 6-489 <LYE>
A; Cross-references: EMBL: Z49273; NID: g809577; PIDN: CAA89274.1; PID: g809584; MIPS: YMR125N
C; Genetics: SGD: STO1; GCR3
A; Gene: SGD: STO1; GCR3
A; Map position: 13R
C; Keywords: DNA binding; nucleus
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C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: F8438
R;Ay;W:V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablc Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A.Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A;Title: Genome sequence of Halobacterium species NRC-1.
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-84 <STO>
A; Cross-references: GB: AE004437; NID: 910581786; PIDN: AAG20474.1; GSPDB: GN00138
C; Genetics:
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      Length 577
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                                                      3; Indels
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Pred. No. 1e+02;
5; Mismatches 4
      2;
    Score 41; DB 2
Pred. No. 67;
3; Mismatches
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    49.48; 57.18;
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FGRKIRRMSKMAVD 576
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                      Similarity 57.1
8; Conservative
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Query Match
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A;Molecule type: DNA
A;Residues: 1-275 <STO>
A;Cross-references: GB:AE005174; NID:g12517451; PIDN:AAG58045.1; GSPDB:GN00145; UWGP:242
                                                                                                                                 Nymical to the EMBL Data Library, July 1999
A; Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome strut A; Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome strut A; Description: A75001
A; Reference number: A75001
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-219 < KAN>
A; Residues: 1-219 < KAN>
A; Residues: 1-219 okan>
A; Cross-references: GB:AJ248286; GB:AL096836; NID:g5458366; PIDN:CAB50006.1; PID:e15159C
C; Genetics: A; Gene: PAB1640
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                       C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C;Accession: A75088
R;anonymous, Genoscope
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 275; 46;
hypothetical protein PAB1640 - Pyrococcus abyssi (strain Orsay)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48.2%; Score 40; DB 2; Length 219; 47.1%; Pred. No. 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Indels
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7
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Pred. No. 46;
3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48.2%;
50.0%;
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35 YGRKLNALSKVFID 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 50.0*
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Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
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R.Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A)Cross references: GB:AE000375; GB:U00096; NID:g1789282; PIDN:AAC75956.1; PID:g1789; A)Experimental source: strain K-12, substrain MG1655
C;Superfamily: naphthoate synthase; encyl-CoA hydratase homology
F;40-192/Domain: encyl-CoA hydratase homology <ECH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-275 <BLAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                      C.Species: Escherichia coli
C.Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C.Accession: F65076
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0
                          C;Genetics:
A;Gene: ygfG
C;Superfamily: naphthoate synthase; enoyl-CoA hydratase homology
                                                                                                                                      Length 275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A)Title: The complete genome sequence of Escherichia coli K-12. A;Reference number: A64720; MUID:97426617; PMID:9278503 A;Accession: F65076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein b2919 - Escherichia coli (strain K-12)
A; Experimental source: strain 0157:H7, substrain EDL933
                                                                                                                                    DB 2;
46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 46;
3; Mismatches
                                                                                                                                                                                          3; Mismatches
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                                                                                                                                      Score 40;
Pred. No.
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                                                                                                                                      48.2%;
50.0%;
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                                                                                                                                                                                                                                             3 YGRELRRMSDEFVD 16
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35 YGRKLNALSKVFID 48
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Best Local Similarity 50.0°
Matches 7; Conservative
                                                                                                                                                            Best Local Similarity 50.0 Matches 7; Conservative
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Gaps